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(54) Title: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING METABOLIC PATHWAY PROTEINS

(57) Abstract: Isolated nucleic acid molecules, designated MP nucleic acid molecules, which encode novel MP proteins from *Corynebacterium glutamicum* are described. The invention also provides antisense nucleic acid molecules, recombinant expression vectors containing MP nucleic acid molecules, and host cells into which the expression vectors have been introduced. The invention still further provides isolated MP proteins, mutated MP proteins, fusion proteins, antigenic peptides and methods for the improvement of production of a desired compound from *C. glutamicum* based on genetic engineering of MP genes in this organism.

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***CORYNEBACTERIUM GLUTAMICUM* GENES ENCODING METABOLIC  
PATHWAY PROTEINS**

**Related Applications**

- The present application claims priority to prior filed U.S. Provisional Patent
- 5 Application Serial No. 60/141031, filed June 25, 1999, U.S. Provisional Patent  
Application Serial No. 60/142101, filed July 2, 1999, U.S. Provisional Patent  
Application Serial No. 60/148613, filed August 12, 1999, and also to U.S. Provisional  
Patent Application Serial No. 60/187970, filed March 9, 2000. The present application  
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- 10 1, 1999, German Patent Application No. 19931415.2, filed July 8, 1999, German Patent  
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- 15 19931434.9, filed July 8, 1999, German Patent Application No. 19931435.7, filed July  
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- 20 Application No. 19931510.8, filed July 8, 1999, German Patent Application No.  
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- 25 8, 1999, German Patent Application No. 19932125.6, filed July 9, 1999, German Patent  
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### **Background of the Invention**

Certain products and by-products of naturally-occurring metabolic processes in cells have utility in a wide array of industries, including the food, feed, cosmetics, and pharmaceutical industries. These molecules, collectively termed 'fine chemicals', include organic acids, both proteinogenic and non-proteinogenic amino acids, nucleotides and nucleosides, lipids and fatty acids, diols, carbohydrates, aromatic compounds, vitamins and cofactors, and enzymes. Their production is most conveniently performed through large-scale culture of bacteria developed to produce and secrete large quantities of a particular desired molecule. One particularly useful organism for this purpose is *Corynebacterium glutamicum*, a gram positive, nonpathogenic bacterium. Through strain selection, a number of mutant strains have

been developed which produce an array of desirable compounds. However, selection of strains improved for the production of a particular molecule is a time-consuming and difficult process.

## 5 Summary of the Invention

The invention provides novel bacterial nucleic acid molecules which have a variety of uses. These uses include the identification of microorganisms which can be used to produce fine chemicals, the modulation of fine chemical production in *C. glutamicum* or related bacteria, the typing or identification of *C. glutamicum* or related  
10 bacteria, as reference points for mapping the *C. glutamicum* genome, and as markers for transformation. These novel nucleic acid molecules encode proteins, referred to herein as metabolic pathway (MP) proteins.

*C. glutamicum* is a gram positive, aerobic bacterium which is commonly used in industry for the large-scale production of a variety of fine chemicals, and also for the  
15 degradation of hydrocarbons (such as in petroleum spills) and for the oxidation of terpenoids. The MP nucleic acid molecules of the invention, therefore, can be used to identify microorganisms which can be used to produce fine chemicals, e.g., by fermentation processes. Modulation of the expression of the MP nucleic acids of the invention, or modification of the sequence of the MP nucleic acid molecules of the  
20 invention, can be used to modulate the production of one or more fine chemicals from a microorganism (e.g., to improve the yield or production of one or more fine chemicals from a *Corynebacterium* or *Brevibacterium* species).

The MP nucleic acids of the invention may also be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof, or to identify the  
25 presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain  
30 whether this organism is present. Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to species pathogenic in humans, such as *Corynebacterium*

*diphtheriae* (the causative agent of diphtheria); the detection of such organisms is of significant clinical relevance.

The MP nucleic acid molecules of the invention may also serve as reference points for mapping of the *C. glutamicum* genome, or of genomes of related organisms.

5 Similarly, these molecules, or variants or portions thereof, may serve as markers for genetically engineered *Corynebacterium* or *Brevibacterium* species.

The MP proteins encoded by the novel nucleic acid molecules of the invention are capable of, for example, performing an enzymatic step involved in the metabolism of certain fine chemicals, including amino acids, vitamins, cofactors, nutraceuticals,  
10 nucleotides, nucleosides, and trehalose. Given the availability of cloning vectors for use in *Corynebacterium glutamicum*, such as those disclosed in Sinskey *et al.*, U.S. Patent No. 4,649,119, and techniques for genetic manipulation of *C. glutamicum* and the related *Brevibacterium* species (*e.g.*, *lactofermentum*) (Yoshihama *et al.*, *J. Bacteriol.* 162: 591-597 (1985); Katsumata *et al.*, *J. Bacteriol.* 159: 306-311 (1984); and  
15 Santamaria *et al.*, *J. Gen. Microbiol.* 130: 2237-2246 (1984)), the nucleic acid molecules of the invention may be utilized in the genetic engineering of this organism to make it a better or more efficient producer of one or more fine chemicals.

This improved production or efficiency of production of a fine chemical may be due to a direct effect of manipulation of a gene of the invention, or it may be due to an  
20 indirect effect of such manipulation. Specifically, alterations in *C. glutamicum* metabolic pathways for amino acids, vitamins, cofactors, nucleotides, and trehalose may have a direct impact on the overall production of one or more of these desired compounds from this organism. For example, optimizing the activity of a lysine biosynthetic pathway protein or decreasing the activity of a lysine degradative pathway  
25 protein may result in an increase in the yield or efficiency of production of lysine from such an engineered organism. Alterations in the proteins involved in these metabolic pathways may also have an indirect impact on the production or efficiency of production of a desired fine chemical. For example, a reaction which is in competition for an intermediate necessary for the production of a desired molecule may be eliminated, or a  
30 pathway necessary for the production of a particular intermediate for a desired compound may be optimized. Further, modulations in the biosynthesis or degradation of, for example, an amino acid, a vitamin, or a nucleotide may increase the overall

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ability of the microorganism to rapidly grow and divide, thus increasing the number and/or production capacities of the microorganism in culture and thereby increasing the possible yield of the desired fine chemical.

The nucleic acid and protein molecules of the invention may be utilized to

5 directly improve the production or efficiency of production of one or more desired fine chemicals from *Corynebacterium glutamicum*. Using recombinant genetic techniques well known in the art, one or more of the biosynthetic or degradative enzymes of the invention for amino acids, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, or trehalose may be manipulated such that its function is modulated. For example, a

10 biosynthetic enzyme may be improved in efficiency, or its allosteric control region destroyed such that feedback inhibition of production of the compound is prevented. Similarly, a degradative enzyme may be deleted or modified by substitution, deletion, or addition such that its degradative activity is lessened for the desired compound without impairing the viability of the cell. In each case, the overall yield or rate of production of

15 the desired fine chemical may be increased.

It is also possible that such alterations in the protein and nucleotide molecules of the invention may improve the production of other fine chemicals besides the amino acids, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, and trehalose through indirect mechanisms. Metabolism of any one compound is necessarily

20 intertwined with other biosynthetic and degradative pathways within the cell, and necessary cofactors, intermediates, or substrates in one pathway are likely supplied or limited by another such pathway. Therefore, by modulating the activity of one or more of the proteins of the invention, the production or efficiency of activity of another fine chemical biosynthetic or degradative pathway may be impacted. For example, amino

25 acids serve as the structural units of all proteins, yet may be present intracellularly in levels which are limiting for protein synthesis; therefore, by increasing the efficiency of production or the yields of one or more amino acids within the cell, proteins, such as biosynthetic or degradative proteins, may be more readily synthesized. Likewise, an alteration in a metabolic pathway enzyme such that a particular side reaction becomes

30 more or less favored may result in the over- or under-production of one or more compounds which are utilized as intermediates or substrates for the production of a desired fine chemical.

This invention provides novel nucleic acid molecules which encode proteins, referred to herein as metabolic pathway proteins (MP), which are capable of, for example, performing an enzymatic step involved in the metabolism of molecules important for the normal functioning of cells, such as amino acids, vitamins, cofactors, nucleotides and nucleosides, or trehalose. Nucleic acid molecules encoding an MP protein are referred to herein as MP nucleic acid molecules. In a preferred embodiment, the MP protein performs an enzymatic step related to the metabolism of one or more of the following: amino acids, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, and trehalose. Examples of such proteins include those encoded by the genes set forth in Table 1.

Accordingly, one aspect of the invention pertains to isolated nucleic acid molecules (*e.g.*, cDNAs, DNAs, or RNAs) comprising a nucleotide sequence encoding an MP protein or biologically active portions thereof, as well as nucleic acid fragments suitable as primers or hybridization probes for the detection or amplification of MP-encoding nucleic acid (*e.g.*, DNA or mRNA). In particularly preferred embodiments, the isolated nucleic acid molecule comprises one of the nucleotide sequences set forth as the odd-numbered SEQ ID NOs in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7....), or the coding region or a complement thereof of one of these nucleotide sequences. In other particularly preferred embodiments, the isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes to or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80% or 90%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence set forth as an odd-numbered SEQ ID NO in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7....), or a portion thereof. In other preferred embodiments, the isolated nucleic acid molecule encodes one of the amino acid sequences set forth as an even-numbered SEQ ID NO in the Sequence Listing (*e.g.*, SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8....). The preferred MP proteins of the present invention also preferably possess at least one of the MP activities described herein.

In another embodiment, the isolated nucleic acid molecule encodes a protein or portion thereof wherein the protein or portion thereof includes an amino acid sequence which is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a

sequence having an even-numbered SEQ ID NO: in the Sequence Listing), *e.g.*, sufficiently homologous to an amino acid sequence of the invention such that the protein or portion thereof maintains an MP activity. Preferably, the protein or portion thereof encoded by the nucleic acid molecule maintains the ability to perform an enzymatic reaction in a amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway. In one embodiment, the protein encoded by the nucleic acid molecule is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90% and most preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to an amino acid sequence of the invention (*e.g.*, an entire amino acid sequence selected from those having an even-numbered SEQ ID NO in the Sequence Listing). In another preferred embodiment, the protein is a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of the invention (encoded by an open reading frame shown in the corresponding odd-numbered SEQ ID NOs in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7....)).

In another preferred embodiment, the isolated nucleic acid molecule is derived from *C. glutamicum* and encodes a protein (*e.g.*, an MP fusion protein) which includes a biologically active domain which is at least about 50% or more homologous to one of the amino acid sequences of the invention (*e.g.*, a sequence of one of the even-numbered SEQ ID NOs in the Sequence Listing) and is able to catalyze a reaction in a metabolic pathway for an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose, or one or more of the activities set forth in Table 1, and which also includes heterologous nucleic acid sequences encoding a heterologous polypeptide or regulatory regions.

In another embodiment, the isolated nucleic acid molecule is at least 15 nucleotides in length and hybridizes under stringent conditions to a nucleic acid molecule comprising a nucleotide sequence of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO in the Sequence Listing). Preferably, the isolated nucleic acid molecule corresponds to a naturally-occurring nucleic acid molecule. More preferably, the isolated nucleic acid encodes a naturally-occurring *C. glutamicum* MP protein, or a biologically active portion thereof.

Another aspect of the invention pertains to vectors, *e.g.*, recombinant expression vectors, containing the nucleic acid molecules of the invention, and host cells into which such vectors have been introduced. In one embodiment, such a host cell is used to produce an MP protein by culturing the host cell in a suitable medium. The MP protein  
5 can be then isolated from the medium or the host cell.

Yet another aspect of the invention pertains to a genetically altered microorganism in which an MP gene has been introduced or altered. In one embodiment, the genome of the microorganism has been altered by introduction of a nucleic acid molecule of the invention encoding wild-type or mutated MP sequence as a  
10 transgene. In another embodiment, an endogenous MP gene within the genome of the microorganism has been altered, *e.g.*, functionally disrupted, by homologous recombination with an altered MP gene. In another embodiment, an endogenous or introduced MP gene in a microorganism has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional MP protein. In still  
15 another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of an MP gene in a microorganism has been altered (*e.g.*, by deletion, truncation, inversion, or point mutation) such that the expression of the MP gene is modulated. In a preferred embodiment, the microorganism belongs to the genus *Corynebacterium* or *Brevibacterium*, with *Corynebacterium glutamicum* being  
20 particularly preferred. In a preferred embodiment, the microorganism is also utilized for the production of a desired compound, such as an amino acid, with lysine being particularly preferred.

In another aspect, the invention provides a method of identifying the presence or activity of *Corynebacterium diphtheriae* in a subject. This method includes detection of  
25 one or more of the nucleic acid or amino acid sequences of the invention (*e.g.*, the sequences set forth in the Sequence Listing as SEQ ID NOs 1 through 1156) in a subject, thereby detecting the presence or activity of *Corynebacterium diphtheriae* in the subject.

Still another aspect of the invention pertains to an isolated MP protein or a  
30 portion, *e.g.*, a biologically active portion, thereof. In a preferred embodiment, the isolated MP protein or portion thereof can catalyze an enzymatic reaction involved in one or more pathways for the metabolism of an amino acid, a vitamin, a cofactor, a



nutraceutical, a nucleotide, a nucleoside, or trehalose. In another preferred embodiment, the isolated MP protein or portion thereof is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: in the Sequence Listing) such that the protein or portion thereof maintains the ability to

5 catalyze an enzymatic reaction involved in one or more pathways for the metabolism of an amino acid, a vitamin, a cofactor, a nutraceutical, a nucleotide, a nucleoside, or trehalose.

The invention also provides an isolated preparation of an MP protein. In preferred embodiments, the MP protein comprises an amino acid sequence of the

10 invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing). In another preferred embodiment, the invention pertains to an isolated full length protein which is substantially homologous to an entire amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) (encoded by an open reading frame set forth in a corresponding odd-numbered SEQ ID NO: of the

15 Sequence Listing). In yet another embodiment, the protein is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90%, and most preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to an entire amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing). In other embodiments, the isolated MP protein

20 comprises an amino acid sequence which is at least about 50% or more homologous to one of the amino acid sequences of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) and is able to catalyze an enzymatic reaction in an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway, or has one or more of the activities set forth in Table 1.

25 Alternatively, the isolated MP protein can comprise an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80%, or 90%, and even more preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to a nucleotide sequence of one of

30 the even-numbered SEQ ID NOs set forth in the Sequence Listing. It is also preferred that the preferred forms of MP proteins also have one or more of the MP bioactivities described herein.

The MP polypeptide, or a biologically active portion thereof, can be operatively linked to a non-MP polypeptide to form a fusion protein. In preferred embodiments, this fusion protein has an activity which differs from that of the MP protein alone. In other preferred embodiments, this fusion protein, when introduced into a *C. glutamicum* pathway for the metabolism of an amino acid, vitamin, cofactor, nutraceutical, results in increased yields and/or efficiency of production of a desired fine chemical from *C. glutamicum*. In particularly preferred embodiments, integration of this fusion protein into an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway of a host cell modulates production of a desired compound from the cell.

In another aspect, the invention provides methods for screening molecules which modulate the activity of an MP protein, either by interacting with the protein itself or a substrate or binding partner of the MP protein, or by modulating the transcription or translation of an MP nucleic acid molecule of the invention.

Another aspect of the invention pertains to a method for producing a fine chemical. This method involves the culturing of a cell containing a vector directing the expression of an MP nucleic acid molecule of the invention, such that a fine chemical is produced. In a preferred embodiment, this method further includes the step of obtaining a cell containing such a vector, in which a cell is transfected with a vector directing the expression of an MP nucleic acid. In another preferred embodiment, this method further includes the step of recovering the fine chemical from the culture. In a particularly preferred embodiment, the cell is from the genus *Corynebacterium* or *Brevibacterium*, or is selected from those strains set forth in Table 3.

Another aspect of the invention pertains to methods for modulating production of a molecule from a microorganism. Such methods include contacting the cell with an agent which modulates MP protein activity or MP nucleic acid expression such that a cell associated activity is altered relative to this same activity in the absence of the agent. In a preferred embodiment, the cell is modulated for one or more *C. glutamicum* amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathways, such that the yields or rate of production of a desired fine chemical by this microorganism is improved. The agent which modulates MP protein activity can be an agent which stimulates MP protein activity or MP nucleic acid expression.

Examples of agents which stimulate MP protein activity or MP nucleic acid expression include small molecules, active MP proteins, and nucleic acids encoding MP proteins that have been introduced into the cell. Examples of agents which inhibit MP activity or expression include small molecules, and antisense MP nucleic acid molecules.

5           Another aspect of the invention pertains to methods for modulating yields of a desired compound from a cell, involving the introduction of a wild-type or mutant MP gene into a cell, either maintained on a separate plasmid or integrated into the genome of the host cell. If integrated into the genome, such integration can be random, or it can take place by homologous recombination such that the native gene is replaced by the  
10 introduced copy, causing the production of the desired compound from the cell to be modulated. In a preferred embodiment, said yields are increased. In another preferred embodiment, said chemical is a fine chemical. In a particularly preferred embodiment, said fine chemical is an amino acid. In especially preferred embodiments, said amino acid is L-lysine.

15

#### **Detailed Description of the Invention**

The present invention provides MP nucleic acid and protein molecules which are involved in the metabolism of certain fine chemicals in *Corynebacterium glutamicum*, including amino acids, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, and  
20 trehalose. The molecules of the invention may be utilized in the modulation of production of fine chemicals from microorganisms, such as *C. glutamicum*, either directly (*e.g.*, where modulation of the activity of a lysine biosynthesis protein has a direct impact on the production or efficiency of production of lysine from that organism), or may have an indirect impact which nonetheless results in an increase of  
25 yield or efficiency of production of the desired compound (*e.g.*, where modulation of the activity of a nucleotide biosynthesis protein has an impact on the production of an organic acid or a fatty acid from the bacterium, perhaps due to improved growth or an increased supply of necessary co-factors, energy compounds, or precursor molecules). Aspects of the invention are further explicated below.

30

## I. Fine Chemicals

The term 'fine chemical' is art-recognized and includes molecules produced by an organism which have applications in various industries, such as, but not limited to, the pharmaceutical, agriculture, and cosmetics industries. Such compounds include

5 organic acids, such as tartaric acid, itaconic acid, and diaminopimelic acid, both proteinogenic and non-proteinogenic amino acids, purine and pyrimidine bases, nucleosides, and nucleotides (as described *e.g.* in Kuninaka, A. (1996) Nucleotides and related compounds, p. 561-612, in *Biotechnology* vol. 6, Rehm *et al.*, eds. VCH: Weinheim, and references contained therein), lipids, both saturated and unsaturated fatty

10 acids (*e.g.*, arachidonic acid), diols (*e.g.*, propane diol, and butane diol), carbohydrates (*e.g.*, hyaluronic acid and trehalose), aromatic compounds (*e.g.*, aromatic amines, vanillin, and indigo), vitamins and cofactors (as described in Ullmann's Encyclopedia of Industrial Chemistry, vol. A27, "Vitamins", p. 443-613 (1996) VCH: Weinheim and references therein; and Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids,

15 Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCS Press, (1995)), enzymes, polyketides (Cane *et al.* (1998) *Science* 282: 63-68), and all other chemicals described in Gutcho (1983) *Chemicals by Fermentation*, Noyes Data Corporation, ISBN:

20 0818805086 and references therein. The metabolism and uses of certain of these fine chemicals are further explicated below.

### *A. Amino Acid Metabolism and Uses*

Amino acids comprise the basic structural units of all proteins, and as such are

25 essential for normal cellular functioning in all organisms. The term "amino acid" is art-recognized. The proteinogenic amino acids, of which there are 20 species, serve as structural units for proteins, in which they are linked by peptide bonds, while the nonproteinogenic amino acids (hundreds of which are known) are not normally found in proteins (see Ullmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97 VCH:

30 Weinheim (1985)). Amino acids may be in the D- or L- optical configuration, though L-amino acids are generally the only type found in naturally-occurring proteins. Biosynthetic and degradative pathways of each of the 20 proteinogenic amino acids

have been well characterized in both prokaryotic and eukaryotic cells (see, for example, Stryer, L. Biochemistry, 3<sup>rd</sup> edition, pages 578-590 (1988)). The 'essential' amino acids (histidine, isoleucine, leucine, lysine, methionine, phenylalanine, threonine, tryptophan, and valine), so named because they are generally a nutritional requirement due to the complexity of their biosyntheses, are readily converted by simple biosynthetic pathways to the remaining 11 'nonessential' amino acids (alanine, arginine, asparagine, aspartate, cysteine, glutamate, glutamine, glycine, proline, serine, and tyrosine). Higher animals do retain the ability to synthesize some of these amino acids, but the essential amino acids must be supplied from the diet in order for normal protein synthesis to occur.

Aside from their function in protein biosynthesis, these amino acids are interesting chemicals in their own right, and many have been found to have various applications in the food, feed, chemical, cosmetics, agriculture, and pharmaceutical industries. Lysine is an important amino acid in the nutrition not only of humans, but also of monogastric animals such as poultry and swine. Glutamate is most commonly used as a flavor additive (mono-sodium glutamate, MSG) and is widely used throughout the food industry, as are aspartate, phenylalanine, glycine, and cysteine. Glycine, L-methionine and tryptophan are all utilized in the pharmaceutical industry. Glutamine, valine, leucine, isoleucine, histidine, arginine, proline, serine and alanine are of use in both the pharmaceutical and cosmetics industries. Threonine, tryptophan, and D/ L-methionine are common feed additives. (Leuchtenberger, W. (1996) Amino acids – technical production and use, p. 466-502 in Rehm *et al.* (eds.) Biotechnology vol. 6, chapter 14a, VCH: Weinheim). Additionally, these amino acids have been found to be useful as precursors for the synthesis of synthetic amino acids and proteins, such as N-acetylcysteine, S-carboxymethyl-L-cysteine, (S)-5-hydroxytryptophan, and others described in Ulmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97, VCH: Weinheim, 1985.

The biosynthesis of these natural amino acids in organisms capable of producing them, such as bacteria, has been well characterized (for review of bacterial amino acid biosynthesis and regulation thereof, see Umbarger, H.E.(1978) *Ann. Rev. Biochem.* 47: 533-606). Glutamate is synthesized by the reductive amination of  $\alpha$ -ketoglutarate, an intermediate in the citric acid cycle. Glutamine, proline, and arginine are each subsequently produced from glutamate. The biosynthesis of serine is a three-

step process beginning with 3-phosphoglycerate (an intermediate in glycolysis), and resulting in this amino acid after oxidation, transamination, and hydrolysis steps. Both cysteine and glycine are produced from serine; the former by the condensation of homocysteine with serine, and the latter by the transfer of the side-chain  $\beta$ -carbon atom to tetrahydrofolate, in a reaction catalyzed by serine transhydroxymethylase. Phenylalanine, and tyrosine are synthesized from the glycolytic and pentose phosphate pathway precursors erythrose 4-phosphate and phosphoenolpyruvate in a 9-step biosynthetic pathway that differ only at the final two steps after synthesis of prephenate. Tryptophan is also produced from these two initial molecules, but its synthesis is an 11-step pathway. Tyrosine may also be synthesized from phenylalanine, in a reaction catalyzed by phenylalanine hydroxylase. Alanine, valine, and leucine are all biosynthetic products of pyruvate, the final product of glycolysis. Aspartate is formed from oxaloacetate, an intermediate of the citric acid cycle. Asparagine, methionine, threonine, and lysine are each produced by the conversion of aspartate. Isoleucine is formed from threonine. A complex 9-step pathway results in the production of histidine from 5-phosphoribosyl-1-pyrophosphate, an activated sugar.

Amino acids in excess of the protein synthesis needs of the cell cannot be stored, and are instead degraded to provide intermediates for the major metabolic pathways of the cell (for review see Stryer, L. Biochemistry 3<sup>rd</sup> ed. Ch. 21 "Amino Acid Degradation and the Urea Cycle" p. 495-516 (1988)). Although the cell is able to convert unwanted amino acids into useful metabolic intermediates, amino acid production is costly in terms of energy, precursor molecules, and the enzymes necessary to synthesize them. Thus it is not surprising that amino acid biosynthesis is regulated by feedback inhibition, in which the presence of a particular amino acid serves to slow or entirely stop its own production (for overview of feedback mechanisms in amino acid biosynthetic pathways, see Stryer, L. Biochemistry, 3<sup>rd</sup> ed. Ch. 24: "Biosynthesis of Amino Acids and Heme" p. 575-600 (1988)). Thus, the output of any particular amino acid is limited by the amount of that amino acid present in the cell.

### 30 B. Vitamin, Cofactor, and Nutraceutical Metabolism and Uses

Vitamins, cofactors, and nutraceuticals comprise another group of molecules which the higher animals have lost the ability to synthesize and so must ingest, although

they are readily synthesized by other organisms, such as bacteria. These molecules are either bioactive substances themselves, or are precursors of biologically active substances which may serve as electron carriers or intermediates in a variety of metabolic pathways. Aside from their nutritive value, these compounds also have significant industrial value as coloring agents, antioxidants, and catalysts or other processing aids. (For an overview of the structure, activity, and industrial applications of these compounds, see, for example, Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996.) The term "vitamin" is art-recognized, and includes nutrients which are required by an organism for normal functioning, but which that organism cannot synthesize by itself. The group of vitamins may encompass cofactors and nutraceutical compounds. The language "cofactor" includes nonproteinaceous compounds required for a normal enzymatic activity to occur. Such compounds may be organic or inorganic; the cofactor molecules of the invention are preferably organic. The term "nutraceutical" includes dietary supplements having health benefits in plants and animals, particularly humans. Examples of such molecules are vitamins, antioxidants, and also certain lipids (e.g., polyunsaturated fatty acids).

The biosynthesis of these molecules in organisms capable of producing them, such as bacteria, has been largely characterized (Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996; Michal, G. (1999) Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, John Wiley & Sons; Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCS Press: Champaign, IL X, 374 S).

Thiamin (vitamin B<sub>1</sub>) is produced by the chemical coupling of pyrimidine and thiazole moieties. Riboflavin (vitamin B<sub>2</sub>) is synthesized from guanosine-5'-triphosphate (GTP) and ribose-5'-phosphate. Riboflavin, in turn, is utilized for the synthesis of flavin mononucleotide (FMN) and flavin adenine dinucleotide (FAD). The family of compounds collectively termed 'vitamin B<sub>6</sub>' (e.g., pyridoxine, pyridoxamine, pyridoxa-5'-phosphate, and the commercially used pyridoxin hydrochloride) are all derivatives of the common structural unit, 5-hydroxy-6-methylpyridine. Pantothenate (pantothenic

acid, (R)-(+)-N-(2,4-dihydroxy-3,3-dimethyl-1-oxobutyl)- $\beta$ -alanine) can be produced either by chemical synthesis or by fermentation. The final steps in pantothenate biosynthesis consist of the ATP-driven condensation of  $\beta$ -alanine and pantoic acid. The enzymes responsible for the biosynthesis steps for the conversion to pantoic acid, to  $\beta$ -alanine and for the condensation to panthotenic acid are known. The metabolically active form of pantothenate is Coenzyme A, for which the biosynthesis proceeds in 5 enzymatic steps. Pantothenate, pyridoxal-5'-phosphate, cysteine and ATP are the precursors of Coenzyme A. These enzymes not only catalyze the formation of panthothante, but also the production of (R)-pantoic acid, (R)-pantolacton, (R)-panthenol (provitamin B<sub>5</sub>), pantetheine (and its derivatives) and coenzyme A.

Biotin biosynthesis from the precursor molecule pimeloyl-CoA in microorganisms has been studied in detail and several of the genes involved have been identified. Many of the corresponding proteins have been found to also be involved in Fe-cluster synthesis and are members of the nifS class of proteins. Lipic acid is derived from octanoic acid, and serves as a coenzyme in energy metabolism, where it becomes part of the pyruvate dehydrogenase complex and the  $\alpha$ -ketoglutarate dehydrogenase complex. The folates are a group of substances which are all derivatives of folic acid, which is turn is derived from L-glutamic acid, p-amino-benzoic acid and 6-methylpterin. The biosynthesis of folic acid and its derivatives, starting from the metabolism intermediates guanosine-5'-triphosphate (GTP), L-glutamic acid and p-amino-benzoic acid has been studied in detail in certain microorganisms.

Corrinoids (such as the cobalamines and particularly vitamin B<sub>12</sub>) and porphyrines belong to a group of chemicals characterized by a tetrapyrrole ring system. The biosynthesis of vitamin B<sub>12</sub> is sufficiently complex that it has not yet been completely characterized, but many of the enzymes and substrates involved are now known. Nicotinic acid (nicotinate), and nicotinamide are pyridine derivatives which are also termed 'niacin'. Niacin is the precursor of the important coenzymes NAD (nicotinamide adenine dinucleotide) and NADP (nicotinamide adenine dinucleotide phosphate) and their reduced forms.

The large-scale production of these compounds has largely relied on cell-free chemical syntheses, though some of these chemicals have also been produced by large-scale culture of microorganisms, such as riboflavin, Vitamin B<sub>6</sub>, pantothenate, and



biotin. Only Vitamin B<sub>12</sub> is produced solely by fermentation, due to the complexity of its synthesis. *In vitro* methodologies require significant inputs of materials and time, often at great cost.

5 C. Purine, Pyrimidine, Nucleoside and Nucleotide Metabolism and Uses

Purine and pyrimidine metabolism genes and their corresponding proteins are important targets for the therapy of tumor diseases and viral infections. The language "purine" or "pyrimidine" includes the nitrogenous bases which are constituents of nucleic acids, co-enzymes, and nucleotides. The term "nucleotide" includes the basic structural units of nucleic acid molecules, which are comprised of a nitrogenous base, a pentose sugar (in the case of RNA, the sugar is ribose; in the case of DNA, the sugar is D-deoxyribose), and phosphoric acid. The language "nucleoside" includes molecules which serve as precursors to nucleotides, but which are lacking the phosphoric acid moiety that nucleotides possess. By inhibiting the biosynthesis of these molecules, or their mobilization to form nucleic acid molecules, it is possible to inhibit RNA and DNA synthesis; by inhibiting this activity in a fashion targeted to cancerous cells, the ability of tumor cells to divide and replicate may be inhibited. Additionally, there are nucleotides which do not form nucleic acid molecules, but rather serve as energy stores (*i.e.*, AMP) or as coenzymes (*i.e.*, FAD and NAD).

Several publications have described the use of these chemicals for these medical indications, by influencing purine and/or pyrimidine metabolism (*e.g.* Christopherson, R.I. and Lyons, S.D. (1990) "Potent inhibitors of *de novo* pyrimidine and purine biosynthesis as chemotherapeutic agents." *Med. Res. Reviews* 10: 505-548). Studies of enzymes involved in purine and pyrimidine metabolism have been focused on the development of new drugs which can be used, for example, as immunosuppressants or anti-proliferants (Smith, J.L., (1995) "Enzymes in nucleotide synthesis." *Curr. Opin. Struct. Biol.* 5: 752-757; (1995) *Biochem Soc. Transact.* 23: 877-902). However, purine and pyrimidine bases, nucleosides and nucleotides have other utilities: as intermediates in the biosynthesis of several fine chemicals (*e.g.*, thiamine, S-adenosyl-methionine, folates, or riboflavin), as energy carriers for the cell (*e.g.*, ATP or GTP), and for chemicals themselves, commonly used as flavor enhancers (*e.g.*, IMP or GMP) or for several medicinal applications (see, for example, Kuninaka, A. (1996) Nucleotides and

Related Compounds in Biotechnology vol. 6, Rehm *et al.*, eds. VCH: Weinheim, p. 561-612). Also, enzymes involved in purine, pyrimidine, nucleoside, or nucleotide metabolism are increasingly serving as targets against which chemicals for crop protection, including fungicides, herbicides and insecticides, are developed.

- 5           The metabolism of these compounds in bacteria has been characterized (for reviews see, for example, Zalkin, H. and Dixon, J.E. (1992) "*de novo* purine nucleotide biosynthesis", in: Progress in Nucleic Acid Research and Molecular Biology, vol. 42, Academic Press:, p. 259-287; and Michal, G. (1999) "Nucleotides and Nucleosides", Chapter 8 in: Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology,
- 10   Wiley: New York). Purine metabolism has been the subject of intensive research, and is essential to the normal functioning of the cell. Impaired purine metabolism in higher animals can cause severe disease, such as gout. Purine nucleotides are synthesized from ribose-5-phosphate, in a series of steps through the intermediate compound inosine-5'-phosphate (IMP), resulting in the production of guanosine-5'-monophosphate (GMP) or
- 15   adenosine-5'-monophosphate (AMP), from which the triphosphate forms utilized as nucleotides are readily formed. These compounds are also utilized as energy stores, so their degradation provides energy for many different biochemical processes in the cell. Pyrimidine biosynthesis proceeds by the formation of uridine-5'-monophosphate (UMP) from ribose-5-phosphate. UMP, in turn, is converted to cytidine-5'-triphosphate (CTP).
- 20   The deoxy- forms of all of these nucleotides are produced in a one step reduction reaction from the diphosphate ribose form of the nucleotide to the diphosphate deoxyribose form of the nucleotide. Upon phosphorylation, these molecules are able to participate in DNA synthesis.

25   D. *Trehalose Metabolism and Uses*

- Trehalose consists of two glucose molecules, bound in  $\alpha$ ,  $\alpha$ -1,1 linkage. It is commonly used in the food industry as a sweetener, an additive for dried or frozen foods, and in beverages. However, it also has applications in the pharmaceutical, cosmetics and biotechnology industries (see, for example, Nishimoto *et al.*, (1998) U.S.
- 30   Patent No. 5,759,610; Singer, M.A. and Lindquist, S. (1998) *Trends Biotech.* 16: 460-467; Paiva, C.L.A. and Panek, A.D. (1996) *Biotech. Ann. Rev.* 2: 293-314; and Shiosaka, M. (1997) *J. Japan* 172: 97-102). Trehalose is produced by enzymes from

many microorganisms and is naturally released into the surrounding medium, from which it can be collected using methods known in the art.

## II. Elements and Methods of the Invention

5           The present invention is based, at least in part, on the discovery of novel molecules, referred to herein as MP nucleic acid and protein molecules, which play a role in or function in one or more cellular metabolic pathways. In one embodiment, the MP molecules catalyze an enzymatic reaction involving one or more amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic  
10 pathways. In a preferred embodiment, the activity of the MP molecules of the present invention in one or more *C. glutamicum* metabolic pathways for amino acids, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides or trehalose has an impact on the production of a desired fine chemical by this organism. In a particularly preferred embodiment, the MP molecules of the invention are modulated in activity, such that the  
15 *C. glutamicum* metabolic pathways in which the MP proteins of the invention are involved are modulated in efficiency or output, which either directly or indirectly modulates the production or efficiency of production of a desired fine chemical by *C. glutamicum*.

          The language, "MP protein" or "MP polypeptide" includes proteins which play  
20 a role in, *e.g.*, catalyze an enzymatic reaction, in one or more amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside or trehalose metabolic pathways. Examples of MP proteins include those encoded by the MP genes set forth in Table 1 and by the odd-numbered SEQ ID NOs. The terms "MP gene" or "MP nucleic acid sequence" include nucleic acid sequences encoding an MP protein, which consist of a  
25 coding region and also corresponding untranslated 5' and 3' sequence regions. Examples of MP genes include those set forth in Table 1. The terms "production" or "productivity" are art-recognized and include the concentration of the fermentation product (for example, the desired fine chemical) formed within a given time and a given fermentation volume (*e.g.*, kg product per hour per liter). The term "efficiency of  
30 production" includes the time required for a particular level of production to be achieved (for example, how long it takes for the cell to attain a particular rate of output of a fine chemical). The term "yield" or "product/carbon yield" is art-recognized and includes

the efficiency of the conversion of the carbon source into the product (*i.e.*, fine chemical). This is generally written as, for example, kg product per kg carbon source. By increasing the yield or production of the compound, the quantity of recovered molecules, or of useful recovered molecules of that compound in a given amount of culture over a given amount of time is increased. The terms "biosynthesis" or a "biosynthetic pathway" are art-recognized and include the synthesis of a compound, preferably an organic compound, by a cell from intermediate compounds in what may be a multistep and highly regulated process. The terms "degradation" or a "degradation pathway" are art-recognized and include the breakdown of a compound, preferably an organic compound, by a cell to degradation products (generally speaking, smaller or less complex molecules) in what may be a multistep and highly regulated process. The language "metabolism" is art-recognized and includes the totality of the biochemical reactions that take place in an organism. The metabolism of a particular compound, then, (*e.g.*, the metabolism of an amino acid such as glycine) comprises the overall biosynthetic, modification, and degradation pathways in the cell related to this compound.

In another embodiment, the MP molecules of the invention are capable of modulating the production of a desired molecule, such as a fine chemical, in a microorganism such as *C. glutamicum*. Using recombinant genetic techniques, one or more of the biosynthetic or degradative enzymes of the invention for amino acids, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, or trehalose may be manipulated such that its function is modulated. For example, a biosynthetic enzyme may be improved in efficiency, or its allosteric control region destroyed such that feedback inhibition of production of the compound is prevented. Similarly, a degradative enzyme may be deleted or modified by substitution, deletion, or addition such that its degradative activity is lessened for the desired compound without impairing the viability of the cell. In each case, the overall yield or rate of production of one of these desired fine chemicals may be increased.

It is also possible that such alterations in the protein and nucleotide molecules of the invention may improve the production of other fine chemicals besides the amino acids, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, and trehalose. Metabolism of any one compound is necessarily intertwined with other biosynthetic and

degradative pathways within the cell, and necessary cofactors, intermediates, or substrates in one pathway are likely supplied or limited by another such pathway.

Therefore, by modulating the activity of one or more of the proteins of the invention, the production or efficiency of activity of another fine chemical biosynthetic or degradative pathway may be impacted. For example, amino acids serve as the structural units of all proteins, yet may be present intracellularly in levels which are limiting for protein synthesis; therefore, by increasing the efficiency of production or the yields of one or more amino acids within the cell, proteins, such as biosynthetic or degradative proteins, may be more readily synthesized. Likewise, an alteration in a metabolic pathway enzyme such that a particular side reaction becomes more or less favored may result in the over- or under-production of one or more compounds which are utilized as intermediates or substrates for the production of a desired fine chemical.

The isolated nucleic acid sequences of the invention are contained within the genome of a *Corynebacterium glutamicum* strain available through the American Type Culture Collection, given designation ATCC 13032. The nucleotide sequence of the isolated *C. glutamicum* MP DNAs and the predicted amino acid sequences of the *C. glutamicum* MP proteins are shown in the Sequence Listing as odd-numbered SEQ ID NOs and even-numbered SEQ ID NOs, respectively. Computational analyses were performed which classified and/or identified these nucleotide sequences as sequences which encode metabolic pathway proteins.

The present invention also pertains to proteins which have an amino acid sequence which is substantially homologous to an amino acid sequence of the invention (e.g., the sequence of an even-numbered SEQ ID NO of the Sequence Listing). As used herein, a protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence is least about 50% homologous to the selected amino acid sequence, e.g., the entire selected amino acid sequence. A protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence can also be least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, or 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to the selected amino acid sequence.

The MP protein or a biologically active portion or fragment thereof of the invention can catalyze an enzymatic reaction in one or more amino acid, vitamin,

cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathways, or have one or more of the activities set forth in Table 1.

Various aspects of the invention are described in further detail in the following subsections:

5

*A. Isolated Nucleic Acid Molecules*

One aspect of the invention pertains to isolated nucleic acid molecules that encode MP polypeptides or biologically active portions thereof, as well as nucleic acid fragments sufficient for use as hybridization probes or primers for the identification or  
10 amplification of MP-encoding nucleic acid (*e.g.*, MP DNA). As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (*e.g.*, cDNA or genomic DNA) and RNA molecules (*e.g.*, mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. This term also encompasses untranslated sequence located at both the 3' and 5' ends of the coding region of the gene: at least about 100 nucleotides  
15 of sequence upstream from the 5' end of the coding region and at least about 20 nucleotides of sequence downstream from the 3' end of the coding region of the gene. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA. An "isolated" nucleic acid molecule is one which is separated from other nucleic acid molecules which are present in the natural source of the nucleic  
20 acid. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (*i.e.*, sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated MP nucleic acid molecule can contain less than about 5 kb, 4kb, 3kb, 2kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank  
25 the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived (*e.g.*, a *C. glutamicum* cell). Moreover, an "isolated" nucleic acid molecule, such as a DNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized.

30 A nucleic acid molecule of the present invention, *e.g.*, a nucleic acid molecule having a nucleotide sequence of an odd-numbered SEQ ID NO of the Sequence Listing, or a portion thereof, can be isolated using standard molecular biology techniques and the

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sequence information provided herein. For example, a *C. glutamicum* MP DNA can be isolated from a *C. glutamicum* library using all or portion of one of the odd-numbered SEQ ID NO sequences of the Sequence Listing as a hybridization probe and standard hybridization techniques (e.g., as described in Sambrook, J., Fritsh, E. F., and Maniatis, 5 T. *Molecular Cloning: A Laboratory Manual*. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989). Moreover, a nucleic acid molecule encompassing all or a portion of one of the nucleic acid sequences of the invention (e.g., an odd-numbered SEQ ID NO:) can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this 10 sequence (e.g., a nucleic acid molecule encompassing all or a portion of one of the nucleic acid sequences of the invention (e.g., an odd-numbered SEQ ID NO of the Sequence Listing) can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this same sequence). For example, mRNA can be isolated from normal endothelial cells (e.g., by the guanidinium-thiocyanate 15 extraction procedure of Chirgwin *et al.* (1979) *Biochemistry* 18: 5294-5299) and DNA can be prepared using reverse transcriptase (e.g., Moloney MLV reverse transcriptase, available from Gibco/BRL, Bethesda, MD; or AMV reverse transcriptase, available from Seikagaku America, Inc., St. Petersburg, FL). Synthetic oligonucleotide primers for polymerase chain reaction amplification can be designed based upon one of the 20 nucleotide sequences shown in the Sequence Listing. A nucleic acid of the invention can be amplified using cDNA or, alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to an MP nucleotide sequence can be prepared by standard synthetic techniques, e.g., 25 using an automated DNA synthesizer.

In a preferred embodiment, an isolated nucleic acid molecule of the invention comprises one of the nucleotide sequences shown in the Sequence Listing. The nucleic acid sequences of the invention, as set forth in the Sequence Listing, correspond to the 30 *Corynebacterium glutamicum* MP DNAs of the invention. This DNA comprises sequences encoding MP proteins (*i.e.*, the "coding region", indicated in each odd-numbered SEQ ID NO: sequence in the Sequence Listing), as well as 5' untranslated

sequences and 3' untranslated sequences, also indicated in each odd-numbered SEQ ID NO: in the Sequence Listing. Alternatively, the nucleic acid molecule can comprise only the coding region of any of the nucleic acid sequences of the Sequence Listing.

For the purposes of this application, it will be understood that each of the nucleic acid and amino acid sequences set forth in the Sequence Listing has an identifying RXA, RXN, RXS, or RXC number having the designation "RXA", "RXN", "RXS", or "RXC" followed by 5 digits (*i.e.*, RXA00007, RXN00023, RXS00116, or RXC00128). Each of the nucleic acid sequences comprises up to three parts: a 5' upstream region, a coding region, and a downstream region. Each of these three regions is identified by the same RXA, RXN, RXS, or RXC designation to eliminate confusion. The recitation "one of the odd-numbered sequences of the Sequence Listing", then, refers to any of the nucleic acid sequences in the Sequence Listing, which may also be distinguished by their differing RXA, RXN, RXS, or RXC designations. The coding region of each of these sequences is translated into a corresponding amino acid sequence, which is also set forth in the Sequence Listing, as an even-numbered SEQ ID NO: immediately following the corresponding nucleic acid sequence. For example, the coding region for RXA02229 is set forth in SEQ ID NO:1, while the amino acid sequence which it encodes is set forth as SEQ ID NO:2. The sequences of the nucleic acid molecules of the invention are identified by the same RXA, RXN, RXS, or RXC designations as the amino acid molecules which they encode, such that they can be readily correlated. For example, the amino acid sequences designated RXA02229, RX00351, RXS02970, and RXC02390 are translations of the coding regions of the nucleotide sequences of nucleic acid molecules RXA02229, RX00351, RXS02970, and RXC02390, respectively. The correspondence between the RXA, RXN, RXS, and RXC nucleotide and amino acid sequences of the invention and their assigned SEQ ID NOs is set forth in Table 1.

Several of the genes of the invention are "F-designated genes". An F-designated gene includes those genes set forth in Table 1 which have an 'F' in front of the RXA, RXN, RXS, or RXC designation. For example, SEQ ID NO:5, designated, as indicated on Table 1, as "F RXA01009", is an F-designated gene, as are SEQ ID NOs: 73, 75, and 77 (designated on Table 1 as "F RXA00007", "F RXA00364", and "F RXA00367", respectively).



In one embodiment, the nucleic acid molecules of the present invention are not intended to include *C. glutamicum* those compiled in Table 2. In the case of the dapD gene, a sequence for this gene was published in Wehrmann, A., *et al.* (1998) *J. Bacteriol.* 180(12): 3159-3165. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

In another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule which is a complement of one of the nucleotide sequences of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing), or a portion thereof. A nucleic acid molecule which is complementary to one of the nucleotide sequences of the invention is one which is sufficiently complementary to one of the nucleotide sequences shown in the Sequence Listing (*e.g.*, the sequence of an odd-numbered SEQ ID NO:) such that it can hybridize to one of the nucleotide sequences of the invention, thereby forming a stable duplex.

In still another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing), or a portion thereof. Ranges and identity values intermediate to the above-recited ranges, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In an additional preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to one of the nucleotide sequences of the invention, or a portion thereof.

Moreover, the nucleic acid molecule of the invention can comprise only a portion of the coding region of the sequence of one of the odd-numbered SEQ ID NOs

of the Sequence Listing, for example a fragment which can be used as a probe or primer or a fragment encoding a biologically active portion of an MP protein. The nucleotide sequences determined from the cloning of the MP genes from *C. glutamicum* allows for the generation of probes and primers designed for use in identifying and/or cloning MP

5 homologues in other cell types and organisms, as well as MP homologues from other *Corynebacteria* or related species. The probe/primer typically comprises substantially purified oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, preferably about 25, more preferably about 40, 50 or 75 consecutive nucleotides of a sense strand of one

10 of the nucleotide sequences of the invention (*e.g.*, a sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing), an anti-sense sequence of one of these sequences, or naturally occurring mutants thereof. Primers based on a nucleotide sequence of the invention can be used in PCR reactions to clone MP homologues. Probes based on the MP nucleotide sequences can be used to detect transcripts or

15 genomic sequences encoding the same or homologous proteins. In preferred embodiments, the probe further comprises a label group attached thereto, *e.g.* the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as a part of a diagnostic test kit for identifying cells which misexpress an MP protein, such as by measuring a level of an MP-encoding

20 nucleic acid in a sample of cells from a subject *e.g.*, detecting MP mRNA levels or determining whether a genomic MP gene has been mutated or deleted.

In one embodiment, the nucleic acid molecule of the invention encodes a protein or portion thereof which includes an amino acid sequence which is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-

25 numbered SEQ ID NO of the Sequence Listing) such that the protein or portion thereof maintains the ability to catalyze an enzymatic reaction in an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway. As used herein, the language "sufficiently homologous" refers to proteins or portions thereof which have amino acid sequences which include a minimum number of identical or

30 equivalent (*e.g.*, an amino acid residue which has a similar side chain as an amino acid residue in a sequence of one of the even-numbered SEQ ID NOs of the Sequence Listing) amino acid residues to an amino acid sequence of the invention such that the

protein or portion thereof is able to catalyze an enzymatic reaction in a *C. glutamicum* amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside or trehalose metabolic pathway. Protein members of such metabolic pathways, as described herein, function to catalyze the biosynthesis or degradation of one or more of: amino acids, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, or trehalose. Examples of such activities are also described herein. Thus, "the function of an MP protein" contributes to the overall functioning of one or more such metabolic pathway and contributes, either directly or indirectly, to the yield, production, and/or efficiency of production of one or more fine chemicals. Examples of MP protein activities are set forth in Table 1.

In another embodiment, the protein is at least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing).

Portions of proteins encoded by the MP nucleic acid molecules of the invention are preferably biologically active portions of one of the MP proteins. As used herein, the term "biologically active portion of an MP protein" is intended to include a portion, *e.g.*, a domain/motif, of an MP protein that catalyzes an enzymatic reaction in one or more *C. glutamicum* amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathways, or has an activity as set forth in Table 1. To determine whether an MP protein or a biologically active portion thereof can catalyze an enzymatic reaction in an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway, an assay of enzymatic activity may be performed. Such assay methods are well known to those of ordinary skill in the art, as detailed in Example 8 of the Exemplification.

Additional nucleic acid fragments encoding biologically active portions of an MP protein can be prepared by isolating a portion of one of the amino acid sequences of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing), expressing the encoded portion of the MP protein or peptide (*e.g.*, by recombinant expression *in vitro*) and assessing the activity of the encoded portion of the MP protein or peptide.

The invention further encompasses nucleic acid molecules that differ from one of the nucleotide sequences of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing) (and portions thereof) due to degeneracy of the genetic code and thus encode the same MP protein as that encoded by the nucleotide sequences of the invention. In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in the Sequence Listing (*e.g.*, an even-numbered SEQ ID NO:). In a still further embodiment, the nucleic acid molecule of the invention encodes a full length *C. glutamicum* protein which is substantially homologous to an amino acid sequence of the invention (encoded by an open reading frame shown in an odd-numbered SEQ ID NO: of the Sequence Listing).

It will be understood by one of ordinary skill in the art that in one embodiment the sequences of the invention are not meant to include the sequences of the prior art, such as those Genbank sequences set forth in Tables 2 or 4 which were available prior to the present invention. In one embodiment, the invention includes nucleotide and amino acid sequences having a percent identity to a nucleotide or amino acid sequence of the invention which is greater than that of a sequence of the prior art (*e.g.*, a Genbank sequence (or the protein encoded by such a sequence) set forth in Tables 2 or 4). For example, the invention includes a nucleotide sequence which is greater than and/or at least 40% identical to the nucleotide sequence designated RXA00115 (SEQ ID NO:185), a nucleotide sequence which is greater than and/or at least % identical to the nucleotide sequence designated RXA00131 (SEQ ID NO:991), and a nucleotide sequence which is greater than and/or at least 39% identical to the nucleotide sequence designated RXA00219 (SEQ ID NO:345). One of ordinary skill in the art would be able to calculate the lower threshold of percent identity for any given sequence of the invention by examining the GAP-calculated percent identity scores set forth in Table 4 for each of the three top hits for the given sequence, and by subtracting the highest GAP-calculated percent identity from 100 percent. One of ordinary skill in the art will also appreciate that nucleic acid and amino acid sequences having percent identities greater than the lower threshold so calculated (*e.g.*, at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%,

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74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more identical) are also encompassed by the invention.

In addition to the *C. glutamicum* MP nucleotide sequences set forth in the

5 Sequence Listing as odd-numbered SEQ ID NOs, it will be appreciated by one of ordinary skill in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of MP proteins may exist within a population (e.g., the *C. glutamicum* population). Such genetic polymorphism in the MP gene may exist among individuals within a population due to natural variation. As used herein, the terms

10 "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding an MP protein, preferably a *C. glutamicum* MP protein. Such natural variations can typically result in 1-5% variance in the nucleotide sequence of the MP gene. Any and all such nucleotide variations and resulting amino acid

15 polymorphisms in MP that are the result of natural variation and that do not alter the functional activity of MP proteins are intended to be within the scope of the invention.

Nucleic acid molecules corresponding to natural variants and non-*C. glutamicum* homologues of the *C. glutamicum* MP DNA of the invention can be isolated based on their homology to the *C. glutamicum* MP nucleic acid disclosed herein using the *C. glutamicum* DNA, or a portion thereof, as a hybridization probe according to standard

20 hybridization techniques under stringent hybridization conditions. Accordingly, in another embodiment, an isolated nucleic acid molecule of the invention is at least 15 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising a nucleotide sequence of an odd-numbered SEQ ID NO: of the Sequence Listing. In other embodiments, the nucleic acid is at least 30, 50, 100, 250 or

25 more nucleotides in length. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other. Preferably, the conditions are such that sequences at least about 65%, more preferably at least about 70%, and even more preferably at least about

30 75% or more homologous to each other typically remain hybridized to each other. Such stringent conditions are known to one of ordinary skill in the art and can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6.

A preferred, non-limiting example of stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2 X SSC, 0.1% SDS at 50-65°C. Preferably, an isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to a  
5 nucleotide sequence of the invention corresponds to a naturally-occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (*e.g.*, encodes a natural protein). In one embodiment, the nucleic acid encodes a natural *C. glutamicum* MP protein.

10 In addition to naturally-occurring variants of the MP sequence that may exist in the population, one of ordinary skill in the art will further appreciate that changes can be introduced by mutation into a nucleotide sequence of the invention, thereby leading to changes in the amino acid sequence of the encoded MP protein, without altering the functional ability of the MP protein. For example, nucleotide substitutions leading to  
15 amino acid substitutions at "non-essential" amino acid residues can be made in a nucleotide sequence of the invention. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of one of the MP proteins (*e.g.*, an even-numbered SEQ ID NO: of the Sequence Listing) without altering the activity of said MP protein, whereas an "essential" amino acid residue is required for MP protein activity.  
20 Other amino acid residues, however, (*e.g.*, those that are not conserved or only semi-conserved in the domain having MP activity) may not be essential for activity and thus are likely to be amenable to alteration without altering MP activity.

Accordingly, another aspect of the invention pertains to nucleic acid molecules encoding MP proteins that contain changes in amino acid residues that are not essential  
25 for MP activity. Such MP proteins differ in amino acid sequence from a sequence of an even-numbered SEQ ID NO: of the Sequence Listing yet retain at least one of the MP activities described herein. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 50% homologous to an amino acid sequence of the  
30 invention and is capable of catalyzing an enzymatic reaction in an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway, or has one or more activities set forth in Table 1. Preferably, the protein encoded by the nucleic

acid molecule is at least about 50-60% homologous to the amino acid sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing, more preferably at least about 60-70% homologous to one of these sequences, even more preferably at least about 70-80%, 80-90%, 90-95% homologous to one of these sequences, and most preferably at least about 96%, 97%, 98%, or 99% homologous to one of the amino acid sequences of the invention.

To determine the percent homology of two amino acid sequences (*e.g.*, one of the amino acid sequences of the invention and a mutant form thereof) or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of one protein or nucleic acid for optimal alignment with the other protein or nucleic acid). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in one sequence (*e.g.*, one of the amino acid sequences of the invention) is occupied by the same amino acid residue or nucleotide as the corresponding position in the other sequence (*e.g.*, a mutant form of the amino acid sequence), then the molecules are homologous at that position (*i.e.*, as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity"). The percent homology between the two sequences is a function of the number of identical positions shared by the sequences (*i.e.*, % homology = # of identical positions/total # of positions x 100).

An isolated nucleic acid molecule encoding an MP protein homologous to a protein sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) can be created by introducing one or more nucleotide substitutions, additions or deletions into a nucleotide sequence of the invention such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein. Mutations can be introduced into one of the nucleotide sequences of the invention by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic

acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in an MP protein is preferably replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of an MP coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for an MP activity described herein to identify mutants that retain MP activity. Following mutagenesis of the nucleotide sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing, the encoded protein can be expressed recombinantly and the activity of the protein can be determined using, for example, assays described herein (see Example 8 of the Exemplification).

In addition to the nucleic acid molecules encoding MP proteins described above, another aspect of the invention pertains to isolated nucleic acid molecules which are antisense thereto. An "antisense" nucleic acid comprises a nucleotide sequence which is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded DNA molecule or complementary to an mRNA sequence. Accordingly, an antisense nucleic acid can hydrogen bond to a sense nucleic acid. The antisense nucleic acid can be complementary to an entire MP coding strand, or to only a portion thereof. In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding an MP protein. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues (*e.g.*, the entire coding region of SEQ ID NO. 1 (RXA02229) comprises nucleotides 1 to 825). In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding MP. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding MP disclosed herein (*e.g.*, the sequences set forth as odd-numbered SEQ ID NOs in the Sequence Listing), antisense



nucleic acids of the invention can be designed according to the rules of Watson and Crick base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of MP mRNA, but more preferably is an oligonucleotide which is antisense to only a portion of the coding or noncoding region of MP mRNA. For

5 example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of MP mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an

10 antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used. Examples of modified

15 nucleotides which can be used to generate the antisense nucleic acid include 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine,

20 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-

25 methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5- oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from

30 the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a cell or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding an MCT protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by  
5 conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule which binds to DNA duplexes, through specific interactions in the major groove of the double helix. The antisense molecule can be modified such that it specifically binds to a receptor or an antigen expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecule to a peptide or  
10 an antibody which binds to a cell surface receptor or antigen. The antisense nucleic acid molecule can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of the antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong prokaryotic, viral, or eukaryotic promoter are preferred.

15 In yet another embodiment, the antisense nucleic acid molecule of the invention is an  $\alpha$ -anomeric nucleic acid molecule. An  $\alpha$ -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual  $\beta$ -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res.* 15:6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res.* 15:6131-6148) or a  
20 chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett.* 215:327-330).

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity which are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they  
25 have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave MP mRNA transcripts to thereby inhibit translation of MP mRNA. A ribozyme having specificity for an MP-encoding nucleic acid can be designed based upon the nucleotide sequence of an MP DNA disclosed herein (*i.e.*, SEQ ID NO: 1  
30 (RXA02229). For example, a derivative of a *Tetrahymena* L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an MP-encoding mRNA. See, *e.g.*, Cech *et al.*

U.S. Patent No. 4,987,071 and Cech *et al.* U.S. Patent No. 5,116,742. Alternatively, MP mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel, D. and Szostak, J.W. (1993) *Science* 261:1411-1418.

- 5           Alternatively, MP gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of an MP nucleotide sequence (*e.g.*, an MP promoter and/or enhancers) to form triple helical structures that prevent transcription of an MP gene in target cells. See generally, Helene, C. (1991) *Anticancer Drug Des.* 6(6):569-84; Helene, C. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and
- 10   Maher, L.J. (1992) *Bioassays* 14(12):807-15.

#### *B. Recombinant Expression Vectors and Host Cells*

- Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding an MP protein (or a portion thereof). As
- 15   used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of
- 20   autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to
- 25   which they are operatively linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors,
- 30   such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

- The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is
- 5 operatively linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory
- 10 sequence" is intended to include promoters, repressor binding sites, activator binding sites, enhancers and other expression control elements (*e.g.*, terminators, polyadenylation signals, or other elements of mRNA secondary structure). Such regulatory sequences are described, for example, in Goeddel; *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990).
- 15 Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in many types of host cell and those which direct expression of the nucleotide sequence only in certain host cells. Preferred regulatory sequences are, for example, promoters such as *cos*-, *tac*-, *trp*-, *tet*-, *trp-tet*-, *lpp*-, *lac*-, *lpp-lac*-, *lacI<sup>q</sup>*-, *T7*-, *T5*-, *T3*-, *gal*-, *trc*-, *ara*-, *SP6*-, *amy*, *SPO2*,  $\lambda$ -*P<sub>R</sub>*- or  $\lambda$  *P<sub>L</sub>*, which are used preferably in bacteria.
- 20 Additional regulatory sequences are, for example, promoters from yeasts and fungi, such as *ADC1*, *MF $\alpha$* , *AC*, *P-60*, *CYC1*, *GAPDH*, *TEF*, *rp28*, *ADH*, promoters from plants such as *CaMV/35S*, *SSU*, *OCS*, *lib4*, *usp*, *STLS1*, *B33*, *nos* or ubiquitin- or phaseolin-promoters. It is also possible to use artificial promoters. It will be appreciated by one of ordinary skill in the art that the design of the expression vector can depend on such
- 25 factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein (*e.g.*, MP proteins, mutant forms of MP proteins, fusion proteins, etc.).
- 30 The recombinant expression vectors of the invention can be designed for expression of MP proteins in prokaryotic or eukaryotic cells. For example, MP genes can be expressed in bacterial cells such as *C. glutamicum*, insect cells (using baculovirus

expression vectors), yeast and other fungal cells (see Romanos, M.A. *et al.* (1992) "Foreign gene expression in yeast: a review", *Yeast* 8: 423-488; van den Hondel, C.A.M.J.J. *et al.* (1991) "Heterologous gene expression in filamentous fungi" in: More Gene Manipulations in Fungi, J.W. Bennet & L.L. Lasure, eds., p. 396-428: Academic Press: San Diego; and van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, Peberdy, J.F. *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge), algae and multicellular plant cells (see Schmidt, R. and Willmitzer, L. (1988) High efficiency *Agrobacterium tumefaciens* -mediated transformation of *Arabidopsis thaliana* leaf and cotyledon explants" *Plant Cell Rep.*: 583-586), or mammalian cells. Suitable host cells are discussed further in Goeddel, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Expression of proteins in prokaryotes is most often carried out with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein but also to the C-terminus or fused within suitable regions in the proteins. Such fusion vectors typically serve three purposes: 1) to increase expression of recombinant protein; 2) to increase the solubility of the recombinant protein; and 3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase.

Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith, D.B. and Johnson, K.S. (1988) *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein. In one embodiment, the coding sequence of the MP protein is cloned into a pGEX expression vector to create a vector encoding a fusion protein comprising, from

the N-terminus to the C-terminus, GST-thrombin cleavage site-X protein. The fusion protein can be purified by affinity chromatography using glutathione-agarose resin. Recombinant MP protein unfused to GST can be recovered by cleavage of the fusion protein with thrombin.

- 5           Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amann *et al.*, (1988) *Gene* 69:301-315) pLG338, pACYC184, pBR322, pUC18, pUC19, pKC30, pRep4, pHS1, pHS2, pPLc236, pMBL24, pLG200, pUR290, pIN-III113-B1,  $\lambda$ gt11, pBdCl, and pET 11d (Studier *et al.*, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 60-89; and
- 10   Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York ISBN 0 444 904018). Target gene expression from the pTrc vector relies on host RNA polymerase transcription from a hybrid trp-lac fusion promoter. Target gene expression from the pET 11d vector relies on transcription from a T7 gn10-lac fusion promoter mediated by a coexpressed viral RNA polymerase (T7 gn1). This viral polymerase is supplied by
- 15   host strains BL21(DE3) or HMS174(DE3) from a resident  $\lambda$  prophage harboring a T7 gn1 gene under the transcriptional control of the lacUV 5 promoter. For transformation of other varieties of bacteria, appropriate vectors may be selected. For example, the plasmids pIJ101, pIJ364, pIJ702 and pIJ361 are known to be useful in transforming *Streptomyces*, while plasmids pUB110, pC194, or pBD214 are suited for transformation
- 20   of *Bacillus* species. Several plasmids of use in the transfer of genetic information into *Corynebacterium* include pHM1519, pBL1, pSA77, or pAJ667 (Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York ISBN 0 444 904018).

- One strategy to maximize recombinant protein expression is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the
- 25   recombinant protein (Gottesman, S., *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 119-128). Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in the bacterium chosen for expression, such as *C. glutamicum*
- 30   (Wada *et al.* (1992) *Nucleic Acids Res.* 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

In another embodiment, the MP protein expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari, *et al.*, (1987) *Embo J.* 6:229-234), , 2  $\mu$ , pAG-1, Yep6, Yep13, pEMBL Ye23, pMFa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz *et al.*, (1987) 5 *Gene* 54:113-123), and pYES2 (Invitrogen Corporation, San Diego, CA). Vectors and methods for the construction of vectors appropriate for use in other fungi, such as the filamentous fungi, include those detailed in: van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, J.F. Peberdy, *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge, and Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: 10 New York (IBSN 0 444 904018).

Alternatively, the MP proteins of the invention can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*, Sf 9 cells) include the pAc series (Smith *et al.* 15 (1983) *Mol. Cell Biol.* 3:2156-2165) and the pVL series (Lucklow and Summers (1989) *Virology* 170:31-39).

In another embodiment, the MP proteins of the invention may be expressed in unicellular plant cells (such as algae) or in plant cells from higher plants (*e.g.*, the spermatophytes, such as crop plants). Examples of plant expression vectors include 20 those detailed in: Becker, D., Kemper, E., Schell, J. and Masterson, R. (1992) "New plant binary vectors with selectable markers located proximal to the left border", *Plant Mol. Biol.* 20: 1195-1197; and Bevan, M.W. (1984) "Binary *Agrobacterium* vectors for plant transformation", *Nucl. Acid. Res.* 12: 8711-8721, and include pLGV23, pGHIac+, pBIN19, pAK2004, and pDH51 (Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: 25 New York IBSN 0 444 904018).

In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed, B. (1987) *Nature* 329:840) and pMT2PC (Kaufman *et al.* (1987) *EMBO J.* 6:187-195). When used in mammalian cells, the 30 expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. For other suitable expression systems for both

prokaryotic and eukaryotic cells see chapters 16 and 17 of Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989.*

- 5 In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (e.g., tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert *et al.* 10 (1987) *Genes Dev.* 1:268-277), lymphoid-specific promoters (Calame and Eaton (1988) *Adv. Immunol.* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore (1989) *EMBO J.* 8:729-733) and immunoglobulins (Banerji *et al.* (1983) *Cell* 33:729-740; Queen and Baltimore (1983) *Cell* 33:741-748), neuron-specific promoters (e.g., the neurofilament promoter; Byrne and Ruddle (1989) *PNAS* 86:5473-5477), 15 pancreas-specific promoters (Edlund *et al.* (1985) *Science* 230:912-916), and mammary gland-specific promoters (e.g., milk whey promoter; U.S. Patent No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, for example the murine hox promoters (Kessel and Gruss (1990) *Science* 249:374-379) and the  $\alpha$ -fetoprotein promoter (Campes and Tilghman (1989) 20 *Genes Dev.* 3:537-546).

- The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively linked to a regulatory sequence in a manner which allows for expression (by transcription of the DNA molecule) of an 25 RNA molecule which is antisense to MP mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the antisense orientation can be chosen which direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen which direct constitutive, tissue specific or cell type specific expression of antisense RNA.
- 30 The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell



type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub, H. *et al.*, Antisense RNA as a molecular tool for genetic analysis, *Reviews - Trends in Genetics*, Vol. 1(1) 1986.

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, an MP protein can be expressed in bacterial cells such as *C. glutamicum*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those of ordinary skill in the art. Microorganisms related to *Corynebacterium glutamicum* which may be conveniently used as host cells for the nucleic acid and protein molecules of the invention are set forth in Table 3.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection", "conjugation" and "transduction" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (*e.g.*, linear DNA or RNA (*e.g.*, a linearized vector or a gene construct alone without a vector) or nucleic acid in the form of a vector (*e.g.*, a plasmid, phage, phasmid, phagemid, transposon or other DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, natural competence, chemical-mediated transfer, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (*Molecular Cloning: A Laboratory Manual. 2nd, ed.*, Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these

integrants, a gene that encodes a selectable marker (*e.g.*, resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those which confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be  
5 introduced into a host cell on the same vector as that encoding an MP protein or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

To create a homologous recombinant microorganism, a vector is prepared which  
10 contains at least a portion of an MP gene into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, functionally disrupt, the MP gene. Preferably, this MP gene is a *Corynebacterium glutamicum* MP gene, but it can be a homologue from a related bacterium or even from a mammalian, yeast, or insect source. In a preferred embodiment, the vector is designed such that, upon homologous  
15 recombination, the endogenous MP gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a "knock out" vector). Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous MP gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the  
20 endogenous MP protein). In the homologous recombination vector, the altered portion of the MP gene is flanked at its 5' and 3' ends by additional nucleic acid of the MP gene to allow for homologous recombination to occur between the exogenous MP gene carried by the vector and an endogenous MP gene in a microorganism. The additional flanking MP nucleic acid is of sufficient length for successful homologous  
25 recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector (see *e.g.*, Thomas, K.R., and Capecchi, M.R. (1987) Cell 51: 503 for a description of homologous recombination vectors). The vector is introduced into a microorganism (*e.g.*, by electroporation) and cells in which the introduced MP gene has homologously recombined with the  
30 endogenous MP gene are selected, using art-known techniques.

In another embodiment, recombinant microorganisms can be produced which contain selected systems which allow for regulated expression of the introduced gene.

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For example, inclusion of an MP gene on a vector placing it under control of the lac operon permits expression of the MP gene only in the presence of IPTG. Such regulatory systems are well known in the art.

In another embodiment, an endogenous MP gene in a host cell is disrupted (*e.g.*,  
5 by homologous recombination or other genetic means known in the art) such that expression of its protein product does not occur. In another embodiment, an endogenous or introduced MP gene in a host cell has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional MP protein. In still another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or  
10 inducer) of an MP gene in a microorganism has been altered (*e.g.*, by deletion, truncation, inversion, or point mutation) such that the expression of the MP gene is modulated. One of ordinary skill in the art will appreciate that host cells containing more than one of the described MP gene and protein modifications may be readily produced using the methods of the invention, and are meant to be included in the present  
15 invention.

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) an MP protein. Accordingly, the invention further provides methods for producing MP proteins using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of  
20 invention (into which a recombinant expression vector encoding an MP protein has been introduced, or into which genome has been introduced a gene encoding a wild-type or altered MP protein) in a suitable medium until MP protein is produced. In another embodiment, the method further comprises isolating MP proteins from the medium or the host cell.

25

### *C. Isolated MP Proteins*

Another aspect of the invention pertains to isolated MP proteins, and biologically active portions thereof. An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material when produced by recombinant DNA  
30 techniques, or chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of MP protein in which the protein is separated from cellular components of the cells in which

it is naturally or recombinantly produced. In one embodiment, the language "substantially free of cellular material" includes preparations of MP protein having less than about 30% (by dry weight) of non-MP protein (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-MP protein, still more preferably less than about 10% of non-MP protein, and most preferably less than about 5% non-MP protein. When the MP protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein preparation. The language "substantially free of chemical precursors or other chemicals" includes preparations of MP protein in which the protein is separated from chemical precursors or other chemicals which are involved in the synthesis of the protein. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of MP protein having less than about 30% (by dry weight) of chemical precursors or non-MP chemicals, more preferably less than about 20% chemical precursors or non-MP chemicals, still more preferably less than about 10% chemical precursors or non-MP chemicals, and most preferably less than about 5% chemical precursors or non-MP chemicals. In preferred embodiments, isolated proteins or biologically active portions thereof lack contaminating proteins from the same organism from which the MP protein is derived. Typically, such proteins are produced by recombinant expression of, for example, a *C. glutamicum* MP protein in a microorganism such as *C. glutamicum*.

An isolated MP protein or a portion thereof of the invention can catalyze an enzymatic reaction in an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway, or has one or more of the activities set forth in Table 1. In preferred embodiments, the protein or portion thereof comprises an amino acid sequence which is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) such that the protein or portion thereof maintains the ability to catalyze an enzymatic reaction in an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway. The portion of the protein is preferably a biologically active portion as described herein. In another preferred embodiment, an MP protein of

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the invention has an amino acid sequence set forth as an even-numbered SEQ ID NO: of the Sequence Listing. In yet another preferred embodiment, the MP protein has an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to a nucleotide sequence of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing). In still another preferred embodiment, the MP protein has an amino acid sequence which is encoded by a nucleotide sequence that is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to one of the nucleic acid sequences of the invention, or a portion thereof. Ranges and identity values intermediate to the above-recited values, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. The preferred MP proteins of the present invention also preferably possess at least one of the MP activities described herein. For example, a preferred MP protein of the present invention includes an amino acid sequence encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to a nucleotide sequence of the invention, and which can catalyze an enzymatic reaction in an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway, or which has one or more of the activities set forth in Table 1.

In other embodiments, the MP protein is substantially homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) and retains the functional activity of the protein of one of the amino acid sequences of the invention yet differs in amino acid sequence due to natural variation or mutagenesis, as described in detail in subsection I above. Accordingly, in another embodiment, the MP protein is a protein which comprises an amino acid sequence which is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%,

78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of the invention and which has at least one of the MP activities described herein. Ranges and identity values  
5 intermediate to the above-recited values, (e.g., 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In another embodiment, the invention pertains to a full length *C. glutamicum* protein which is substantially homologous to an entire  
10 amino acid sequence of the invention.

Biologically active portions of an MP protein include peptides comprising amino acid sequences derived from the amino acid sequence of an MP protein, e.g., an amino acid sequence of an even-numbered SEQ ID NO: of the Sequence Listing or the amino acid sequence of a protein homologous to an MP protein, which include fewer amino  
15 acids than a full length MP protein or the full length protein which is homologous to an MP protein, and exhibit at least one activity of an MP protein. Typically, biologically active portions (peptides, e.g., peptides which are, for example, 5, 10, 15, 20, 30, 35, 36, 37, 38, 39, 40, 50, 100 or more amino acids in length) comprise a domain or motif with at least one activity of an MP protein. Moreover, other biologically active portions, in  
20 which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the activities described herein. Preferably, the biologically active portions of an MP protein include one or more selected domains/motifs or portions thereof having biological activity.

MP proteins are preferably produced by recombinant DNA techniques. For  
25 example, a nucleic acid molecule encoding the protein is cloned into an expression vector (as described above), the expression vector is introduced into a host cell (as described above) and the MP protein is expressed in the host cell. The MP protein can then be isolated from the cells by an appropriate purification scheme using standard protein purification techniques. Alternative to recombinant expression, an MP protein,  
30 polypeptide, or peptide can be synthesized chemically using standard peptide synthesis techniques. Moreover, native MP protein can be isolated from cells (e.g., endothelial

cells), for example using an anti-MP antibody, which can be produced by standard techniques utilizing an MP protein or fragment thereof of this invention.

The invention also provides MP chimeric or fusion proteins. As used herein, an MP "chimeric protein" or "fusion protein" comprises an MP polypeptide operatively  
5 linked to a non-MP polypeptide. An "MP polypeptide" refers to a polypeptide having an amino acid sequence corresponding to MP, whereas a "non-MP polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein which is not substantially homologous to the MP protein, *e.g.*, a protein which is different from the MP protein and which is derived from the same or a different organism. Within the  
10 fusion protein, the term "operatively linked" is intended to indicate that the MP polypeptide and the non-MP polypeptide are fused in-frame to each other. The non-MP polypeptide can be fused to the N-terminus or C-terminus of the MP polypeptide. For example, in one embodiment the fusion protein is a GST-MP fusion protein in which the MP sequences are fused to the C-terminus of the GST sequences. Such fusion proteins  
15 can facilitate the purification of recombinant MP proteins. In another embodiment, the fusion protein is an MP protein containing a heterologous signal sequence at its N-terminus. In certain host cells (*e.g.*, mammalian host cells), expression and/or secretion of an MP protein can be increased through use of a heterologous signal sequence.

Preferably, an MP chimeric or fusion protein of the invention is produced by  
20 standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, for example by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid  
25 undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed and reamplified to generate a chimeric  
30 gene sequence (see, for example, *Current Protocols in Molecular Biology*, eds. Ausubel *et al.* John Wiley & Sons: 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). An MP-

encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the MP protein.

Homologues of the MP protein can be generated by mutagenesis, *e.g.*, discrete point mutation or truncation of the MP protein. As used herein, the term "homologue" refers to a variant form of the MP protein which acts as an agonist or antagonist of the activity of the MP protein. An agonist of the MP protein can retain substantially the same, or a subset, of the biological activities of the MP protein. An antagonist of the MP protein can inhibit one or more of the activities of the naturally occurring form of the MP protein, by, for example, competitively binding to a downstream or upstream member of the MP cascade which includes the MP protein. Thus, the *C. glutamicum* MP protein and homologues thereof of the present invention may modulate the activity of one or more metabolic pathways in which MP proteins play a role in this microorganism.

In an alternative embodiment, homologues of the MP protein can be identified by screening combinatorial libraries of mutants, *e.g.*, truncation mutants, of the MP protein for MP protein agonist or antagonist activity. In one embodiment, a variegated library of MP variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of MP variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential MP sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (*e.g.*, for phage display) containing the set of MP sequences therein. There are a variety of methods which can be used to produce libraries of potential MP homologues from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential MP sequences. Methods for synthesizing degenerate oligonucleotides are known in the art (see, *e.g.*, Narang, S.A. (1983) *Tetrahedron* 39:3; Itakura *et al.* (1984) *Annu. Rev. Biochem.* 53:323; Itakura *et al.* (1984) *Science* 198:1056; Ike *et al.* (1983) *Nucleic Acid Res.* 11:477.



In addition, libraries of fragments of the MP protein coding can be used to generate a variegated population of MP fragments for screening and subsequent selection of homologues of an MP protein. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of an MP coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA which can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes N-terminal, C-terminal and internal fragments of various sizes of the MP protein.

Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of MP homologues. The most widely used techniques, which are amenable to high through-put analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique which enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify MP homologues (Arkin and Yourvan (1992) *PNAS* 89:7811-7815; Delgrave *et al.* (1993) *Protein Engineering* 6(3):327-331).

In another embodiment, cell based assays can be exploited to analyze a variegated MP library, using methods well known in the art.

#### *D. Uses and Methods of the Invention*

The nucleic acid molecules, proteins, protein homologues, fusion proteins, primers, vectors, and host cells described herein can be used in one or more of the following methods: identification of *C. glutamicum* and related organisms; mapping of genomes of organisms related to *C. glutamicum*; identification and localization of *C.*

*glutamicum* sequences of interest; evolutionary studies; determination of MP protein regions required for function; modulation of an MP protein activity; modulation of the activity of an MP pathway; and modulation of cellular production of a desired compound, such as a fine chemical.

- 5           The MP nucleic acid molecules of the invention have a variety of uses. First, they may be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof. Also, they may be used to identify the presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the
- 10   extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present. Although *Corynebacterium glutamicum* itself is not pathogenic to humans, it is related to species which are human pathogens, such as *Corynebacterium diphtheriae*.
- 15   *Corynebacterium diphtheriae* is the causative agent of diphtheria, a rapidly developing, acute, febrile infection which involves both local and systemic pathology. In this disease, a local lesion develops in the upper respiratory tract and involves necrotic injury to epithelial cells; the bacilli secrete toxin which is disseminated through this lesion to distal susceptible tissues of the body. Degenerative changes brought about by the
- 20   inhibition of protein synthesis in these tissues, which include heart, muscle, peripheral nerves, adrenals, kidneys, liver and spleen, result in the systemic pathology of the disease. Diphtheria continues to have high incidence in many parts of the world, including Africa, Asia, Eastern Europe and the independent states of the former Soviet Union. An ongoing epidemic of diphtheria in the latter two regions has resulted in at
- 25   least 5,000 deaths since 1990.

          In one embodiment, the invention provides a method of identifying the presence or activity of *Corynebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (*e.g.*, the sequences set forth as odd-numbered or even-numbered SEQ ID NOs, respectively, in

30   the Sequence Listing) in a subject, thereby detecting the presence or activity of *Corynebacterium diphtheriae* in the subject. *C. glutamicum* and *C. diphtheriae* are related bacteria, and many of the nucleic acid and protein molecules in *C. glutamicum*

are homologous to *C. diphtheriae* nucleic acid and protein molecules, and can therefore be used to detect *C. diphtheriae* in a subject.

The nucleic acid and protein molecules of the invention may also serve as markers for specific regions of the genome. This has utility not only in the mapping of the genome, but also for functional studies of *C. glutamicum* proteins. For example, to identify the region of the genome to which a particular *C. glutamicum* DNA-binding protein binds, the *C. glutamicum* genome could be digested, and the fragments incubated with the DNA-binding protein. Those which bind the protein may be additionally probed with the nucleic acid molecules of the invention, preferably with readily detectable labels; binding of such a nucleic acid molecule to the genome fragment enables the localization of the fragment to the genome map of *C. glutamicum*, and, when performed multiple times with different enzymes, facilitates a rapid determination of the nucleic acid sequence to which the protein binds. Further, the nucleic acid molecules of the invention may be sufficiently homologous to the sequences of related species such that these nucleic acid molecules may serve as markers for the construction of a genomic map in related bacteria, such as *Brevibacterium lactofermentum*.

The MP nucleic acid molecules of the invention are also useful for evolutionary and protein structural studies. The metabolic processes in which the molecules of the invention participate are utilized by a wide variety of prokaryotic and eukaryotic cells; by comparing the sequences of the nucleic acid molecules of the present invention to those encoding similar enzymes from other organisms, the evolutionary relatedness of the organisms can be assessed. Similarly, such a comparison permits an assessment of which regions of the sequence are conserved and which are not, which may aid in determining those regions of the protein which are essential for the functioning of the enzyme. This type of determination is of value for protein engineering studies and may give an indication of what the protein can tolerate in terms of mutagenesis without losing function.

Manipulation of the MP nucleic acid molecules of the invention may result in the production of MP proteins having functional differences from the wild-type MP proteins. These proteins may be improved in efficiency or activity, may be present in greater numbers in the cell than is usual, or may be decreased in efficiency or activity.

The invention also provides methods for screening molecules which modulate the activity of an MP protein, either by interacting with the protein itself or a substrate or binding partner of the MP protein, or by modulating the transcription or translation of an MP nucleic acid molecule of the invention. In such methods, a microorganism  
5 expressing one or more MP proteins of the invention is contacted with one or more test compounds, and the effect of each test compound on the activity or level of expression of the MP protein is assessed.

When the desired fine chemical to be isolated from large-scale fermentative culture of *C. glutamicum* is an amino acid, a vitamin, a cofactor, a nutraceutical, a  
10 nucleotide, a nucleoside, or trehalose, modulation of the activity or efficiency of activity of one or more of the proteins of the invention by recombinant genetic mechanisms may directly impact the production of one of these fine chemicals. For example, in the case of an enzyme in a biosynthetic pathway for a desired amino acid, improvement in efficiency or activity of the enzyme (including the presence of multiple copies of the  
15 gene) should lead to an increased production or efficiency of production of that desired amino acid. In the case of an enzyme in a biosynthetic pathway for an amino acid whose synthesis is in competition with the synthesis of a desired amino acid, any decrease in the efficiency or activity of this enzyme (including deletion of the gene) should result in an increase in production or efficiency of production of the desired amino acid, due to  
20 decreased competition for intermediate compounds and/or energy. In the case of an enzyme in a degradation pathway for a desired amino acid, any decrease in efficiency or activity of the enzyme should result in a greater yield or efficiency of production of the desired product due to a decrease in its degradation. Lastly, mutagenesis of an enzyme involved in the biosynthesis of a desired amino acid such that this enzyme is no longer is  
25 capable of feedback inhibition should result in increased yields or efficiency of production of the desired amino acid. The same should apply to the biosynthetic and degradative enzymes of the invention involved in the metabolism of vitamins, cofactors, nutraceuticals, nucleotides, nucleosides and trehalose.

Similarly, when the desired fine chemical is not one of the aforementioned  
30 compounds, the modulation of activity of one of the proteins of the invention may still impact the yield and/or efficiency of production of the compound from large-scale culture of *C. glutamicum*. The metabolic pathways of any organism are closely

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interconnected; the intermediate used by one pathway is often supplied by a different pathway. Enzyme expression and function may be regulated based on the cellular levels of a compound from a different metabolic process, and the cellular levels of molecules necessary for basic growth, such as amino acids and nucleotides, may critically affect the viability of the microorganism in large-scale culture. Thus, modulation of an amino acid biosynthesis enzyme, for example, such that it is no longer responsive to feedback inhibition or such that it is improved in efficiency or turnover may result in increased cellular levels of one or more amino acids. In turn, this increased pool of amino acids provides not only an increased supply of molecules necessary for protein synthesis, but also of molecules which are utilized as intermediates and precursors in a number of other biosynthetic pathways. If a particular amino acid had been limiting in the cell, its increased production might increase the ability of the cell to perform numerous other metabolic reactions, as well as enabling the cell to more efficiently produce proteins of all kinds, possibly increasing the overall growth rate or survival ability of the cell in large scale culture. Increased viability improves the number of cells capable of producing the desired fine chemical in fermentative culture, thereby increasing the yield of this compound. Similar processes are possible by the modulation of activity of a degradative enzyme of the invention such that the enzyme no longer catalyzes, or catalyzes less efficiently, the degradation of a cellular compound which is important for the biosynthesis of a desired compound, or which will enable the cell to grow and reproduce more efficiently in large-scale culture. It should be emphasized that optimizing the degradative activity or decreasing the biosynthetic activity of certain molecules of the invention may also have a beneficial effect on the production of certain fine chemicals from *C. glutamicum*. For example, by decreasing the efficiency of activity of a biosynthetic enzyme in a pathway which competes with the biosynthetic pathway of a desired compound for one or more intermediates, more of those intermediates should be available for conversion to the desired product. A similar situation may call for the improvement of degradative ability or efficiency of one or more proteins of the invention.

This aforementioned list of mutagenesis strategies for MP proteins to result in increased yields of a desired compound is not meant to be limiting; variations on these mutagenesis strategies will be readily apparent to one of ordinary skill in the art. By

these mechanisms, the nucleic acid and protein molecules of the invention may be utilized to generate *C. glutamicum* or related strains of bacteria expressing mutated MP nucleic acid and protein molecules such that the yield, production, and/or efficiency of production of a desired compound is improved. This desired compound may be any

5 natural product of *C. glutamicum*, which includes the final products of biosynthesis pathways and intermediates of naturally-occurring metabolic pathways, as well as molecules which do not naturally occur in the metabolism of *C. glutamicum*, but which are produced by a *C. glutamicum* strain of the invention.

This invention is further illustrated by the following examples which should not

10 be construed as limiting. The contents of all references, patent applications, patents, published patent applications, Tables, and the sequence listing cited throughout this application are hereby incorporated by reference.

TABLE 1: Included Genes

**Lysine biosynthesis**

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
1	2	RXA02229	GR00653	2793	3617	DIAMINOPELATE EPIMERASE (EC 5.1.1.7)
3	4	RXS02970				ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
5	6	F RXA01009	GR00287	4714	5943	ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
7	8	RXC02390				MEMBRANE SPANNING PROTEIN INVOLVED IN LYSINE METABOLISM
9	10	RXC01796				MEMBRANE ASSOCIATED PROTEIN INVOLVED IN LYSINE METABOLISM
11	12	RXC01207				CYTOSOLIC PROTEIN INVOLVED IN METABOLISM OF LYSINE AND THREONINE
13	14	RXC00657				TRANSCRIPTIONAL REGULATOR INVOLVED IN LYSINE METABOLISM
15	16	RXC00552				CYTOSOLIC PROTEIN INVOLVED IN LYSINE METABOLISM

**Trehalose**

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
17	18	RXN00351	VW0135	37078	38532	ALPHA,ALPHA-TREHALOSE-PHOSPHATE SYNTHASE (UDP-FORMING) 56 KD SUBUNIT (EC 2.4.1.15)
19	20	F RXA00351	GR00066	1486	2931	ALPHA,ALPHA-TREHALOSE-PHOSPHATE SYNTHASE (UDP-FORMING) 56 KD SUBUNIT (EC 2.4.1.15)
21	22	RXA00873	GR00241	3	758	trehalose synthase (EC 2.4.1.-)
23	24	RXA00891	GR00243	1005	4	trehalose synthase (EC 2.4.1.-)

**Lysine biosynthesis**

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
25	26	RXA00534	GR00137	4758	3496	ASPARTOKINASE ALPHA AND BETA SUBUNITS (EC 2.7.2.4)
27	28	RXA00533	GR00137	3489	2438	ASPARTATE-SEMIALDEHYDE DEHYDROGENASE (EC 1.2.1.11)
29	30	RXA02843	GR00842	543	4	2,3,4,5-TETRAHYDROPYRIDINE-2-CARBOXYLATE N-SUCCINYLTRANSFERASE (EC 2.3.1.117)
31	32	RXA02022	GR00613	2063	3169	SUCCINYL-DIAMINOPIMELATE DESUCCINYLASE (EC 3.5.1.18)
33	34	RXA00044	GR00007	3458	4393	DIHYDRODIPICOLINATE SYNTHASE (EC 4.2.1.52)
35	36	RXA00863	GR00236	896	1639	DIHYDRODIPICOLINATE REDUCTASE (EC 1.3.1.26)
37	38	RXA00864	GR00236	1694	2443	probable 2,3-dihydrodipicolinate N-C6-lyase (cyclizing) (EC 4.3.3.-) Corynebacterium glutamicum
39	40	RXA02843	GR00842	543	4	2,3,4,5-TETRAHYDROPYRIDINE-2-CARBOXYLATE N-SUCCINYLTRANSFERASE (EC 2.3.1.117)
41	42	RXN00355	VW0135	31980	30961	MESO-DIAMINOPIMELATE D-DEHYDROGENASE
43	44	F RXA00352	GR00068	861	4	MESO-DIAMINOPIMELATE D-DEHYDROGENASE (EC 1.4.1.16)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
45	46	RXA00972	GR00274	3	1379	DIAMINOPIMELATE DECARBOXYLASE (EC 4.1.1.20)
47	48	RXA02653	GR00752	5237	7234	DIAMINOPIMELATE DECARBOXYLASE (EC 4.1.1.20)
49	50	RXA01393	GR00408	4249	3380	LYSINE EXPORT REGULATOR PROTEIN
51	52	RXA00241	GR00036	5443	6945	L-LYSINE TRANSPORT PROTEIN
53	54	RXA01394	GR00408	4320	5018	LYSINE EXPORTER PROTEIN
55	56	RXA00865	GR00236	2647	3549	DIHYDRODIPICOLINATE SYNTHASE (EC 4.2.1.52)
57	58	RXS02021				2,3,4,5-TETRAHYDROPYRIDINE-2-CARBOXYLATE N-SUCCINYLTRANSFERASE (EC 2.3.1.117)
59	60	RXS02157				ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
61	62	RXC00733				ABC TRANSPORTER ATP-BINDING PROTEIN INVOLVED IN LYSINE METABOLISM
63	64	RXC00861				PROTEIN INVOLVED IN LYSINE METABOLISM
65	66	RXC00866				ZN-DEPENDENT HYDROLASE INVOLVED IN LYSINE METABOLISM
67	68	RXC02095				ABC TRANSPORTER ATP-BINDING PROTEIN INVOLVED IN LYSINE METABOLISM
69	70	RXC03185				PROTEIN INVOLVED IN LYSINE METABOLISM

## Glutamate and glutamine metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
71	72	RXN00367	VV0196	9744	14273	GLUTAMATE SYNTHASE [NADH] PRECURSOR (EC 1.4.1.14)
73	74	F RXA00007	GR00001	7107	8912	GLUTAMATE SYNTHASE (NADPH) LARGE CHAIN PRECURSOR (EC 1.4.1.13)
75	76	F RXA00364	GR00074	1296	4	GLUTAMATE SYNTHASE (NADPH) LARGE CHAIN PRECURSOR (EC 1.4.1.13)
77	78	F RXA00367	GR00075	1806	964	GLUTAMATE SYNTHASE (NADPH) LARGE CHAIN PRECURSOR (EC 1.4.1.13)
79	80	RXN00076	VV0154	2752	4122	GLUTAMATE SYNTHASE (NADPH) SMALL CHAIN (EC 1.4.1.13)
81	82	F RXA00075	GR00012	2757	3419	GLUTAMATE SYNTHASE (NADPH) SMALL CHAIN (EC 1.4.1.13)
83	84	RXN00198	VV0181	7916	7368	GLUTAMATE SYNTHASE (NADPH) SMALL CHAIN (EC 1.4.1.13)
85	86	F RXA00198	GR00031	2	283	GLUTAMATE SYNTHASE (NADPH) SMALL CHAIN (EC 1.4.1.13)
87	88	RXN00365	VV0196	14607	15233	GLUTAMATE SYNTHASE (NADPH) SMALL CHAIN (EC 1.4.1.13)
89	90	F RXA00365	GR00075	630	4	GLUTAMATE SYNTHASE (NADPH) SMALL CHAIN (EC 1.4.1.13)
91	92	RXA00366	GR00075	961	605	GLUTAMATE SYNTHASE (NADPH) SMALL CHAIN (EC 1.4.1.13)
93	94	RXA02072	GR00628	1259	2599	NADP-SPECIFIC GLUTAMATE DEHYDROGENASE (EC 1.4.1.4)
95	96	RXA00323	GR00057	3855	5192	GLUTAMINE SYNTHETASE (EC 6.3.1.2)
97	98	RXA00335	GR00057	19180	17750	GLUTAMINE SYNTHETASE (EC 6.3.1.2)
99	100	RXA00324	GR00057	5262	8396	GLUTAMATE-AMMONIA-LIGASE ADENYLYLTRANSFERASE (EC 2.7.7.42)
101	102	RXN03176	VV0332	2	862	GLUTAMINASE (EC 3.5.1.2)
103	104	F RXA02879	GR10017	2	862	GLUTAMINASE (EC 3.5.1.2)
105	106	RXA00278	GR00043	2612	1581	GLUTAMINE-BINDING PROTEIN PRECURSOR
107	108	RXA00727	GR00193	614	1525	GLUTAMINE-BINDING PERIPLASMIC PROTEIN PRECURSOR



Table 1 (continued)  
**Alanine and Aspartate and Asparagine metabolism**

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
109	110	RXA02139	GR00639	6739	4901	ASPARAGINE SYNTHETASE (GLUTAMINE-HYDROLYZING) (EC 6.3.5.4)
111	112	RXN00116	VV0100	26974	25814	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
113	114	F RXA00116	GR00018	510	4	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
115	116	RXN00618	VV0135	10288	9182	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
117	118	F RXA00618	GR00163	213	746	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
119	120	F RXA00627	GR00164	854	1138	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
121	122	RXA02550	GR00729	1585	275	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
123	124	RXA02193	GR00645	1942	365	ASPARTATE AMONIA-LYASE (EC 4.3.1.1)
125	126	RXA02432	GR00708	2669	1695	L-ASPARAGINASE (EC 3.5.1.1)
127	128	RXN03003	VV0138	680	6	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
129	130	RXN00508	VV0086	4701	5783	ALANINE RACEMASE (EC 5.1.1.1)
131	132	RXN00636	VV0135	20972	19944	ALANINE RACEMASE; BIOSYNTHETIC (EC 5.1.1.1)

### beta-Alanine metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
133	134	RXA02536	GR00726	8581	7826	BETA-UREIDOPROPIONASE (EC 3.5.1.6)
135	136	RX S00870				METHYLMALONATE-SEMIALDEHYDE DEHYDROGENASE (ACYLATING) (EC 1.2.1.27)
137	138	RX S02299				ASPARTATE 1-DECARBOXYLASE PRECURSOR (EC 4.1.1.11)

### Glycine and serine metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
139	140	RXA01561	GR00435	1113	2042	L-SERINE DEHYDRATASE (EC 4.2.1.13)
141	142	RXA01850	GR00525	481	1827	L-SERINE DEHYDRATASE (EC 4.2.1.13)
143	144	RXA00580	GR00156	7343	6042	SERINE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.1)
145	146	RXA01821	GR00515	10253	9876	SARCOSINE OXIDASE (EC 1.5.3.1)
147	148	RXN02263	VV0202	11783	12160	SARCOSINE OXIDASE (EC 1.5.3.1)
149	150	F RXA02263	GR00654	33454	33813	SARCOSINE OXIDASE (EC 1.5.3.1)
151	152	RXA02176	GR00641	11454	12581	PHOSPHOSERINE AMINOTRANSFERASE (EC 2.6.1.52)
153	154	RXN02758	GR00766	5082	4648	PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3)
155	156	F RXA02479	GR00717	393	4	PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3)
157	158	F RXA02758	GR00766	5082	4648	PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3)
159	160	F RXA02759	GR00766	5330	5220	PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3)
161	162	RXA02501	GR00720	15041	13977	PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3)
163	164	RXN03105	VV0074	15857	15423	SARCOSINE OXIDASE (EC 1.5.3.1)
165	166	RX S01130				D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
167	168	RX S03112				D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)

Table 1 (continued)

## Threonine metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
165	170	RXN00969	VW0149	12053	13387	HOMOSERINE DEHYDROGENASE (EC 1.1.1.3)
171	172	F RXA00974	GR00274	2623	3015	HOMOSERINE DEHYDROGENASE (EC 1.1.1.3)
173	174	RXA00970	GR00273	161	1087	HOMOSERINE KINASE (EC 2.7.1.39)
175	176	RXA00330	GR00057	12968	14410	THREONINE SYNTHASE (EC 4.2.99.2)
177	178	RXN00403	VW0086	70041	68911	HOMOSERINE O-ACETYLTRANSFERASE
179	180	F RXA00403	GR00088	723	1832	HOMOSERINE O-ACETYLTRANSFERASE (EC 2.3.1.11)
181	182	RXC01207				CYTOSOLIC PROTEIN INVOLVED IN METABOLISM OF LYSINE AND THREONINE
183	184	RXC00152				MEMBRANE ASSOCIATED PROTEIN INVOLVED IN THREONINE METABOLISM

## Metabolism of methionine and S-adenosyl methionine

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
185	186	RXA00115	GR00017	5359	4313	HOMOSERINE O-ACETYLTRANSFERASE (EC 2.3.1.31)
187	188	RXN00403	VW0086	70041	68911	HOMOSERINE O-ACETYLTRANSFERASE
189	190	F RXA00403	GR00088	723	1832	HOMOSERINE O-ACETYLTRANSFERASE (EC 2.3.1.11)
191	192	RXS03158				CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9)
193	194	F RXA00254	GR00038	2404	1811	CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9)
195	196	RXA02532	GR00726	3085	2039	CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9)
197	198	RXS03159				CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9)
199	200	F RXA02768	GR00770	1919	2521	CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9)
201	202	RXA00216	GR00032	16286	15297	5-methyltetrahydrofolate-homocysteine methyltransferase (methionine synthetase)
203	204	RXN00402	VW0086	70787	70188	O-ACETYLHOMOSERINE SULFHYDRYLASE (EC 4.2.99.10) / O-ACETYL SERINE SULFHYDRYLASE (EC 4.2.99.8)
205	206	F RXA00402	GR00088	1	576	O-ACETYLHOMOSERINE SULFHYDRYLASE (EC 4.2.99.10) / O-ACETYL SERINE SULFHYDRYLASE (EC 4.2.99.8)
207	208	RXA00405	GR00089	3289	3801	O-ACETYLHOMOSERINE SULFHYDRYLASE (EC 4.2.99.10) / O-ACETYL SERINE SULFHYDRYLASE (EC 4.2.99.8)
209	210	RXA02197	GR00645	4552	4025	5-METHYLTETRAHYDROFOLATE-HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.13)
211	212	RXN02198	VW0302	9228	11726	5-METHYLTETRAHYDROFOLATE-HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.13)
213	214	F RXA02198	GR00646	2483	6	5-METHYLTETRAHYDROFOLATE-HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.13)
215	216	RXN03074	VW0042	2238	1741	S-ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.-.-)
217	218	F RXA02906	GR10044	1142	645	S-ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.-.-)
219	220	RXN00132	VW0124	3612	5045	ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE
221	222	F RXA00132	GR00020	7728	7624	ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
223	224	F RXA01371	GR00398	2339	3634	ADENOSYLHOMOCYSTEINASE (EC 3.3.1.1)
225	226	RXN02085				5-METHYL-TETRAHYDROPTEROYL-TRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
227	228	F RXA02085	GR00629	3496	5295	5-METHYL-TETRAHYDROPTEROYL-TRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
229	230	F RXA02086	GR00629	5252	5731	5-METHYL-TETRAHYDROPTEROYL-TRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
231	232	RXN02648				5-METHYL-TETRAHYDROPTEROYL-TRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
233	234	F RXA02648	GR00751	5254	4730	5-METHYL-TETRAHYDROPTEROYL-TRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
235	236	F RXA02658	GR00752	14764	15447	5-METHYL-TETRAHYDROPTEROYL-TRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
237	238	RXC02238				PROTEIN INVOLVED IN METABOLISM OF S-ADENOSYLMETHIONINE, PURINES AND PANTOTHENATE
239	240	RXC00128				EXPORTED PROTEIN INVOLVED IN METABOLISM OF PYRIDIMES AND ADENOSYLHOMOCYSTEINE

### S-adenosyl methionine (SAM) Biosynthesis

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
241	242	RXA02240	GR00654	7160	8380	S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6)

### Cysteine metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
243	244	RXA00780	GR00206	1689	2234	SERINE ACETYLTRANSFERASE (EC 2.3.1.30)
245	246	RXA00779	GR00206	550	1482	CYSTEINE SYNTHASE (EC 4.2.99.8)
247	248	RXN00402	VV0086	70787	70188	O-ACETYLMOMOSERINE SULFHYDRYLASE (EC 4.2.99.10) / O-ACETYL-SERINE SULFHYDRYLASE (EC 4.2.99.8)
249	250	F RXA00402	GR00088	1	576	O-ACETYLMOMOSERINE SULFHYDRYLASE (EC 4.2.99.10) / O-ACETYLSERINE SULFHYDRYLASE (EC 4.2.99.8)
251	252	RXS00405				O-ACETYLMOMOSERINE SULFHYDRYLASE (EC 4.2.99.10) / O-ACETYLSERINE SULFHYDRYLASE (EC 4.2.99.8)
253	254	RXC00164				ABC TRANSPORTER ATP-BINDING PROTEIN INVOLVED IN CYSTEINE METABOLISM
255	256	RXC01191				ABC TRANSPORTER ATP-BINDING PROTEIN INVOLVED IN CYSTEINE METABOLISM

Table 1 (continued)

## Valine, leucine and isoleucine

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
257	258	RXA02646	GR00751	3856	2598	THREONINE DEHYDRATASE BIOSYNTHETIC (EC 4.2.1.16)
259	260	RXA00766	GR00204	5091	4249	BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE (EC 2.6.1.42)
261	262	RXN01690	VV0246	1296	196	BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE (EC 2.6.1.42)
263	264	F RXA01690	GR00473	1248	196	BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE (EC 2.6.1.42)
265	266	RXN01026	VV0143	9171	7513	3-ISOPROPYLMALATE DEHYDRATASE LARGE SUBUNIT (EC 4.2.1.33)
267	268	F RXA01026	GR00294	1	1602	3-ISOPROPYLMALATE DEHYDRATASE LARGE SUBUNIT (EC 4.2.1.33)
269	270	RXN01127	VV0157	4491	3472	3-ISOPROPYLMALATE DEHYDROGENASE (EC 1.1.1.85)
271	272	F RXA01132	GR00315	1349	1651	3-ISOPROPYLMALATE DEHYDROGENASE (EC 1.1.1.85)
273	274	RXN00536	VV0219	6128	7498	2-ISOPROPYLMALATE SYNTHASE (EC 4.1.3.12)
275	276	F RXA00536	GR00137	6128	7360	2-ISOPROPYLMALATE SYNTHASE (EC 4.1.3.1)
277	278	RXN02965	VV0143	7711	7121	3-ISOPROPYLMALATE DEHYDRATASE SMALL SUBUNIT (EC 4.2.1.33)
279	280	RXN01929	VV0127	47590	48402	3-METHYL-2-OXOBUTANOATE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.11)
281	282	F RXA01929	GR00555	2766	1960	/ DECARBOXYLASE (EC 4.1.1.44)
283	284	RXN01420	VV0122	15584	14643	3-METHYL-2-OXOBUTANOATE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.11)
285	286	RXS01145				4"-MYCAROSYL ISOVALERYL-COA TRANSFERASE (EC 2.---)
287	288	F RXA01145	GR00321	1075	1530	KETOL-ACID REDUCTOISOMERASE (EC 1.1.1.86)
						KETOL-ACID REDUCTOISOMERASE (EC 1.1.1.86)

## Arginine and proline metabolism

## Enzymes of proline biosynthesis:

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
289	290	RXA02375	GR00689	1449	223	GLUTAMATE 5-KINASE (EC 2.7.2.11)
291	292	RXN02382	VV0213	5162	3867	GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (EC 1.2.1.41)
293	294	F RXA02378	GR00690	624	16	GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (EC 1.2.1.41)
295	296	F RXA02382	GR00691	2493	1894	GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (EC 1.2.1.41)
297	298	RXA02499	GR00720	11883	12692	PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2)
299	300	RXS02157				ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
301	302	RXS02262				ORNITHINE CYCLODEAMINASE (EC 4.3.1.12)
303	304	RXS02970				ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
305	306	F RXA01009	GR00287	4714	5943	ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)

Table 1 (continued)

## Enzymes of proline degradation:

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
307	308	RXN00023	VV0127	68158	64703	PROLINE DEHYDROGENASE (EC 1.5.99.8) / DELTA-1- PYRROLINE-5-CARBOXYLATE DEHYDROGENASE (EC 1.5.1.12)
309	310	F RXA00023	GR00003	2	454	PROLINE DEHYDROGENASE (EC 1.5.99.8) / DELTA-1- PYRROLINE-5-CARBOXYLATE DEHYDROGENASE (EC 1.5.1.12)
311	312	F RXA02284	GR00660	3028	5	PROLINE DEHYDROGENASE (EC 1.5.99.8) / DELTA-1- PYRROLINE-5-CARBOXYLATE DEHYDROGENASE (EC 1.5.1.12)
313	314	RXC02498				PROTEIN INVOLVED IN PROLINE METABOLISM

## Synthesis of 3-Hydroxy-proline:

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
315	316	RXA01491	GR00423	5337	4687	DNA FOR L-PROLINE 3-HYDROXYLASE, COMPLETE CDS

## Enzymes of ornithine, arginine and spermidine metabolism:

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
317	318	RXA02155	GR00640	1913	3076	GLUTAMATE N-ACETYLTRANSFERASE (EC 2.3.1.35) / AMINO-ACID ACETYLTRANSFERASE (EC 2.3.1.1)
319	320	RXA02156	GR00640	3125	4075	ACETYLGLUTAMATE KINASE (EC 2.7.2.8)
321	322	RXN02153	VV0122	14106	13327	N-ACETYL-GAMMA-GLUTAMYL-PHOSPHATE REDUCTASE (EC 1.2.1.38)
323	324	F RXA02153	GR00640	757	1536	N-ACETYLGLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE
325	326	RXA02154	GR00640	1536	1826	N-ACETYLGLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE
327	328	RXA02157	GR00640	4079	5251	ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
329	330	RXS02970				ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
331	332	F RXA01009	GR00287	4714	5943	ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
333	334	RXA02158	GR00640	5268	6224	ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
335	336	RXA02160	GR00640	6914	8116	ORNITHINE CARBAMOYLTRANSFERASE (EC 2.1.3.3)
337	338	RXN02162	VV0122	6683	5253	ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5)
339	340	F RXA02161	GR00640	8180	8962	ARGININOSUCCINATE LYASE (EC 4.3.2.1)
341	342	F RXA02162	GR00640	8949	9611	ARGININOSUCCINATE LYASE (EC 4.3.2.1)
343	344	RXA02262	GR00654	32291	33436	ORNITHINE CYCLODEAMINASE (EC 4.3.1.12)
345	346	RXA00219	GR00032	19289	20230	SPERMIDINE SYNTHASE (EC 2.5.1.16)
347	348	RXA01508	GR00424	12652	14190	SPERMIDINE SYNTHASE (EC 2.5.1.16)
349	350	RXA01757	GR00498	2942	2142	PUTRESCINE OXIDASE (EC 1.4.3.10)
351	352	RXA02159	GR00640	6231	6743	ARGININE HYDROXIMATE RESISTANCE PROTEIN
353	354	RXN02154	VV0122	13327	13037	N-ACETYL-GAMMA-GLUTAMYL-PHOSPHATE REDUCTASE (EC 1.2.1.38)
355	356	RXS00147				CARBAMOYL-PHOSPHATE SYNTHASE SMALL CHAIN (EC 6.3.5.5)
357	358	RXS00905				N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)
359	360	RXS00906				N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
361	362	RXS00907				N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)
363	364	RXS02001				N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)
365	366	RXS02101				N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)
367	368	RXS02234				CARBAMOYL-PHOSPHATE SYNTHASE LARGE CHAIN (EC 6.3.5.5)
369	370	F RXA02234	GR00654	1	3198	CARBAMOYL-PHOSPHATE SYNTHASE LARGE CHAIN (EC 6.3.5.5)
371	372	RXS02565				N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)
373	374	RXS02937				N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)

  

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
375	376	RXA02194	GR00645	2897	2055	ATP PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.17)
377	378	RXA02195	GR00645	3186	2917	PHOSPHORIBOSYL-ATP PYROPHOSPHOHYDROLASE (EC 3.6.1.31)
379	380	RXA01097	GR00306	4726	4373	PHOSPHORIBOSYL-AMP CYCLOHYDROLASE (EC 3.5.4.19)
381	382	RXA01100	GR00306	7072	6335	PHOSPHORIBOSYLFORMIMINO-5-AMINOIMIDAZOLE CARBOXAMIDE RIBOTIDE ISOMERASE (EC 5.3.1.16)
383	384	RXA01101	GR00306	7726	7094	AMIDOTRANSFERASE HSH (EC 2.4.2.-)
385	386	RXN01657	VW0010	39950	39351	AMIDOTRANSFERASE HSH (EC 2.4.2.-)
387	388	F RXA01657	GR00460	2444	2944	AMIDOTRANSFERASE HSH (EC 2.4.2.-)
389	390	RXA01098	GR00306	5499	4726	HISF PROTEIN
391	392	RXN01104	VW0059	7037	6432	IMIDAZOLEGLYCEROL-PHOSPHATE DEHYDRATASE (EC 4.2.1.19)
393	394	F RXA01104	GR00306	10927	10322	IMIDAZOLEGLYCEROL-PHOSPHATE DEHYDRATASE (EC 4.2.1.19) / HISTIDINOL-PHOSPHATASE (EC 3.1.3.15)
395	396	RXN00446	VW0112	24181	23318	HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (EC 2.6.1.9)
397	398	F RXA00446	GR00108	4	525	HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (EC 2.6.1.9)
399	400	RXA01105	GR00306	12044	10947	HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (EC 2.6.1.9)
401	402	RXA01106	GR00306	13378	12053	HISTIDINOL DEHYDROGENASE (EC 1.1.1.23)
403	404	RXC00930				PROTEIN INVOLVED IN HISTIDINE METABOLISM
405	406	RXC01096				PROTEIN INVOLVED IN HISTIDINE METABOLISM
407	408	RXC01656				PROTEIN INVOLVED IN HISTIDINE METABOLISM
409	410	RXC01158				MEMBRANE SPANNING PROTEIN INVOLVED IN HISTIDINE METABOLISM

### Histidine metabolism

### Metabolism of aromatic amino acids

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
411	412	RXA02458	GR00712	3056	4345	3-PHOSPHOSHIMIMATE 1-CARBOXYVINYLTRANSFERASE (EC 2.5.1.19)
413	414	RXA02790	GR00777	5806	6948	4-AMINO-4-DEOXYCHORISMATE LYASE (EC 4.1.3.27)
415	416	RXN00954	VW0247	3197	2577	ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.18)
417	418	F RXA00954	GR00263	3	590	ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.18)
419	420	RXN00957	VW0208	1211	2764	ANTHRANILATE SYNTHASE COMPONENT I (EC 4.1.3.27)
421	422	F RXA00957	GR00264	3	1130	ANTHRANILATE SYNTHASE COMPONENT I (EC 4.1.3.27)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
423	424	RXA02687	GR00754	11306	12250	CHORISMATE MUTASE (EC 5.4.99.5) / PREPHENATE DEHYDRATASE (EC 4.2.1.51)
425	426	RXN01698	VV0134	11507	12736	CHORISMATE SYNTHASE (EC 4.6.1.4)
427	428	F RXA01698	GR00477	2	991	CHORISMATE SYNTHASE (EC 4.6.1.4)
429	430	RXA01095	GR00306	3603	2821	INDOLE-3-GLYCEROL PHOSPHATE SYNTHASE (EC 4.1.1.48)
431	432	RXA00955	GR00263	586	2007	INDOLE-3-GLYCEROL PHOSPHATE SYNTHASE (EC 4.1.1.48) / N-(5'-PHOSPHO-RIBOSYL)ANTHRANILATE ISOMERASE (EC 5.3.1.24)
433	434	RXA02814	GR00795	598	128	ISOCHORISMATE MUTASE
435	436	RXA00229	GR00033	1715	936	SHIKIMATE 5-DEHYDROGENASE (EC 1.1.1.25)
437	438	RXA02093	GR00629	12444	13247	SHIKIMATE 5-DEHYDROGENASE (EC 1.1.1.25)
439	440	RXA02791	GR00777	6968	7795	SHIKIMATE 5-DEHYDROGENASE (EC 1.1.1.25)
441	442	RXA01699	GR00477	984	1553	SHIKIMATE KINASE (EC 2.7.1.71)
443	444	RXA00952	GR00262	97	936	TRYPTOPHAN SYNTHASE ALPHA CHAIN (EC 4.2.1.20)
445	446	RXN00956	VV0247	1140	4	TRYPTOPHAN SYNTHASE BETA CHAIN (EC 4.2.1.20)
447	448	F RXA00956	GR00263	2027	3157	TRYPTOPHAN SYNTHASE BETA CHAIN (EC 4.2.1.20)
449	450	RXA00064	GR00010	2499	3776	TYROSINE AMINOTRANSFERASE (EC 2.6.1.5)
451	452	RXN00448	VV0112	33959	32940	PREPHENATE DEHYDROGENASE (EC 1.3.1.12)
453	454	F RXA00448	GR00109	3	668	PREPHENATE DEHYDROGENASE (EC 1.3.1.12)
455	456	F RXA00452	GR00110	854	1099	PREPHENATE DEHYDROGENASE (EC 1.3.1.12)
457	458	RXA00584	GR00156	11384	10260	PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE (EC 4.1.2.15)
459	460	RXA00579	GR00156	5946	4087	PARA-AMINOBENZOATE SYNTHASE COMPONENT I (EC 4.1.3.-)
461	462	RXA00958	GR00264	1130	1753	PARA-AMINOBENZOATE SYNTHASE GLUTAMINE AMIDOTRANSFERASE COMPONENT II (EC 4.1.3.-) / ANTHRANILATE SYNTHASE COMPONENT II (EC 4.1.3.27)
463	464	RXN03007	VV0208	3410	3778	ANTHRANILATE SYNTHASE COMPONENT II (EC 4.1.3.27)
465	466	RXN02918	VV0086	25447	25887	TRYPTOPHAN SYNTHASE BETA CHAIN (EC 4.2.1.20)
467	468	RXN01116	VV0182	7497	6886	3-OXOADIPATE COA-TRANSFERASE SUBUNIT B (EC 2.8.3.6)
469	470	RXN01115	VV0182	10347	11099	3-OXOADIPATE ENOL-LACTONE HYDROLASE (EC 3.1.1.24) / 4-CARBOXYMUCONOLACTONE
471	472	RXS00116	GR00018	510	4	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
473	474	F RXA00116	GR00018	510	4	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
475	476	RXS00391	GR00018	510	4	O-SUCCINYL-BENZOIC ACID--COA LIGASE (EC 6.2.1.26)
477	478	RXS00393	GR00086	4030	4911	1,4-DIHYDROXY-2-NAPHTHOATE OCTAPRENYLTRANSFERASE (EC 2.5.-.-)
479	480	F RXA00393	GR00086	4030	4911	1,4-DIHYDROXY-2-NAPHTHOATE OCTAPRENYLTRANSFERASE (EC 2.5.-.-)
481	482	RXS00446	GR00108	4	525	HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (EC 2.6.1.9)
483	484	F RXA00446	GR00108	4	525	HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (EC 2.6.1.9)
485	486	RXS00618	GR00163	213	746	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
487	488	F RXA00618	GR00163	213	746	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
489	490	F RXA00627	GR00164	854	1138	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
491	492	RXS01105	GR00164	854	1138	HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (EC 2.6.1.9)
493	494	RXS02315	GR00164	854	1138	2-SUCCINYL-6-HYDROXY-2,4-CYCLOHEXADIENE-1-CARBOXYLATE SYNTHASE / 2-OXOGlutarate decarboxylase (EC 4.1.1.71)
495	496	RXS02550	GR00164	854	1138	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
497	498	RXS02319	GR00164	854	1138	NAPHTHOATE SYNTHASE (EC 4.1.3.36)
499	500	RXS02908	GR00164	854	1138	O-SUCCINYL-BENZOIC ACID--COA LIGASE (EC 6.2.1.26)
501	502	RXS03003	GR00164	854	1138	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
503	504	RXS03026	GR00164	854	1138	3-DEHYDROQUINATE DEHYDRATASE (EC 4.2.1.10)

Table 1 (continued)

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
505	506	RXS03074				S-ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.-.-)
507	508	RXC01434				MEMBRANE SPANNING PROTEIN INVOLVED IN METABOLISM OF AROMATIC AMINO ACIDS AND RIBOFLAVIN
509	510	RXC02080				MEMBRANE SPANNING PROTEIN INVOLVED IN METABOLISM OF AROMATIC AMINO ACIDS
511	512	RXC02789				CYTOSOLIC PROTEIN INVOLVED IN METABOLISM OF AROMATIC AMINO ACIDS
513	514	RXC02295				MEMBRANE SPANNING PROTEIN INVOLVED IN METABOLISM OF AROMATIC AMINO ACIDS

### Aminobutyrate metabolism

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
515	516	RXN03063	VV0035	666	1697	4-aminobutyrate aminotransferase (EC 2.6.1.19)
517	518	RXN02970	VV0021	4714	6081	ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
519	520	F RXA01009	GR00287	4714	5943	ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)

## Vitamins, vitamin-like substances (cofactors), nutraceuticals

### Thiamine metabolism

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
521	522	RXA01551	GR00431	2945	4819	THIAMIN BIOSYNTHESIS PROTEIN THIC
523	524	RXA01019	GR00291	6	995	THIAMIN-MONOPHOSPHATE KINASE (EC 2.7.4.16)
525	526	RXA01352	GR00393	609	4	THIAMIN-PHOSPHATE PYROPHOSPHORYLASE (EC 2.5.1.3)
527	528	RXA01381	GR00403	3206	2286	THIF PROTEIN
529	530	RXA01360	GR00394	162	4	THIG PROTEIN
531	532	RXA01361	GR00394	983	378	THIG PROTEIN
533	534	RXA01208	GR00348	229	1032	HYDROXYETHYLTHIAZOLE KINASE (EC 2.7.1.50)
535	536	RXA00838	GR00227	1532	633	APBA PROTEIN
537	538	RXA02400	GR00699	1988	2557	THIAMIN BIOSYNTHESIS PROTEIN X
539	540	RXN01209	VV0270	1019	2446	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
541	542	F RXA01209	GR00348	1019	2446	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
543	544	RXN01413	VV0050	27306	27905	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
545	546	RXN01617	VV0050	22187	22858	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
547	548	F RXA01617	GR00451	2	616	PYRIDOXINE KINASE (EC 2.7.1.35)
549	550	RXS01807				CYTOSOLIC KINASE INVOLVED IN METABOLISM OF SUGARS AND THIAMIN
551	552	RXC01021				



Table 1 (continued)

## Riboflavin metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
553	554	RXN02246	VV0130	4388	5371	diaminohydroxyphosphoribosylaminopyrimidine deaminase (EC 3.5.4.26) / 5-amino-6-(5-phosphoribosylamino)uracil reductase (EC 1.1.1.193)
555	556	F RXA02246	GR00654	14299	15282	RIBG PROTEIN riboflavin-specific deaminase [EC:3.5.4.-]
557	558	RXA02247	GR00654	15286	15918	RIBOFLAVIN SYNTHASE ALPHA CHAIN (EC 2.5.1.9)
559	560	RXN02248	VV0130	6021	7286	GTP CYCLOHYDROLASE II (EC 3.5.4.25) / 3,4-DIHYDROXY-2-BUTANONE 4-PHOSPHATE SYNTHASE
561	562	F RXA02248	GR00654	15932	17197	RIBA PROTEIN - GTP cyclohydrolase II [EC:3.5.4.25]
563	564	RXN02249	VV0130	7301	7777	6,7-DIMETHYL-8-RIBITYLLUMAZINE SYNTHASE (EC 2.5.1.9)
565	566	F RXA02249	GR00654	17212	17688	RIBH PROTEIN - 6,7-dimethyl-8-ribityllumazine synthase (dmrl synthase, lumazine synthase, riboflavin synthase beta chain) [EC:2.5.1.9]
567	568	RXA02250	GR00654	17778	18356	RIBX PROTEIN
569	570	RXA01489	GR00423	3410	2388	RIBOFLAVIN KINASE (EC 2.7.1.26) / FMN ADENYLYLTRANSFERASE (EC 2.7.7.2)
571	572	RXA02135	GR00639	2809	1736	NICOTINATE-NUCLEOTIDE--DIMETHYLBENZIMIDAZOLE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.21)
573	574	RXA01489	GR00423	3410	2388	RIBOFLAVIN KINASE (EC 2.7.1.26) / FMN ADENYLYLTRANSFERASE (EC 2.7.7.2)
575	576	RXN01712	VV0191	8993	8298	RIBOFLAVIN-SPECIFIC DEAMINASE (EC 3.5.4.-)
577	578	F RXA01712	GR00484	2652	2152	RIBOFLAVIN-SPECIFIC DEAMINASE (EC 3.5.4.-)
579	580	RXN02384	VV0213	1386	679	ALPHA-RIBAZOLE-5'-PHOSPHATE PHOSPHATASE (EC 3.1.3.-)
581	582	RXN01560	VV0319	767	438	RIBOFLAVIN-SPECIFIC DEAMINASE (EC 3.5.4.-)
583	584	RXN00667	VV0109	1363	350	DRAP DEAMINASE
585	586	RXC01711				MEMBRANE SPANNING PROTEIN INVOLVED IN RIBOFLAVIN METABOLISM
587	588	RXC02380				PROTEIN INVOLVED IN RIBOFLAVIN METABOLISM
589	590	F RXA02380	GR00691	709	56	Predicted nucleotidyltransferases
591	592	RXC02921				CYTOSOLIC PROTEIN INVOLVED IN METABOLISM OF RIBOFLAVIN AND LIPIDS
593	594	RXC01434				MEMBRANE SPANNING PROTEIN INVOLVED IN METABOLISM OF AROMATIC AMINO ACIDS AND RIBOFLAVIN

## Vitamin B6 metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
595	596	RXA01807	GR00509	7868	7077	PYRIDOXINE KINASE (EC 2.7.1.35), pyridoxal/pyridoxine/pyridoxamine kinase

**Table 1 (continued)**  
**Nicotinate (nicotinic acid), nicotinamide, NAD and NADP**

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
597	598	RXN02754	VV0084	22564	23901	NICOTINATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.11)
599	600	F RXA02405	GR00701	774	4	NICOTINATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.11)
601	602	F RXA02754	GR00766	3	488	NICOTINATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.11)
603	604	RXA02112	GR00632	5600	6436	NICOTINATE-NUCLEOTIDE PYROPHOSPHORYLASE (CARBOXYLATING) (EC 2.4.2.19)
605	606	RXA02111	GR00632	4310	5593	QUINOLINATE SYNTHETASE A

### NAD Biosynthesis

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
607	608	RXA01073	GR00300	1274	2104	NH(3)-DEPENDENT NAD(+) SYNTHETASE (EC 6.3.5.1)
609	610	RXN02754	VV0084	22564	23901	NICOTINATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.11)

### Pantothenate and Coenzyme A (CoA) biosynthesis

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
611	612	RXA02299	GR00662	10452	10859	ASPARTATE 1-DECARBOXYLASE PRECURSOR (EC 4.1.1.11)
613	614	RXA01928	GR00555	1957	1121	PANTOATE--BETA-ALANINE LIGASE (EC 6.3.2.1)
615	616	RXN01929	VV0127	47590	48402	3-METHYL-2-OXOBUTANOATE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.11) / DECARBOXYLASE (EC 4.1.1.44)
617	618	F RXA01929	GR00555	2766	1960	3-METHYL-2-OXOBUTANOATE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.11)
619	620	RXA01521	GR00424	25167	25964	PANTOATE--BETA-ALANINE LIGASE (EC 6.3.2.1)
621	622	RXS01145				KETOL-ACID REDUCTOISOMERASE (EC 1.1.1.86)
623	624	F RXA01145	GR00321	1075	1530	KETOL-ACID REDUCTOISOMERASE (EC 1.1.1.86)
625	626	RXA02239	GR00654	5784	7049	DNA/PANTOTHENATE METABOLISM FLAVOPROTEIN
627	628	RXA00581	GR00156	7572	8540	PANTOTHENATE KINASE (EC 2.7.1.33)
629	630	RXS00838				2-DEHYDROPANTOATE 2-REDUCTASE (EC 1.1.1.169)
631	632	RXC02238				PROTEIN INVOLVED IN METABOLISM OF S-ADENOSYLMETHIONINE, PURINES AND PANTOTHENATE

### Biotin metabolism

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
633	634	RXN03058	VV0028	8272	8754	BIOTIN SYNTHESIS PROTEIN BIOC

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
635	636	F RXA02903	GR10040	11532	12014	BIOTIN SYNTHESIS PROTEIN BIOC
637	638	RXA00166	GR00025	3650	4309	BIOTIN SYNTHESIS PROTEIN BIOC
639	640	RXA00633	GR00166	3556	2288	ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE (EC 2.6.1.62)
641	642	RXA00632	GR00166	2281	1610	DETHIOBIOTIN SYNTHETASE (EC 6.3.3.3)
643	644	RXA00295	GR00047	3407	4408	BIOTIN SYNTHASE (EC 2.8.1.6)
645	646	RXA00223	GR00032	23967	22879	NIFS PROTEIN
647	648	RXN00262	VV0123	16681	15608	NIFS PROTEIN
649	650	F RXA00262	GR00040	79	897	NIFS PROTEIN
651	652	RXN00435	VV0112	10037	11209	NIFS PROTEIN
653	654	F RXA00435	GR00100	3563	2949	NIFS PROTEIN
655	656	F RXA02801	GR00782	438	4	NIFS PROTEIN
657	658	RXA02516	GR00723	1724	2986	NIFS PROTEIN
659	660	RXA02517	GR00723	2989	3435	NIFU PROTEIN

## Lipoic Acid

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
661	662	RXA01747	GR00495	2506	3549	LIPIC ACID SYNTHETASE
663	664	RXA01746	GR00495	1614	2366	LIPATE-PROTEIN LIGASE B (EC 6.---)
665	666	RXA02106	GR00632	472	1527	LIPATE-PROTEIN LIGASE A (EC 6.---)
667	668	RXS01183				DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE COMPONENT (E2) OF 2- OXOGLUTARATE DEHYDROGENASE COMPLEX (EC 2.3.1.61)
669	670	RXS01260				LIPAMIDE DEHYDROGENASE COMPONENT (E3) OF BRANCHED-CHAIN ALPHA-KETO ACID DEHYDROGENASE COMPLEX (EC 1.8.1.4)
671	672	RXS01261				LIPAMIDE DEHYDROGENASE COMPONENT (E3) OF BRANCHED-CHAIN ALPHA-KETO ACID DEHYDROGENASE COMPLEX (EC 1.8.1.4)

## Folate biosynthesis

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
673	674	RXA02717	GR00758	18281	17400	5,10-METHYLENETETRAHYDROFOLATE REDUCTASE (EC 1.7.99.5)
675	676	RXN02027	VV0296	503	1003	5-FORMYLTETRAHYDROFOLATE CYCLO-LIGASE (EC 6.3.3.2)
677	678	F RXA02027	GR00616	500	6	5-FORMYLTETRAHYDROFOLATE CYCLO-LIGASE (EC 6.3.3.2)
679	680	RXA00106	GR00014	17469	17924	DIHYDROFOLATE REDUCTASE (EC 1.5.1.3)
681	682	RXN01321	VV0082	8868	9788	FORMYLTETRAHYDROFOLATE DEFORMYLASE (EC 3.5.1.10)
683	684	F RXA01321	GR00384	23	559	FORMYLTETRAHYDROFOLATE DEFORMYLASE (EC 3.5.1.10)
685	686	RXA00461	GR00116	428	1279	METHYLENETETRAHYDROFOLATE DEHYDROGENASE (EC 1.5.1.5) / METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE (EC 3.5.4.9)
687	688	RXA01514	GR00424	20922	21509	GTP CYCLOHYDROLASE I (EC 3.5.4.16)
689	690	RXA01516	GR00424	22360	22749	DIHYDRONEOPTERIN ALDOLASE (EC 4.1.2.25)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
691	692	RXA01515	GR00424	21513	22364	DIHYDROPTEROATE SYNTHASE (EC 2.5.1.15)
693	694	RXA02024	GR00613	4026	4784	DIHYDROPTEROATE SYNTHASE (EC 2.5.1.15)
695	696	RXA00106	GR00014	17469	17924	DIHYDROFOLATE REDUCTASE (EC 1.5.1.3)
697	698	RXA00989	GR00280	2903	1371	FOLYLPOLYGLUTAMATE SYNTHASE (EC 6.3.2.17)
699	700	RXA01517	GR00424	22752	23228	2-AMINO-4-HYDROXY-5-HYDROXYMETHYLDIHYDROPTERIDINE PYROPHOSPHOKINASE (EC 2.7.6.3)
701	702	RXA00579	GR00156	5946	4087	PARA-AMINOBENZOATE SYNTHASE COMPONENT I (EC 4.1.3.-)
703	704	RXA00958	GR00264	1130	1753	PARA-AMINOBENZOATE SYNTHASE GLUTAMINE AMIDOTRANSFERASE COMPONENT II (EC 4.1.3.-) / ANTHRANILATE SYNTHASE COMPONENT II (EC 4.1.3.27)
705	706	RXA02790	GR00777	5806	6948	4-AMINO-4-DEOXYCHORISMATE LYASE (EC 4.-.-.-)
707	708	RXA00106	GR00014	17469	17924	DIHYDROFOLATE REDUCTASE (EC 1.5.1.3)
709	710	RXN02198	VV0302	9228	11726	5-METHYLTETRAHYDROFOLATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.13)
711	712	F RXA02198	GR00646	2483	6	5-METHYLTETRAHYDROFOLATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.13)
713	714	RXN02085	VV0126	8483	10717	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE
715	716	F RXA02085	GR00629	3496	5295	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
717	718	F RXA02086	GR00629	5252	5731	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
719	720	RXN02648				5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
721	722	F RXA02648	GR00751	5254	4730	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
723	724	F RXA02658	GR00752	14764	15447	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
725	726	RXS02197				5-METHYLTETRAHYDROFOLATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.13)
727	728	RXC00988				PROTEIN INVOLVED IN FOLATE METABOLISM
729	730	RXC01518				MEMBRANE SPANNING PROTEIN INVOLVED IN FOLATE METABOLISM
731	732	RXC01942				ATP-BINDING PROTEIN INVOLVED IN FOLATE METABOLISM

### Molybdopterin Metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
733	734	RXN02802	VV0112	17369	16299	MOLYBDOPTERIN BIOSYNTHESIS MOEB PROTEIN
735	736	F RXA02802	GR00783	7	474	MOLYBDOPTERIN BIOSYNTHESIS MOEB PROTEIN
737	738	F RXA00438	GR00103	362	796	MOLYBDOPTERIN BIOSYNTHESIS MOEB PROTEIN
739	740	RXN00437	VV0112	17824	17369	MOLYBDOPTERIN (MPT) CONVERTING FACTOR, SUBUNIT 2
741	742	F RXA00437	GR00103	3	362	MOLYBDOPTERIN (MPT) CONVERTING FACTOR, SUBUNIT 2
743	744	RXN00439	VV0112	18742	18275	MOLYBDOPTERIN CO-FACTOR SYNTHESIS PROTEIN
745	746	F RXA00439	GR00104	2	196	MOLYBDOPTERIN CO-FACTOR SYNTHESIS PROTEIN
747	748	F RXA00442	GR00105	830	1087	MOLYBDOPTERIN CO-FACTOR SYNTHESIS PROTEIN

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
749	750	RXA00440	GR00104	196	654	MOLYBDENUM COFACTOR BIOSYNTHESIS PROTEIN CB
751	752	RXN00441	VV0112	19942	18779	MOLYBDOPTERIN CO-FACTOR SYNTHESIS PROTEIN
753	754	F RXA00441	GR00105	2	793	MOLYBDOPTERIN CO-FACTOR SYNTHESIS PROTEIN
755	756	RXN02085				5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE
						METHYLTRANSFERASE (EC 2.1.1.14)
757	758	F RXA02085	GR00629	3496	5295	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE
						METHYLTRANSFERASE (EC 2.1.1.14)
759	760	F RXA02086	GR00629	5252	5731	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE
						METHYLTRANSFERASE (EC 2.1.1.14)
761	762	RXN02648				5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE
						METHYLTRANSFERASE (EC 2.1.1.14)
763	764	F RXA02648	GR00751	5254	4730	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE
						METHYLTRANSFERASE (EC 2.1.1.14)
765	766	F RXA02658	GR00752	14764	15447	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE
						METHYLTRANSFERASE (EC 2.1.1.14)
767	768	RXA01516	GR00424	22360	22749	DIHYDRONEOPTERIN ALDOLASE (EC 4.1.2.25)
769	770	RXA01515	GR00424	21513	22364	DIHYDROPTEROATE SYNTHASE (EC 2.5.1.15)
771	772	RXA02024	GR00613	4026	4784	DIHYDROPTEROATE SYNTHASE (EC 2.5.1.15)
773	774	RXA01719	GR00488	1264	704	MOLYBDOPTERIN-GUANINE DINUCLEOTIDE BIOSYNTHESIS PROTEIN A
775	776	RXA01720	GR00488	2476	1268	MOLYBDOPTERIN BIOSYNTHESIS MOEA PROTEIN
777	778	RXS03223				MOLYBDOPTERIN BIOSYNTHESIS MOEA PROTEIN
779	780	F RXA01970	GR00568	2	1207	MOLYBDOPTERIN BIOSYNTHESIS MOEA PROTEIN
781	782	RXA02629	GR00748	1274	690	MOLYBDOPTERIN BIOSYNTHESIS CNX1 PROTEIN
783	784	RXA02318	GR00665	9684	9962	(D90909) pterin-4a-carbinolamine dehydratase [Synecocystis sp.]
785	786	RXA01517	GR00424	22752	23228	2-AMINO-4-HYDROXY-6-HYDROXYMETHYLDIHYDROPTERIDINE
						PYROPHOSPHOKINASE (EC 2.7.6.3)
787	788	RXN01304				MOLYBDOPTERIN BIOSYNTHESIS MOG PROTEIN
789	790	RXS02556	VV0148	4449	4934	FLAVOHEMOPROTEIN / DIHYDROPTERIDINE REDUCTASE (EC 1.6.99.7)
791	792	RXS02560				OXYGEN-INSENSITIVE NAD(P)H NITROREDUCTASE (EC 1.-.-.-) / DIHYDROPTERIDINE REDUCTASE (EC 1.6.99.7)

Vitamin B<sub>12</sub>, porphyrins and heme metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
793	794	RXA00382	GR00082	2752	1451	GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE (EC 5.4.3.8)
795	796	RXA00156	GR00023	10509	9400	FERROCHELATASE (EC 4.99.1.1)
797	798	RXA00624	GR00163	7910	8596	FERROCHELATASE (EC 4.99.1.1)
799	800	RXA00306	GR00051	2206	1274	HEMK PROTEIN
801	802	RXA00884	GR00242	10137	11276	OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III OXIDASE (EC 1.-.-.-)
803	804	RXN02503	VV0007	22456	22854	PORPHOBILINOGEN DEAMINASE (EC 4.3.1.8)
805	806	F RXA02503	GR00720	16906	17340	PORPHOBILINOGEN DEAMINASE (EC 4.3.1.8)
807	808	RXA00377	GR00081	1427	306	UROPORPHYRINOGEN DECARBOXYLASE (EC 4.1.1.37)
809	810	RXN02504	VV0007	22805	23362	PORPHOBILINOGEN DEAMINASE (EC 4.3.1.8)
811	812	F RXA02504	GR00720	17379	17816	PORPHOBILINOGEN DEAMINASE (EC 4.3.1.8)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
813	814	RXN01162	VW0088	1849	524	PRECORRIN-6Y METHYLASE (EC 2.1.1.-)
815	816	F RXA01162	GR00330	1248	4	PRECORRIN-6Y METHYLASE (EC 2.1.1.-)
817	818	RXA01162	GR00474	1498	749	UROPORPHYRIN-III C-METHYLTRANSFERASE (EC 2.1.1.107)
819	820	RXN00371	VW0226	4180	5973	UROPORPHYRIN-III C-METHYLTRANSFERASE (EC 2.1.1.107) / UROPORPHYRIN-III SYNTHASE (EC 4.2.1.75)
821	822	F RXA00371	GR00078	929	6	UROPORPHYRIN-III C-METHYLTRANSFERASE (EC 2.1.1.107) / UROPORPHYRIN-III SYNTHASE (EC 4.2.1.75)
823	824	F RXA00374	GR00079	1102	371	UROPORPHYRIN-III C-METHYLTRANSFERASE (EC 2.1.1.107) / UROPORPHYRIN-III SYNTHASE (EC 4.2.1.75)
825	826	RXN00383	VW0223	4206	2863	PROTOPORPHYRIN-III SYNTHASE (EC 1.3.3.4)
827	828	F RXA00376	GR00081	287	6	PROTOPORPHYRIN-III SYNTHASE (EC 1.3.3.4)
829	830	F RXA00383	GR00082	3876	2863	PROTOPORPHYRIN-III SYNTHASE (EC 1.3.3.4)
831	832	RXA01253	GR00365	2536	1787	PROTOPORPHYRIN-III SYNTHASE (EC 1.3.3.4)
833	834	RXA02134	GR00639	1721	801	COBYRIC ACID SYNTHASE
835	836	RXA02135	GR00639	2809	1736	COBALAMIN (5'-PHOSPHATE) SYNTHASE
837	838	RXA02136	GR00639	3362	2841	NICOTINATE-NUCLEOTIDE--DIMETHYLBENZIMIDAZOLE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.21)
839	840	RXN03114	VW0088	1	552	COBINAMIDE KINASE / COBINAMIDE PHOSPHATE GUANYLYLTRANSFERASE
841	842	RXN01810	VW0082	1739	663	COBG PROTEIN (EC 1.-.-.-)
843	844	RXS03205				HEMIN-BINDING PERIPLASMIC PROTEIN HMUT PRECURSOR
845	846	F RXA00306				HEMK PROTEIN
847	848	RXC01715				HEMK PROTEIN CYTOSOLIC PROTEIN INVOLVED IN PORPHYRIN METABOLISM

## Vitamin C precursors

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
849	850	RXN00420	VW0112	2511	1048	L-GULONOLACTONE OXIDASE (EC 1.1.3.8)
851	852	F RXA00420	GR00096	2	541	L-GULONOLACTONE OXIDASE (EC 1.1.3.8)
853	854	F RXA00426	GR00097	1737	2258	L-GULONOLACTONE OXIDASE (EC 1.1.3.8)
855	856	RXN00708	VW0005	4678	3872	2,5-DIKETO-D-GLUCONIC ACID REDUCTASE (EC 1.1.1.-)
857	858	F RXA00708	GR00185	2030	1359	2,5-DIKETO-D-GLUCONIC ACID REDUCTASE (EC 1.1.1.-)
859	860	RXA02373	GR00688	1540	626	2,5-DIKETO-D-GLUCONIC ACID REDUCTASE (EC 1.1.1.-) oxoglutarate semialdehyde dehydrogenase (EC 1.2.1.-)
861	862	RXS00389				ACETOACETYL-COA REDUCTASE (EC 1.1.1.36)
863	864	RXS00419				MEMBRANE SPANNING PROTEIN INVOLVED IN METABOLISM OF VITAMIN C PRECURSORS
865	866	RXC00416				OXIDOREDUCTASE INVOLVED IN METABOLISM OF VITAMIN C PRECURSORS
867	868	RXC02206				

## Vitamin K2

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
869	870	RXS03074				S-ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.-.-)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
871	872	F RXA02806	GR10044	1142	645	S-ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.-.-)
873	874	RXA02315	GR00665	8011	6383	2-SUCCINYL-6-HYDROXY-2,4-CYCLOHEXADIENE-1-CARBOXYLATE SYNTHASE /2-OXOGLUTARATE DECARBOXYLASE (EC 4.1.1.71)
875	876	RXA02319	GR00665	9977	10933	NAPHTHOATE SYNTHASE (EC 4.1.3.36)
877	878	RXS00393				1,4-DIHYDROXY-2-NAPHTHOATE OCTAPRENYLTRANSFERASE (EC 2.5.-.-)
879	880	F RXA00393	GR00086	4030	4911	1,4-DIHYDROXY-2-NAPHTHOATE OCTAPRENYLTRANSFERASE (EC 2.5.-.-)
881	882	RXA00391	GR00086	2031	2750	O-SUCCINYL BENZOIC ACID--COA LIGASE (EC 6.2.1.26)
883	884	RXS02908				O-SUCCINYL BENZOIC ACID--COA LIGASE (EC 6.2.1.26)

### Ubiquinone biosynthesis

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
885	886	RXA00997	GR00283	2389	1808	3-DEMETHYLBUBIQUINONE-9 3-METHYLTRANSFERASE (EC 2.1.1.64)
887	888	RXA02189	GR00642	986	249	3-DEMETHYLBUBIQUINONE-9 3-METHYLTRANSFERASE (EC 2.1.1.64)
889	890	RXA02311	GR00665	3073	2384	3-DEMETHYLBUBIQUINONE-9 3-METHYLTRANSFERASE (EC 2.1.1.64)
891	892	RXN02912	VV0135	13299	12547	UBIQUINONE/MENAQUINONE BIOSYNTHESIS METHYLTRANSFERASE UBIE (EC 2.1.1.-)
893	894	RXS00998				COMA OPERON PROTEIN 2

## Purines and Pyrimidines and other Nucleotides

### Regulation of purine and pyrimidine biosynthesis pathways

### Purine metabolism

### Purine Biosynthesis

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
895	896	RXA01215	GR00352	1187	213	RIBOSE-PHOSPHATE PYROPHOSPHOKINASE PRPP synthetase (EC 2.7.6.1)
897	898	RXN00558	VV0103	8235	9581	AMIDOPHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.14)
899	900	F RXA00558	GR00148	61	501	AMIDOPHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.14)
901	902	RXN00626	VV0135	11624	10362	PHOSPHORIBOSYLAMINE--GLYCINE LIGASE (EC 6.3.4.13)
903	904	F RXA00629	GR00165	1450	1713	PHOSPHORIBOSYLAMINE--GLYCINE LIGASE (EC 6.3.4.13)
905	906	F RXA00626	GR00164	1	780	PHOSPHORIBOSYLAMINE--GLYCINE LIGASE (EC 6.3.4.13)
907	908	RXA02623	GR00746	4875	4285	PHOSPHORIBOSYLAMINE--GLYCINE LIGASE (EC 6.3.4.13) / PHOSPHORIBOSYLFORMYLGLYCINAMIDE FORMYLTRANSFERASE (EC 2.1.2.-)
909	910	RXA01442	GR00418	10277	9054	PHOSPHORIBOSYLGLYCINAMIDE FORMYLTRANSFERASE (EC 2.1.2.-)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
911	912	RXN00537	VV0103	3351	5636	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE (EC 6.3.5.3)
913	914	F RXA02805	GR00786	54	638	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE (EC 6.3.5.3)
915	916	F RXA00537	GR00138	23	697	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE (EC 6.3.5.3)
917	918	F RXA00561	GR00150	2	280	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE (EC 6.3.5.3)
919	920	RXA00541	GR00139	2269	2937	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE (EC 6.3.5.3)
921	922	RXA00620	GR00163	3049	3939	PHOSPHORIBOSYLAMIDIMIDAZOLE-SUCCINOCARBOXAMIDE SYNTHASE (EC 6.3.2.6)
923	924	RXN00770	VV0103	9614	10783	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE CYCLO-LIGASE (EC 6.3.3.1)
925	926	F RXA00557	GR00147	15	818	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE CYCLO-LIGASE (EC 6.3.3.1)
927	928	F RXA00770	GR00204	7809	7495	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE CYCLO-LIGASE (EC 6.3.3.1)
929	930	RXN02345	VV0078	4788	5984	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE ATPASE SUBUNIT (EC 4.1.1.21)
931	932	F RXA02345	GR00676	1534	725	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE ATPASE SUBUNIT (EC 4.1.1.21)
933	934	RXN02350	VV0078	8369	8863	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE CATALYTIC SUBUNIT (EC 4.1.1.21)
935	936	F RXA02346	GR00677	127	5	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE CATALYTIC SUBUNIT (EC 4.1.1.21)
937	938	F RXA02350	GR00678	1120	911	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE CATALYTIC SUBUNIT (EC 4.1.1.21)
939	940	RXA01087	GR00304	498	1373	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE (EC 4.1.1.21)
941	942	RXA00619	GR00163	793	2220	ADENYLOSUCCINATE LYASE (EC 4.3.2.2)
943	944	RXA02622	GR00746	4274	2715	PHOSPHORIBOSYLAMINOIMIDAZOLECARBOXAMIDE FORMYLTRANSFERASE (EC 2.1.2.3) / IMP CYCLOHYDROLASE (EC 3.5.4.10)

## GMP, GDP, AMP and ADP synthesis, from inosine-5'-monophosphate (IMP)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
945	946	RXN00488	VV0086	19066	20583	INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (EC 1.1.1.205)
947	948	F RXA00492	GR00122	1171	1644	INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (EC 1.1.1.205)
949	950	F RXA00488	GR00121	1	534	INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (EC 1.1.1.205)
951	952	RXA02469	GR00715	1927	497	INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (EC 1.1.1.205)
953	954	RXN00487	VV0086	23734	25302	GMP SYNTHASE [GLUTAMINE-HYDROLYZING] (EC 6.3.5.2)
955	956	F RXA00487	GR00120	712	2097	GMP SYNTHASE (EC 6.3.4.1)
957	958	RXA02237	GR00654	4577	5146	GUANYLATE KINASE (EC 2.7.4.8)
959	960	RXA01446	GR00418	17765	16476	ADENYLOSUCCINATE SYNTHETASE (EC 6.3.4.4)
961	962	RXA00619	GR00163	793	2220	ADENYLOSUCCINATE LYASE (EC 4.3.2.2)
963	964	RXA00688	GR00179	10443	10985	ADENYLYATE KINASE (EC 2.7.4.3)
965	966	RXA00266	GR00040	3769	3362	NUCLEOSIDE DIPHOSPHATE KINASE (EC 2.7.4.6)



Table 1 (continued)

**GMP/AMP degrading activities**

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
967	968	RXA00489	GR00121	654	1775	GMP REDUCTASE (EC 1.6.6.8)
969	970	RXN02281	VV0152	1993	3323	AMP NUCLEOSIDASE (EC 3.2.2.4)
971	972	F RXA02281	GR00659	1101	34	AMP NUCLEOSIDASE (EC 3.2.2.4)

**Pyrimidine metabolism****Pyrimidine biosynthesis de novo:**

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
973	974	RXA00147	GR00022	9722	10900	CARBAMOYL-PHOSPHATE SYNTHASE SMALL CHAIN (EC 6.3.5.5)
975	976	RXA00145	GR00022	7258	8193	ASPARTATE CARBAMOYLTRANSFERASE CATALYTIC CHAIN (EC 2.1.3.2)
977	978	RXA00146	GR00022	8249	9589	DIHYDROOROTASE (EC 3.5.2.3)
979	980	RXA02208	GR00647	2	1003	DIHYDROOROTATE DEHYDROGENASE (EC 1.3.3.1)
981	982	RXA01660	GR00462	591	1142	OROTATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.10)
983	984	RXA02235	GR00654	3207	4040	OROTIDINE 5'-PHOSPHATE DECARBOXYLASE (EC 4.1.1.23)
985	986	RXN01892	VV0150	3020	3748	URIDYLATE KINASE (EC 2.7.4.-)
987	988	F RXA01892	GR00542	47	775	URIDYLATE KINASE (EC 2.7.4.-)
989	990	RXA00105	GR00014	16672	17346	THYMIDYLATE SYNTHASE (EC 2.1.1.45)
991	992	RXA00131	GR00020	7621	7013	THYMIDYLATE KINASE (EC 2.7.4.9)
993	994	RXA00266	GR00040	3769	3362	NUCLEOSIDE DIPHOSPHATE KINASE (EC 2.7.4.6)
995	996	RXA00718	GR00188	4576	5283	CYTIDYLATE KINASE (EC 2.7.4.14)
997	998	RXA01599	GR00447	8780	10441	CTP SYNTHASE (EC 6.3.4.2)
999	1000	RXN02234	VV0134	24708	28046	CARBAMOYL-PHOSPHATE SYNTHASE LARGE CHAIN (EC 6.3.5.5)
1001	1002	F RXA02234	GR00654	1	3198	CARBAMOYL-PHOSPHATE SYNTHASE LARGE CHAIN (EC 6.3.5.5)
1003	1004	RXN00450	VV0112	34491	34814	CYTOSINE DEAMINASE (EC 3.5.4.1)
1005	1006	F RXA00450	GR00110	322	5	CYTOSINE DEAMINASE (EC 3.5.4.1)
1007	1008	RXN02272	VV0020	15566	16810	CYTOSINE DEAMINASE (EC 3.5.4.1)
1009	1010	F RXA02272	GR00655	6691	7935	CREATININE DEAMINASE (EC 3.5.4.21)
1011	1012	RXN03004	VV0237	1862	2341	DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE (EC 3.5.4.13)
1013	1014	RXN03137	VV0129	9680	9579	THYMIDYLATE SYNTHASE (EC 2.1.1.45)
1015	1016	RXN03171	VV0328	568	1080	URACIL PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.9)
1017	1018	F RXA02857	GR10003	570	1082	URACIL PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.9)

**Table 1 (continued)**  
Purine and pyrimidine base, nucleoside and nucleotide salvage, interconversion, reduction and degradation:  
Purines:

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
1019	1020	RXA02771	GR00772	1329	1883	ADENINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.7)
1021	1022	RXA01512	GR00424	17633	18232	HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8)
1023	1024	RXA02031	GR00618	3820	3347	XANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.22)
1025	1026	RXA00981	GR00276	3388	4017	GTP PYROPHOSPHOKINASE (EC 2.7.6.5)
1027	1028	RXN02772	VV0171	2045	1011	GUANOSINE-3',5'-BIS(DIPHOSPHATE) 3'-PYROPHOSPHOHYDROLASE (EC 3.1.7.2)
1029	1030	F RXA02772	GR00772	1962	2741	GUANOSINE-3',5'-BIS(DIPHOSPHATE) 3'-PYROPHOSPHOHYDROLASE (EC 3.1.7.2)
1031	1032	F RXA02773	GR00772	2741	2902	GUANOSINE-3',5'-BIS(DIPHOSPHATE) 3'-PYROPHOSPHOHYDROLASE (EC 3.1.7.2)
1033	1034	RXA01835	GR00517	3147	3677	GUANOSINE-3',5'-BIS(DIPHOSPHATE) 3'-PYROPHOSPHOHYDROLASE (EC 3.1.7.2)
1035	1036	RXA01483	GR00422	19511	18240	DEOXYGUANOSINETRIPHOSPHATE TRIPHOSPHOHYDROLASE (EC 3.1.5.1)
1037	1038	RXN01027	VV0143	5761	6768	DIADENOSINE 5',5''-P <sub>1</sub> ,P <sub>4</sub> -TETRAPHOSPHATE HYDROLASE (EC 3.6.1.17)
1039	1040	F RXA01024	GR00293	661	5	DIADENOSINE 5',5''-P <sub>1</sub> ,P <sub>4</sub> -TETRAPHOSPHATE HYDROLASE (EC 3.6.1.17)
1041	1042	F RXA01027	GR00294	2580	2347	DIADENOSINE 5',5''-P <sub>1</sub> ,P <sub>4</sub> -TETRAPHOSPHATE HYDROLASE (EC 3.6.1.17)
1043	1044	RXA01528	GR00425	5653	5126	DIADENOSINE 5',5''-P <sub>1</sub> ,P <sub>4</sub> -TETRAPHOSPHATE HYDROLASE (EC 3.6.1.17)
1045	1046	RXA00072	GR00012	446	6	PHOSPHOADENOSINE PHOSPHOSULFATE REDUCTASE (EC 1.8.99.4)
1047	1048	RXA01878	GR00537	1239	2117	DIMETHYLADENOSINE TRANSFERASE (EC 2.1.1.-)
1049	1050	RXN02281	VV0152	1893	3323	AMP NUCLEOSIDASE (EC 3.2.2.4)
1051	1052	F RXA02281	GR00659	1101	34	AMP NUCLEOSIDASE (EC 3.2.2.4)
1053	1054	RXN01240	VV0090	30442	29420	GTP PYROPHOSPHOKINASE (EC 2.7.6.5)
1055	1056	RXN02008	VV0171	1138	5	GUANOSINE-3',5'-BIS(DIPHOSPHATE) 3'-PYROPHOSPHOHYDROLASE (EC 3.1.7.2)

#### Pyrimidine and purine metabolism:

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
1057	1058	RXN01940	VV0120	10268	9333	INOSINE-URIDINE PREFERRING NUCLEOSIDE HYDROLASE (EC 3.2.2.1)
1059	1060	F RXA01940	GR00557	3	581	INOSINE-URIDINE PREFERRING NUCLEOSIDE HYDROLASE (EC 3.2.2.1)
1061	1062	RXA02559	GR00731	5418	6320	INOSINE-URIDINE PREFERRING NUCLEOSIDE HYDROLASE (EC 3.2.2.1)
1063	1064	RXA02497	GR00720	10059	10985	EXOPOLYPHOSPHATASE (EC 3.6.1.11)
1065	1066	RXN01079	VV0084	38084	35982	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE ALPHA CHAIN (EC 1.17.4.1)
1067	1068	F RXA01079	GR00301	693	4	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE ALPHA CHAIN (EC 1.17.4.1)
1069	1070	F RXA01084	GR00302	3402	2062	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE ALPHA CHAIN (EC 1.17.4.1)
1071	1072	RXN01920	VV0084	32843	31842	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE 2 BETA CHAIN (EC 1.17.4.1)
1073	1074	F RXA01920	GR00550	1321	908	RIBONUCLEOTIDE REDUCTASE SUBUNIT R2F
1075	1076	RXA01080	GR00301	1240	797	NRDI PROTEIN
1077	1078	RXA00867	GR00237	1	627	POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (EC 2.7.7.8)
1079	1080	RXA01416	GR00413	2	631	POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (EC 2.7.7.8)
1081	1082	RXA01486	GR00423	660	4	POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (EC 2.7.7.8)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
1083	1084	RXA01678	GR00467	7162	7689	2',3'-CYCLIC-NUCLEOTIDE 2'-PHOSPHODIESTERASE (EC 3.1.4.16)
1085	1086	RXA01679	GR00467	7729	8964	2',3'-CYCLIC-NUCLEOTIDE 2'-PHOSPHODIESTERASE (EC 3.1.4.16)
1087	1088	RXN01488	VV0139	39842	40789	INOSINE-URIDINE PREFERRING NUCLEOSIDE HYDROLASE (EC 3.2.2.1)
1089	1090	RXC00540				CYTOSOLIC PROTEIN INVOLVED IN PURINE METABOLISM
1091	1092	RXC00560				PROTEIN INVOLVED IN PURINE METABOLISM
1093	1094	RXC01088				CYTOSOLIC PROTEIN INVOLVED IN PURINE METABOLISM
1095	1096	RXC02624				MEMBRANE SPANNING PROTEIN INVOLVED IN PURINE METABOLISM
1097	1098	RXC02665				PROTEIN INVOLVED IN PURINE METABOLISM
1099	1100	RXC02770				LIPOPROTEIN INVOLVED IN PURINE METABOLISM
1101	1102	RXC02238				PROTEIN INVOLVED IN METABOLISM OF S-ADENOSYLMETHIONINE, PURINES AND PANTOTHENATE
1103	1104	RXC01946				ABC TRANSPORTER ATP-BINDING PROTEIN INVOLVED IN PURINE METABOLISM

## Pyrimidines:

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
1105	1106	RXN03171	VV0328	568	1080	URACIL PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.9)
1107	1108	F RXA02857	GR10003	570	1082	URACIL PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.9)
1109	1110	RXN00450	VV0112	34491	34814	CYTOSINE DEAMINASE (EC 3.5.4.1)
1111	1112	F RXA00450	GR00110	322	5	CYTOSINE DEAMINASE (EC 3.5.4.1)
1113	1114	RXA00465	GR00117	337	828	CYTOSINE DEAMINASE (EC 3.5.4.1)
1115	1116	RXA00717	GR00188	3617	4576	RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE B (EC 4.2.1.70)
1117	1118	RXA01894	GR00542	1622	2476	PHOSPHATIDATE CYTIDYLTRANSFERASE (EC 2.7.7.41)
1119	1120	RXA02536	GR00726	8581	7826	BETA-UREIDOPROPIONASE (EC 3.5.1.6)
1121	1122	RXN01209	VV0270	1019	2446	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
1123	1124	F RXA01209	GR00348	1019	2446	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
1125	1126	RXN01617	VV0050	22187	22858	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
1127	1128	F RXA01617	GR00451	2	616	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
1129	1130	RXC01600				CYTOSOLIC PROTEIN INVOLVED IN PYRIMIDINE METABOLISM
1131	1132	RXC01622				CYTOSOLIC PROTEIN INVOLVED IN PYRIMIDINE METABOLISM
1133	1134	RXC00128				EXPORTED PROTEIN INVOLVED IN METABOLISM OF PYRIDINES AND ADENOSYLMOCYSTEINE
1135	1136	RXC01709				CYTOSOLIC PROTEIN INVOLVED IN PYRIMIDINE METABOLISM
1137	1138	RXC02207				EXPORTED PROTEIN INVOLVED IN PYRIMIDINE METABOLISM

Table 1 (continued)

## Sugars

## Trehalose

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
1139	1140	RXA00347	GR00065	246	1013	TREHALOSE-PHOSPHATASE (EC 3.1.3.12)
1141	1142	RXN01239	VV0090	32921	30489	maltooligosyltrehalose synthase
1143	1144	F RXA01239	GR00358	5147	7579	maltooligosyltrehalose synthase
1145	1146	RXA02645	GR00751	714	2543	maltooligosyltrehalose trehalohydrolase
1147	1148	RXN02355	VV0051	735	4	TREHALOSE/MALTOSE BINDING PROTEIN
1149	1150	RXN02909	VV0135	38532	39017	Hypothetical Trehalose-Binding Protein
1151	1152	RXS00349				Hypothetical Trehalose Transport Protein
1153	1154	RXS03183				TREHALOSE/MALTOSE BINDING PROTEIN
1155	1156	RXC00874				TRANSMEBRANE PROTEIN INVOLVED IN TREHALOSE METABOLISM

TABLE 2 - Excluded Genes

GenBank™ Accession No.	Gene Name	Gene Function	Reference
A09073	ppg	Phosphoenol pyruvate carboxylase	Bachman, B. et al. "DNA fragment coding for phosphoenolpyruvate carboxylase, recombinant DNA carrying said fragment, strains carrying the recombinant DNA and method for producing L-aminino acids using said strains," Patent: EP 0358940-A 3 03/21/90
A45579, A45581, A45583, A45585 A45587		Threonine dehydratase	Moeckel, B. et al. "Production of L-isoleucine by means of recombinant micro-organisms with deregulated threonine dehydratase," Patent: WO 9519442-A 5 07/20/95
AB003132	murC; ftsQ; ftsZ		Kobayashi, M. et al. "Cloning, sequencing, and characterization of the ftsZ gene from coryneform bacteria," <i>Biochem. Biophys. Res. Commun.</i> , 236(2):383-388 (1997)
AB015023	murC; ftsQ		Wachi, M. et al. "A murC gene from Coryneform bacteria," <i>Appl. Microbiol. Biotechnol.</i> , 51(2):223-228 (1999)
AB018530	ftsR		Kimura, E. et al. "Molecular cloning of a novel gene, ftsR, which rescues the detergent sensitivity of a mutant derived from <i>Brevibacterium lactofermentum</i> ," <i>Biosci. Biotechnol. Biochem.</i> , 60(10):1565-1570 (1996)
AB018531	ftsR1; ftsR2		
AB020624	murI	D-glutamate racemase	
AB023377	tkl	transketolase	
AB024708	glbB; gltD	Glutamine 2-oxoglutarate aminotransferase large and small subunits	
AB025424	acn	aconitase	
AB027714	rep	Replication protein	
AB027715	rep; aad	Replication protein; aminoglycoside adenylyltransferase	
AF005242	argC	N-acetylglutamate-5-semialdehyde dehydrogenase	
AF005635	glnA	Glutamine synthetase	
AF030405	hisF	cyclase	
AF030520	argG	Argininosuccinate synthetase	
AF031518	argF	Ornithine carbamoyltransferase	
AF036932	aroD	3-dehydroquinate dehydratase	
AF038548	pyc	Pyruvate carboxylase	

Table 2 (continued)

AF038651	dcfAE; apt; rel	Dipeptide-binding protein; adenine phosphoribosyltransferase; GTP pyrophosphokinase	Wehmeier, L. et al. "The role of the Corynebacterium glutamicum rel gene in (p)ppGpp metabolism," <i>Microbiology</i> , 144:1853-1862 (1998)
AF041436	argR	Arginine repressor	
AF045998	impA	Inositol monophosphate phosphatase	
AF048764	argH	Argininosuccinate lyase	
AF049897	argC; argJ; argB; argD; argF; argR; argG; argH	N-acetylglutamylphosphate reductase; ornithine acetyltransferase; N-acetylglutamate kinase; acetylornithine transaminase; ornithine carbamoyltransferase; arginine repressor; argininosuccinate synthase; argininosuccinate lyase	
AF050109	inhA	Enoyl-acyl carrier protein reductase	
AF050166	hisG	ATP phosphoribosyltransferase	
AF051846	hisA	Phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase	
AF052652	metA	Homoserine O-acetyltransferase	Park, S. et al. "Isolation and analysis of metA, a methionine biosynthetic gene encoding homoserine acetyltransferase in Corynebacterium glutamicum," <i>Mol. Cells</i> , 8(3):286-294 (1998)
AF053071	aroB	Dehydroquinase synthetase	
AF060558	hisH	Glutamine amidotransferase	
AF086704	hisE	Phosphoribosyl-ATP-pyrophosphohydrolase	
AF114233	aroA	5-enolpyruvylshikimate 3-phosphate synthase	
AF116184	panD	L-aspartate-alpha-decarboxylase precursor	Dusch, N. et al. "Expression of the Corynebacterium glutamicum panD gene encoding L-aspartate-alpha-decarboxylase leads to pantothenate overproduction in Escherichia coli," <i>Appl. Environ. Microbiol.</i> , 65(4):1530-1539 (1999)
AF124518	aroD; aroE	3-dehydroquinase; shikimate dehydrogenase	
AF124600	aroC; aroK; aroB; pepQ	Chorismate synthase; shikimate kinase; 3-dehydroquinase synthase; putative cytoplasmic peptidase	
AF145897	inhA		
AF145898	inhA		

Table 2 (continued)

AJ001436	ectP	Transport of ectoine, glycine betaine, proline	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)
AJ004934	dapD	Tetrahydrodipicolinate succinylase (incomplete)	Wehrmann, A. et al. "Different modes of diaminopimelate synthesis and their role in cell wall integrity: A study with <i>Corynebacterium glutamicum</i> ," <i>J. Bacteriol.</i> , 180(12):3159-3165 (1998)
AJ007732	ppc; secG; amt; ocd; soxA	Phosphoenolpyruvate-carboxylase; ?; high affinity ammonium uptake protein; putative ornithine-cyclodecarboxylase; sarcosine oxidase	
AJ010319	ftsY, glnB, glnD; srp; amtP	Involved in cell division; PII protein; uridylyltransferase (uridylyl-removing enzyme); signal recognition particle; low affinity ammonium uptake protein	Jakoby, M. et al. "Nitrogen regulation in <i>Corynebacterium glutamicum</i> ; Isolation of genes involved in biochemical characterization of corresponding proteins," <i>FEMS Microbiol.</i> , 173(2):303-310 (1999)
AJ132968	cat	Chloramphenicol acetyl transferase	
AJ224946	mgo	L-malate: quinone oxidoreductase	Molenaar, D. et al. "Biochemical and genetic characterization of the membrane-associated malate dehydrogenase (acceptor) from <i>Corynebacterium glutamicum</i> ," <i>Eur. J. Biochem.</i> , 254(2):395-403 (1998)
AJ238250	ndh	NADH dehydrogenase	
AJ238703	porA	Porin	Lichtinger, T. et al. "Biochemical and biophysical characterization of the cell wall porin of <i>Corynebacterium glutamicum</i> : The channel is formed by a low molecular mass polypeptide," <i>Biochemistry</i> , 37(43):15024-15032 (1998)
D17429		Transposable element IS31831	Vertes et al. "Isolation and characterization of IS31831, a transposable element from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 11(4):739-746 (1994)
D84102	odhA	2-oxoglutarate dehydrogenase	Usuda, Y. et al. "Molecular cloning of the <i>Corynebacterium glutamicum</i> (Brevibacterium lactofermentum AJ12036) odhA gene encoding a novel type of 2-oxoglutarate dehydrogenase," <i>Microbiology</i> , 142:3347-3354 (1996)
E01358	hdh; hk	Homoserine dehydrogenase; homoserine kinase	Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 198732392-A 1 10/12/87
E01359		Upstream of the start codon of homoserine kinase gene	Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 198732392-A 2 10/12/87
E01375		Tryptophan operon	
E01376	trpL; trpE	Leader peptide; anthranilate synthase	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87

Table 2 (continued)

E01377	Promoter and operator regions of tryptophan operon	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E03937	Biotin-synthase	Hatakeyama, K. et al. "DNA fragment containing gene capable of coding biotin synthetase and its utilization," Patent: JP 1992278088-A 1 10/02/92
E04040	Diamino pelargonic acid aminotransferase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04041	Desthiobiotinsynthetase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04307	Flavum aspartase	Kurusu, Y. et al. "Gene DNA coding aspartase and utilization thereof," Patent: JP 1993030977-A 1 02/09/93
E04376	Isocitric acid lyase	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04377	Isocitric acid lyase N-terminal fragment	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04484	Prephenate dehydratase	Sotouchi, N. et al. "Production of L-phenylalanine by fermentation," Patent: JP 1993076352-A 2 03/30/93
E05108	Aspartokinase	Fugono, N. et al. "Gene DNA coding Aspartokinase and its use," Patent: JP 1993184366-A 1 07/27/93
E05112	Dihydro-dipichorinate synthetase	Hatakeyama, K. et al. "Gene DNA coding dihydrodipicolinic acid synthetase and its use," Patent: JP 1993184371-A 1 07/27/93
E05776	Diaminopimelic acid dehydrogenase	Kobayashi, M. et al. "Gene DNA coding Diaminopimelic acid dehydrogenase and its use," Patent: JP 1993284970-A 1 11/02/93
E05779	Threonine synthase	Kohama, K. et al. "Gene DNA coding threonine synthase and its use," Patent: JP 1993284972-A 1 11/02/93
E06110	Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06111	Mutated Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06146	Acetohydroxy acid synthetase	Inui, M. et al. "Gene capable of coding Acetohydroxy acid synthetase and its use," Patent: JP 1993344893-A 1 12/27/93
E06825	Aspartokinase	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06826	Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94



Table 2 (continued)

E06827		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E07701	secY		Honno, N. et al. "Gene DNA participating in integration of membrane protein to membrane," Patent: JP 1994169780-A 1 06/21/94
E08177		Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08178, E08179, E08180, E08181, E08182		Feedback inhibition-released Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08232		Acetohydroxy-acid isomeroreductase	Inui, M. et al. "Gene DNA coding acetohydroxy acid isomeroreductase," Patent: JP 1994277067-A 1 10/04/94
E08234	secE		Asai, Y. et al. "Gene DNA coding for translocation machinery of protein," Patent: JP 1994277073-A 1 10/04/94
E08643		FT aminotransferase and desthiobiotin synthetase promoter region	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95
E08646		Biotin synthetase	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95
E08649		Aspartase	Kohama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031478-A 1 02/03/95
E08900		Dihydrodipicolinate reductase	Madori, M. et al. "DNA fragment containing gene coding Dihydrodipicolinate acid reductase and utilization thereof," Patent: JP 1995075578-A 1 03/20/95
E08901		Diaminopimelic acid decarboxylase	Madori, M. et al. "DNA fragment containing gene coding Diaminopimelic acid decarboxylase and utilization thereof," Patent: JP 1995075579-A 1 03/20/95
E12594		Serine hydroxymethyltransferase	Hatakeyama, K. et al. "Production of L-tryptophan," Patent: JP 1997028391-A 1 02/04/97
E12760, E12759, E12758		transposase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12764		Arginyl-tRNA synthetase; diaminopimelic acid decarboxylase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12767		Dihydrodipicolinic acid synthetase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12770		aspartokinase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12773		Dihydrodipicolinic acid reductase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97

Table 2 (continued)

E13655		Glucose-6-phosphate dehydrogenase	Hatakeyama, K. et al. "Glucose-6-phosphate dehydrogenase and DNA capable of coding the same," Patent: JP 1997224661-A 1 09/02/97
L01508	ilvA	Threonine dehydratase	Moeckel, B. et al. "Functional and structural analysis of the threonine dehydratase of Corynebacterium glutamicum," <i>J. Bacteriol.</i> , 174:8065-8072 (1992)
L07603	EC 4.2.1.15	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase	Chen, C. et al. "The cloning and nucleotide sequence of Corynebacterium glutamicum 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase gene," <i>FEMS Microbiol. Lett.</i> , 107:223-230 (1993)
L09232	ilvB; ilvN; ilvC	Acetohydroxy acid synthase large subunit; Acetohydroxy acid synthase small subunit; Acetohydroxy acid isomeroreductase	Keilhauer, C. et al. "Isolation and synthesis in Corynebacterium glutamicum: molecular analysis of the ilvB-ilvN-ilvC operon," <i>J. Bacteriol.</i> , 175(17):5595-5603 (1993)
L18874	PtsM	Phosphoenolpyruvate sugar phosphotransferase	Fouet, A. et al. "Bacillus subtilis sucrose-specific enzyme II of the phosphotransferase system: expression in Escherichia coli and homology to enzymes II from enteric bacteria," <i>PNAS USA</i> , 84(24):8773-8777 (1987); Lee, J.K. et al. "Nucleotide sequence of the gene encoding the Corynebacterium glutamicum mannose enzyme II and analyses of the deduced protein sequence," <i>FEMS Microbiol. Lett.</i> , 119(1-2):137-145 (1994)
L27123	aceB	Malate synthase	Lee, H-S. et al. "Molecular characterization of aceB, a gene encoding malate synthase in Corynebacterium glutamicum," <i>J. Microbiol. Biotechnol.</i> , 4(4):256-263 (1994)
L27126		Pyruvate kinase	Jetten, M. S. et al. "Structural and functional analysis of pyruvate kinase from Corynebacterium glutamicum," <i>Appl. Environ. Microbiol.</i> , 60(7):2501-2507 (1994)
L28760	aceA	Isocitrate lyase	
L35906	dtxR	Diphtheria toxin repressor	Oguiza, J.A. et al. "Molecular cloning, DNA sequence analysis, and characterization of the Corynebacterium diphtheriae dtxR from Brevibacterium lactofermentum," <i>J. Bacteriol.</i> , 177(2):465-467 (1995)
M13774		Prephenate dehydratase	Follettie, M.T. et al. "Molecular cloning and nucleotide sequence of the Corynebacterium glutamicum pheA gene," <i>J. Bacteriol.</i> , 167:695-702 (1986)
M16175	5S rRNA		Park, Y-H. et al. "Phylogenetic analysis of the coryneform bacteria by 5S rRNA sequences," <i>J. Bacteriol.</i> , 169:1801-1806 (1987)
M16663	trpE	Anthranelate synthase, 5' end	Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)
M16664	trpA	Tryptophan synthase, 3' end	Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)

Table 2 (continued)

		Phosphoenolpyruvate carboxylase	
M25819			O'Regan, M. et al. "Cloning and nucleotide sequence of the Phosphoenolpyruvate carboxylase-coding gene of <i>Corynebacterium glutamicum</i> ATCC13032," <i>Gene</i> , 77(2):237-251 (1989)
M85106		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992)
M85107, M85108		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992)
M89931	accD; brnQ; yhbW	Beta C-S lyase; branched-chain amino acid uptake carrier; hypothetical protein yhbW	Rossol, I. et al. "The <i>Corynebacterium glutamicum</i> accD gene encodes a C-S lyase with alpha, beta-elimination activity that degrades aminoethylcysteine," <i>J. Bacteriol.</i> , 174(9):2968-2977 (1992); Tauch, A. et al. "Isoleucine uptake in <i>Corynebacterium glutamicum</i> ATCC 13032 is directed by the brnQ gene product," <i>Arch. Microbiol.</i> , 169(4):303-312 (1998)
S59299	trp	Leader gene (promoter)	Herry, D.M. et al. "Cloning of the trp gene cluster from a tryptophan-hyperproducing strain of <i>Corynebacterium glutamicum</i> : identification of a mutation in the trp leader sequence," <i>Appl. Environ. Microbiol.</i> , 59(3):791-799 (1993)
U11545	trpD	Anthraniolate phosphoribosyltransferase	O'Gara, J.P. and Dunican, L.K. (1994) Complete nucleotide sequence of the <i>Corynebacterium glutamicum</i> ATCC 21850 trpD gene." Thesis, Microbiology Department, University College Galway, Ireland.
U13922	cgIIIM; cgIIR; cglIIR	Putative type II 5-cytosine methyltransferase; putative type II restriction endonuclease; putative type I or type III restriction endonuclease	Schafer, A. et al. "Cloning and characterization of a DNA region encoding a stress-sensitive restriction system from <i>Corynebacterium glutamicum</i> ATCC 13032 and analysis of its role in intergeneric conjugation with <i>Escherichia coli</i> ," <i>J. Bacteriol.</i> , 176(23):7309-7319 (1994); Schafer, A. et al. "The <i>Corynebacterium glutamicum</i> cgIIIM gene encoding a 5-cytosine in an McrBC-deficient <i>Escherichia coli</i> strain," <i>Gene</i> , 203(2):95-101 (1997)
U14965	recA		
U31224	ppx		Ankri, S. et al. "Mutations in the <i>Corynebacterium glutamicum</i> proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31225	proC	L-proline: NADP+ 5-oxido-reductase	Ankri, S. et al. "Mutations in the <i>Corynebacterium glutamicum</i> proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31230	obg; proB; unkdh	?; gamma glutamyl kinase; similar to D-isomer specific 2-hydroxyacid dehydrogenases	Ankri, S. et al. "Mutations in the <i>Corynebacterium glutamicum</i> proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)

Table 2 (continued)

U31281	bioB	Biotin synthase	Serebriskii, I.G., "Two new members of the bio B superfamily: Cloning, sequencing and expression of bio B genes of <i>Methylobacillus flagellatum</i> and <i>Corynebacterium glutamicum</i> ," <i>Gene</i> , 175:15-22 (1996)
U35023	thiR; accBC	Thiosulfate sulfurtransferase; acyl CoA carboxylase	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene encoding a two-domain protein similar to biotin carboxylases and biotin-carboxyl-carrier proteins," <i>Arch. Microbiol.</i> , 166(2):76-82 (1996)
U43535	cmr	Multidrug resistance protein	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene conferring multidrug resistance in the heterologous host <i>Escherichia coli</i> ," <i>J. Bacteriol.</i> , 179(7):2449-2451 (1997)
U43536	clpB	Heat shock ATP-binding protein	
U53587	aphA-3	3'5'-aminoglycoside phosphotransferase	
U89648		<i>Corynebacterium glutamicum</i> unidentified sequence involved in histidine biosynthesis, partial sequence	
X04960	trpA; trpB; trpC; trpD; trpE; trpG; trpL	Tryptophan operon	
X07563	lys A	DAP decarboxylase (meso-diaminopimelate decarboxylase, EC 4.1.1.20)	Matsui, K. et al. "Complete nucleotide and deduced amino acid sequences of the <i>Brevibacterium lactofermentum</i> tryptophan operon," <i>Nucleic Acids Res.</i> , 14(24):10113-10114 (1986)
X14234	EC 4.1.1.31	Phosphoenolpyruvate carboxylase	Yeh, P. et al. "Nucleic sequence of the <i>lysA</i> gene of <i>Corynebacterium glutamicum</i> and possible mechanisms for modulation of its expression," <i>Mol. Gen. Genet.</i> , 212(1):112-119 (1988)
			Eikmanns, B.J. et al. "The Phosphoenolpyruvate carboxylase gene of <i>Corynebacterium glutamicum</i> : Molecular cloning, nucleotide sequence, and expression," <i>Mol. Gen. Genet.</i> , 218(2):330-339 (1989); Lepiniec, L. et al. "Sorghum Phosphoenolpyruvate carboxylase gene family: structure, function and molecular evolution," <i>Plant. Mol. Biol.</i> , 21(3):487-502 (1993)
X17313	fda	Fructose-bisphosphate aldolase	Von der Osten, C.H. et al. "Molecular cloning, nucleotide sequence and fine-structural analysis of the <i>Corynebacterium glutamicum</i> <i>fda</i> gene: structural comparison of <i>C. glutamicum</i> fructose-1, 6-bisphosphate aldolase to class I and class II aldolases," <i>Mol. Microbiol.</i>
X53993	dapA	L-2, 3-dihydrodipicolinate synthetase (EC 4.2.1.52)	Bonnassie, S. et al. "Nucleic sequence of the <i>dapA</i> gene from <i>Corynebacterium glutamicum</i> ," <i>Nucleic Acids Res.</i> , 18(21):6421 (1990)
X54223		AttB-related site	Gianciotto, N. et al. "DNA sequence homology between att B-related sites of <i>Corynebacterium diphtheriae</i> , <i>Corynebacterium ulcerans</i> , <i>Corynebacterium glutamicum</i> , and the attP site of lambdacorynephage," <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990)
X54740	argS; lysA	Arginyl-tRNA synthetase; Diaminopimelate decarboxylase	Marcel, T. et al. "Nucleotide sequence and organization of the upstream region of the <i>Corynebacterium glutamicum</i> <i>lysA</i> gene," <i>Mol. Microbiol.</i> , 4(1):1819-1830 (1990)

Table 2 (continued)

X55994	trpL; trpE	Putative leader peptide; anthranilate synthase component 1	Heery, D.M. et al. "Nucleotide sequence of the <i>Corynebacterium glutamicum</i> trpE gene," <i>Nucleic Acids Res.</i> , 18(23):7138 (1990)
X56037	thrC	Threonine synthase	Han, K.S. et al. "The molecular structure of the <i>Corynebacterium glutamicum</i> threonine synthase gene," <i>Mol. Microbiol.</i> , 4(10):1693-1702 (1990)
X56075	attB-related site	Attachment site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of <i>Corynebacterium diphtheriae</i> , <i>Corynebacterium ulcerans</i> , <i>Corynebacterium glutamicum</i> , and the attP site of <i>lambdacorynephage</i> ," <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990)
X57226	lysC-alpha; lysC-beta; asd	Aspartokinase-alpha subunit; Aspartokinase-beta subunit; aspartate beta semialdehyde dehydrogenase	Kalinowski, J. et al. "Genetic and biochemical analysis of the Aspartokinase from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 5(5):1197-1204 (1991); Kalinowski, J. et al. "Aspartokinase genes lysC alpha and lysC beta overlap and are adjacent to the aspartate beta-semialdehyde dehydrogenase gene asd in <i>Corynebacterium glutamicum</i> ," <i>Mol. Gen. Genet.</i> , 224(3):317-324 (1990)
X59403	gap;pgk; tpi	Glyceraldehyde-3-phosphate; phosphoglycerate kinase; triosephosphate isomerase	Eikmanns, B.J. "Identification, sequence analysis, and expression of a <i>Corynebacterium glutamicum</i> gene cluster encoding the three glycolytic enzymes glyceraldehyde-3-phosphate dehydrogenase, 3-phosphoglycerate kinase, and triosephosphate isomerase," <i>J. Bacteriol.</i> , 174(19):6076-6086 (1992)
X59404	gdh	Glutamate dehydrogenase	Bormann, E.R. et al. "Molecular analysis of the <i>Corynebacterium glutamicum</i> gdh gene encoding glutamate dehydrogenase," <i>Mol. Microbiol.</i> , 6(3):317-326 (1992)
X60312	lysI	L-lysine permease	Seep-Feldhaus, A.H. et al. "Molecular analysis of the <i>Corynebacterium glutamicum</i> lysI gene involved in lysine uptake," <i>Mol. Microbiol.</i> , 5(12):2995-3005 (1991)
X66078	copI	Psl protein	Joliff, G. et al. "Cloning and nucleotide sequence of the <i>copI</i> gene encoding Psl, one of the two major secreted proteins of <i>Corynebacterium glutamicum</i> : The deduced N-terminal region of Psl is similar to the Mycobacterium antigen 85 complex," <i>Mol. Microbiol.</i> , 6(16):2349-2362 (1992)
X66112	glt	Citrate synthase	Eikmanns, B.J. et al. "Cloning sequence, expression and transcriptional analysis of the <i>Corynebacterium glutamicum</i> gltA gene encoding citrate synthase," <i>Microbiol.</i> , 140:1817-1828 (1994)
X67737	dapB	Dihydrodipicolinate reductase	
X69103	esp2	Surface layer protein PS2	Peyret, J.L. et al. "Characterization of the <i>espB</i> gene encoding PS2, an ordered surface-layer protein in <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 9(1):97-109 (1993)
X69104		IS3 related insertion element	Bonamy, C. et al. "Identification of IS1206, a <i>Corynebacterium glutamicum</i> IS3-related insertion sequence and phylogenetic analysis," <i>Mol. Microbiol.</i> , 14(3):571-581 (1994)

Table 2 (continued)

	leuA	Isopropylmalate synthase	
X70959			Patek, M. et al. "Leucine synthesis in <i>Corynebacterium glutamicum</i> : enzyme activities, structure of leuA, and effect of leuA inactivation on lysine synthesis," <i>Appl. Environ. Microbiol.</i> , 60(1):133-140 (1994)
X71489	icd	Isocitrate dehydrogenase (NADP+)	Eikmanns, B.J. et al. "Cloning sequence analysis, expression, and inactivation of the <i>Corynebacterium glutamicum</i> icd gene encoding isocitrate dehydrogenase and biochemical characterization of the enzyme," <i>J. Bacteriol.</i> , 177(3):774-782 (1995)
X72855	GDHA	Glutamate dehydrogenase (NADP+)	
X75083, X70584	mtaA	5-methyltryptophan resistance	Heery, D.M. et al. "A sequence from a tryptophan-hyperproducing strain of <i>Corynebacterium glutamicum</i> encoding resistance to 5-methyltryptophan," <i>Biochem. Biophys. Res. Commun.</i> , 201(3):1255-1262 (1994)
X75085	recA		Fitzpatrick, R. et al. "Construction and characterization of recA mutant strains of <i>Corynebacterium glutamicum</i> and <i>Brevibacterium lactofermentum</i> ," <i>Appl. Microbiol. Biotechnol.</i> , 42(4):575-580 (1994)
X75504	aceA; thiX	Partial Isocitrate lyase; ?	Reinscheid, D.J. et al. "Characterization of the isocitrate lyase gene from <i>Corynebacterium glutamicum</i> and biochemical analysis of the enzyme," <i>J. Bacteriol.</i> , 176(12):3474-3483 (1994)
X76875		ATPase beta-subunit	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993)
X77034	tuf	Elongation factor Tu	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993)
X77384	recA		Billman-Jacobe, H. "Nucleotide sequence of a recA gene from <i>Corynebacterium glutamicum</i> ," <i>DNA Seq.</i> , 4(6):403-404 (1994)
X78491	aceB	Malate synthase	Reinscheid, D.J. et al. "Malate synthase from <i>Corynebacterium glutamicum</i> pta-ack operon encoding phosphotransacetylase: sequence analysis," <i>Microbiology</i> , 140:3099-3108 (1994)
X80629	16S rDNA	16S ribosomal RNA	Rainey, F.A. et al. "Phylogenetic analysis of the genera <i>Rhodococcus</i> and <i>Norcardia</i> and evidence for the evolutionary origin of the genus <i>Norcardia</i> from within the radiation of <i>Rhodococcus</i> species," <i>Microbiol.</i> , 141:523-528 (1995)
X81191	gluA; gluB; gluC; gluD	Glutamate uptake system	Kronmeyer, W. et al. "Structure of the gluABCD cluster encoding the glutamate uptake system of <i>Corynebacterium glutamicum</i> ," <i>J. Bacteriol.</i> , 177(5):1152-1158 (1995)
X81379	dapE	Succinylidiaminopimelate desuccinylase	Wehrmann, A. et al. "Analysis of different DNA fragments of <i>Corynebacterium glutamicum</i> complementing dapE of <i>Escherichia coli</i> ," <i>Microbiology</i> , 40:3349-56 (1994)

Table 2 (continued)

	16S rDNA	16S ribosomal RNA	
X82061			Ruimy, R. et al. "Phylogeny of the genus <i>Corynebacterium</i> deduced from analyses of small-subunit ribosomal DNA sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):740-746 (1995)
X82928	asd; lysC	Aspartate-semialdehyde dehydrogenase; ?	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X82929	proA	Gamma-glutamyl phosphate reductase	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X84257	16S rDNA	16S ribosomal RNA	Pascual, C. et al. "Phylogenetic analysis of the genus <i>Corynebacterium</i> based on 16S rRNA gene sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):724-728 (1995)
X85965	aroP; dapE	Aromatic amino acid permease; ?	Wehrmann et al. "Functional analysis of sequences adjacent to dapE of <i>C. glutamicum</i> proline reveals the presence of aroP, which encodes the aromatic amino acid transporter," <i>J. Bacteriol.</i> , 177(20):5991-5993 (1995)
X86157	argB; argC; argD; argF; argJ	Acetylglutamate kinase; N-acetyl-gamma-glutamyl-phosphate reductase; acetylornithine aminotransferase; ornithine carbamoyltransferase; glutamate N-acetyltransferase	Sakanyan, V. et al. "Genes and enzymes of the acetyl cycle of arginine biosynthesis in <i>Corynebacterium glutamicum</i> : enzyme evolution in the early steps of the arginine pathway," <i>Microbiology</i> , 142:99-108 (1996)
X89084	pta; ackA	Phosphate acetyltransferase; acetate kinase	Reinscheid, D.J. et al. "Cloning, sequence analysis, expression and inactivation of the <i>Corynebacterium glutamicum</i> pta-ack operon encoding phosphotransacetylase and acetate kinase," <i>Microbiology</i> , 145:503-513 (1999)
X89850	attB	Attachment site	Le Marrec, C. et al. "Genetic characterization of site-specific integration functions of phi AAU2 infecting 'Arthrobacter aureus C70,' <i>J. Bacteriol.</i> , 178(7):1996-2004 (1996)
X90356		Promoter fragment F1	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90357		Promoter fragment F2	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90358		Promoter fragment F10	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90359		Promoter fragment F13	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)

Table 2 (continued)

X90360	Promoter fragment F22	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90361	Promoter fragment F34	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90362	Promoter fragment F37	Patek, M. et al. "Promoters from <i>C. glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90363	Promoter fragment F45	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90364	Promoter fragment F64	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90365	Promoter fragment F75	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90366	Promoter fragment PF101	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90367	Promoter fragment PF104	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90368	Promoter fragment PF109	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X93513	Ammonium transport system	Siewe, R.M. et al. "Functional and genetic characterization of the (methyl) ammonium uptake carrier of <i>Corynebacterium glutamicum</i> ," <i>J. Biol. Chem.</i> , 271(10):5398-5403 (1996)
X93514	Glycine betaine transport system	Peter, H. et al. "Isolation, characterization, and expression of the <i>Corynebacterium glutamicum</i> betP gene, encoding the transport system for the compatible solute glycine betaine," <i>J. Bacteriol.</i> , 178(17):5229-5234 (1996)
X95649	orf4	Patek, M. et al. "Identification and transcriptional analysis of the dapB-ORF2-dapA-ORF4 operon of <i>Corynebacterium glutamicum</i> , encoding two enzymes involved in L-lysine synthesis," <i>Biotechnol. Lett.</i> , 19:1113-1117 (1997)
X96471	Lysine exporter protein; Lysine export regulator protein	Vrljic, M. et al. "A new type of transporter with a new type of cellular function: L-lysine export from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 22(5):815-826 (1996)



Table 2 (continued)

X96580	panB; panC; xylB	3-methyl-2-oxobutanoate hydroxymethyltransferase; pantoate-beta-alanine ligase; xylulokinase	Sahm, H. et al. "D-pantothenate synthesis in Corynebacterium glutamicum and use of panBC and genes encoding L-valine synthesis for D-pantothenate overproduction," <i>Appl. Environ. Microbiol.</i> , 65(5):1973-1979 (1999)
X96962		Insertion sequence IS1207 and transposase	
X99289		Elongation factor P	Ramos, A. et al. "Cloning, sequencing and expression of the gene encoding elongation factor P in the amino-acid producer Brevibacterium lactofermentum (Corynebacterium glutamicum ATCC 13869)," <i>Gene</i> , 198:217-222 (1997)
Y00140	thrB	Homoserine kinase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine kinase (thrB) gene of the Brevibacterium lactofermentum," <i>Nucleic Acids Res.</i> , 15(9):3922 (1987)
Y00151	ddh	Meso-diaminopimelate D-dehydrogenase (EC 1.4.1.16)	Ishino, S. et al. "Nucleotide sequence of the meso-diaminopimelate D-dehydrogenase gene from Corynebacterium glutamicum," <i>Nucleic Acids Res.</i> , 15(9):3917 (1987)
Y00476	thrA	Homoserine dehydrogenase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine dehydrogenase (thrA) gene of the Brevibacterium lactofermentum," <i>Nucleic Acids Res.</i> , 15(24):10598 (1987)
Y00546	hom; thrB	Homoserine dehydrogenase; homoserine kinase	Peoples, O.P. et al. "Nucleotide sequence and fine structural analysis of the Corynebacterium glutamicum hom-thrB operon," <i>Mol. Microbiol.</i> , 2(1):63-72 (1988)
Y08964	murC; ftsQ/divD; ftsZ	UPD-N-acetylmuramate-alanine ligase; division initiation protein or cell division protein; cell division protein	Honrubia, M.P. et al. "Identification, characterization, and chromosomal organization of the ftsZ gene from Brevibacterium lactofermentum," <i>Mol. Gen. Genet.</i> , 259(1):97-104 (1998)
Y09163	putP	High affinity proline transport system	Peter, H. et al. "Isolation of the putP gene of Corynebacterium glutamicumproline and characterization of a low-affinity uptake system for compatible solutes," <i>Arch. Microbiol.</i> , 168(2):143-151 (1997)
Y09548	pyc	Pyruvate carboxylase	Peters-Wendisch, P.G. et al. "Pyruvate carboxylase from Corynebacterium glutamicum: characterization, expression and inactivation of the pyc gene," <i>Microbiology</i> , 144:915-927 (1998)
Y09578	leuB	3-isopropylmalate dehydrogenase	Patek, M. et al. "Analysis of the leuB gene from Corynebacterium glutamicum," <i>Appl. Microbiol. Biotechnol.</i> , 50(1):42-47 (1998)
Y12472		Attachment site bacteriophage Phi-16	Moreau, S. et al. "Site-specific integration of corynebacteriophage Phi-16: The construction of an integration vector," <i>Microbiol.</i> , 145:539-548 (1999)
Y12537	proP	Proline/ectoine uptake system protein	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)

Table 2 (continued)

	glnA	Glutamine synthetase I	
Y13221			Jakoby, M. et al. "Isolation of <i>Corynebacterium glutamicum</i> glnA gene encoding glutamine synthetase I," <i>FEMS Microbiol. Lett.</i> , 154(1):81-88 (1997)
Y16642	lpd	Dihydrolipoamide dehydrogenase	
Y18059		Attachment site <i>Corynebacterium</i> 304L	
Z21501	argS; lysA	Arginyl-tRNA synthetase; diaminopimelate decarboxylase (partial)	Moreau, S. et al. "Analysis of the integration functions of &phi;304L: An integrase module among corynephages," <i>Virology</i> , 255(1):150-159 (1999)
Z21502	dapA; dapB	Dihydrodipicolinate synthase; dihydrodipicolinate reductase	Oguiza, J.A. et al. "A gene encoding arginyl-tRNA synthetase is located in the upstream region of the lysA gene in <i>Brevibacterium lactofermentum</i> : Regulation of argS-lysA cluster expression by arginine," <i>J. Bacteriol.</i> , 175(22):7356-7362 (1993)
Z29563	thrC	Threonine synthase	Pisabarro, A. et al. "A cluster of three genes (dapA, orf2, and dapB) of <i>Brevibacterium lactofermentum</i> encodes dihydrodipicolinate reductase, and a third polypeptide of unknown function," <i>J. Bacteriol.</i> , 175(9):2743-2749 (1993)
Z46753	16S rDNA	Gene for 16S ribosomal RNA	Malumbres, M. et al. "Analysis and expression of the thrC gene of the encoded threonine synthase," <i>Appl. Environ. Microbiol.</i> , 60(7):2209-2219 (1994)
Z49822	sigA	SigA sigma factor	Oguiza, J.A. et al. "Multiple sigma factor genes in <i>Brevibacterium lactofermentum</i> : Characterization of sigA and sigB," <i>J. Bacteriol.</i> , 178(2):550-553 (1996)
Z49823	galE; dtxR	Catalytic activity UDP-galactose 4-epimerase; diphtheria toxin regulatory protein	Oguiza, J.A. et al. "The galE gene encoding the UDP-galactose 4-epimerase of <i>Brevibacterium lactofermentum</i> is coupled transcriptionally to the dmdR gene," <i>Gene</i> , 177:103-107 (1996)
Z49824	orf1; sigB	?; SigB sigma factor	Oguiza, J.A. et al. "Multiple sigma factor genes in <i>Brevibacterium lactofermentum</i> : Characterization of sigA and sigB," <i>J. Bacteriol.</i> , 178(2):550-553 (1996)
Z66534		Transposase	Correia, A. et al. "Cloning and characterization of an IS-like element present in the genome of <i>Brevibacterium lactofermentum</i> ATCC 13869," <i>Gene</i> , 170(1):91-94 (1996)
A sequence for this gene was published in the indicated reference. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.			

TABLE 3: *Corynebacterium* and *Brevibacterium* Strains Which May be Used in the Practice of the Invention

Genus	Species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
<i>Brevibacterium</i>	<i>ammoniagenes</i>	21054							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19350							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19351							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19352							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19353							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19354							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19355							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19356							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	21055							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	21077							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	21553							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	21580							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	39101							
<i>Brevibacterium</i>	<i>butanicum</i>	21196							
<i>Brevibacterium</i>	<i>divaricatum</i>	21792	P928						
<i>Brevibacterium</i>	<i>flavum</i>	21474							
<i>Brevibacterium</i>	<i>flavum</i>	21129							
<i>Brevibacterium</i>	<i>flavum</i>	21518							
<i>Brevibacterium</i>	<i>flavum</i>			B11474					
<i>Brevibacterium</i>	<i>flavum</i>			B11472					
<i>Brevibacterium</i>	<i>flavum</i>	21127							
<i>Brevibacterium</i>	<i>flavum</i>	21128							
<i>Brevibacterium</i>	<i>flavum</i>	21427							
<i>Brevibacterium</i>	<i>flavum</i>	21475							
<i>Brevibacterium</i>	<i>flavum</i>	21517							
<i>Brevibacterium</i>	<i>flavum</i>	21528							
<i>Brevibacterium</i>	<i>flavum</i>	21529							
<i>Brevibacterium</i>	<i>flavum</i>			B11477					
<i>Brevibacterium</i>	<i>flavum</i>			B11478					
<i>Brevibacterium</i>	<i>flavum</i>	21127							
<i>Brevibacterium</i>	<i>flavum</i>			B11474					
<i>Brevibacterium</i>	<i>healii</i>	15527							
<i>Brevibacterium</i>	<i>ketoglutamicum</i>	21004							
<i>Brevibacterium</i>	<i>ketoglutamicum</i>	21089							
<i>Brevibacterium</i>	<i>ketosoreductum</i>	21914							
<i>Brevibacterium</i>	<i>lactofermentum</i>				70				
<i>Brevibacterium</i>	<i>lactofermentum</i>				74				
<i>Brevibacterium</i>	<i>lactofermentum</i>				77				
<i>Brevibacterium</i>	<i>lactofermentum</i>	21798							
<i>Brevibacterium</i>	<i>lactofermentum</i>	21799							
<i>Brevibacterium</i>	<i>lactofermentum</i>	21800							
<i>Brevibacterium</i>	<i>lactofermentum</i>	21801							
<i>Brevibacterium</i>	<i>lactofermentum</i>			B11470					
<i>Brevibacterium</i>	<i>lactofermentum</i>			B11471					

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	CGTC	DSMZ
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	21420							
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	31269							
Brevibacterium	linens	9174							
Brevibacterium	linens	19391							
Brevibacterium	linens	8377							
Brevibacterium	paraffinolyticum					11160			
Brevibacterium	spec.						717.73		
Brevibacterium	spec.						717.73		
Brevibacterium	spec.	14604							
Brevibacterium	spec.	21860							
Brevibacterium	spec.	21864							
Brevibacterium	spec.	21865							
Brevibacterium	spec.	21866							
Brevibacterium	spec.	19240							
Corynebacterium	acetoacidophilum	21476							
Corynebacterium	acetoacidophilum	13870							
Corynebacterium	acetoglutamicum			B11473					
Corynebacterium	acetoglutamicum			B11475					
Corynebacterium	acetoglutamicum	15806							
Corynebacterium	acetoglutamicum	21491							
Corynebacterium	acetoglutamicum	31270							
Corynebacterium	acetophilum			B3671					
Corynebacterium	ammoniagenes	6872						2399	
Corynebacterium	ammoniagenes	15511							
Corynebacterium	fujikense	21496							
Corynebacterium	glutamicum	14067							
Corynebacterium	glutamicum	39137							
Corynebacterium	glutamicum	21254							
Corynebacterium	glutamicum	21255							
Corynebacterium	glutamicum	31830							
Corynebacterium	glutamicum	13032							
Corynebacterium	glutamicum	14305							
Corynebacterium	glutamicum	15455							
Corynebacterium	glutamicum	13058							
Corynebacterium	glutamicum	13059							
Corynebacterium	glutamicum	13060							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum	21513							
Corynebacterium	glutamicum	21526							
Corynebacterium	glutamicum	21543							
Corynebacterium	glutamicum	13287							
Corynebacterium	glutamicum	21851							
Corynebacterium	glutamicum	21253							
Corynebacterium	glutamicum	21514							
Corynebacterium	glutamicum	21516							
Corynebacterium	glutamicum	21299							

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Corynebacterium	glutamicum	21300							
Corynebacterium	glutamicum	39684							
Corynebacterium	glutamicum	21488							
Corynebacterium	glutamicum	21649							
Corynebacterium	glutamicum	21650							
Corynebacterium	glutamicum	19223							
Corynebacterium	glutamicum	13869							
Corynebacterium	glutamicum	21157							
Corynebacterium	glutamicum	21158							
Corynebacterium	glutamicum	21159							
Corynebacterium	glutamicum	21355							
Corynebacterium	glutamicum	31808							
Corynebacterium	glutamicum	21674							
Corynebacterium	glutamicum	21562							
Corynebacterium	glutamicum	21563							
Corynebacterium	glutamicum	21564							
Corynebacterium	glutamicum	21565							
Corynebacterium	glutamicum	21566							
Corynebacterium	glutamicum	21567							
Corynebacterium	glutamicum	21568							
Corynebacterium	glutamicum	21569							
Corynebacterium	glutamicum	21570							
Corynebacterium	glutamicum	21571							
Corynebacterium	glutamicum	21572							
Corynebacterium	glutamicum	21573							
Corynebacterium	glutamicum	21579							
Corynebacterium	glutamicum	19049							
Corynebacterium	glutamicum	19050							
Corynebacterium	glutamicum	19051							
Corynebacterium	glutamicum	19052							
Corynebacterium	glutamicum	19053							
Corynebacterium	glutamicum	19054							
Corynebacterium	glutamicum	19055							
Corynebacterium	glutamicum	19056							
Corynebacterium	glutamicum	19057							
Corynebacterium	glutamicum	19058							
Corynebacterium	glutamicum	19059							
Corynebacterium	glutamicum	19060							
Corynebacterium	glutamicum	19185							
Corynebacterium	glutamicum	13286							
Corynebacterium	glutamicum	21515							
Corynebacterium	glutamicum	21527							
Corynebacterium	glutamicum	21544							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum			B8183					
Corynebacterium	glutamicum			B8182					
Corynebacterium	glutamicum			B12416					
Corynebacterium	glutamicum			B12417					

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Corynebacterium	glutamicum			B12418					
Corynebacterium	glutamicum			B11476					
Corynebacterium	glutamicum	21608							
Corynebacterium	lilium		P973						
Corynebacterium	nitrilophilus	21419				11594			
Corynebacterium	spec.		P4445						
Corynebacterium	spec.		P4446						
Corynebacterium	spec.	31088							
Corynebacterium	spec.	31089							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	15954							20145
Corynebacterium	spec.	21857							
Corynebacterium	spec.	21862							
Corynebacterium	spec.	21863							

ATCC: American Type Culture Collection, Rockville, MD, USA

FERM: Fermentation Research Institute, Chiba, Japan

NRRL: ARS Culture Collection, Northern Regional Research Laboratory, Peoria, IL, USA

CECT: Coleccion Espanola de Cultivos Tipo, Valencia, Spain

NCIMB: National Collection of Industrial and Marine Bacteria Ltd., Aberdeen, UK

CBS: Centraalbureau voor Schimmelcultures, Baarn, NL

NCTC: National Collection of Type Cultures, London, UK

DSMZ: Deutsche Sammlung von Mikroorganismen und Zellkulturen, Braunschweig, Germany

For reference see Sugawara, H. et al. (1993) World directory of collections of cultures of microorganisms: Bacteria, fungi and yeasts (4<sup>th</sup> edn), World federation for culture collections world data center on microorganisms, Saimata, Japan.

Table 4: Alignment Results

ID #	length (NT)	Genbank Hit	Length	Accession	Name of Genbank Hit	Source of Genbank Hit	% homology (GAP)	Date of Deposit
rx00023	3579	GB_EST33:AI776129	483	AI776129	EST257217 tomato resistant, Cornell Lycopersicon esculentum cDNA clone cLER17D3, mRNA sequence.	Lycopersicon esculentum	40,956	29-Jun-99
		GB_EST33:AI776129	483	AI776129	EST257217 tomato resistant, Cornell Lycopersicon esculentum cDNA clone cLER17D3, mRNA sequence.	Lycopersicon esculentum	40,956	29-Jun-99
rx00044	1059	EM_PAT:E11760	6911	E11760	Base sequence of sucrase gene.	Corynebacterium glutamicum	42,979	08-OCT- 1997 (Rel. 52, Created) 07-OCT- 1996
		GB_PAT:I26124	6911	I26124	Sequence 4 from patent US 5556776.	Unknown.	42,979	17-DEC- 1993
rx00064	1401	GB_BA2:ECOUW89	176195	U00006	E. coli chromosomal region from 89.2 to 92.8 minutes.	Escherichia coli	39,097	28-Jul-99
		GB_PAT:E16763	2517	E16763	gDNA encoding aspartate transferase (AAT).	Corynebacterium glutamicum	95,429	2-Aug-99
		GB_HTG2:AC007892	134257	AC007892	Drosophila melanogaster chromosome 3 clone BACR02003 (D797) RPCI-98 02.O.3 map 99B-99B strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 113 unordered pieces.	Drosophila melanogaster	31,111	2-Aug-99
rx00072		GB_HTG2:AC007892	134257	AC007892	Drosophila melanogaster chromosome 3 clone BACR02003 (D797) RPCI-98 02.O.3 map 99B-99B strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 113 unordered pieces.	Drosophila melanogaster	31,111	2-Aug-99
rx00105	798	GB_BA1:MTV002	56414	AL008967	Mycobacterium tuberculosis H37Rv complete genome; segment 122/162.	Mycobacterium tuberculosis	37,753	17-Jun-98
		GB_BA1:ECU29581	71128	U29581	Escherichia coli K-12 genome; approximately 63 to 64 minutes.	Escherichia coli	35,669	14-Jan-97
		GB_BA2:AE000366	10405	AE000366	Escherichia coli K-12 MG1655 section 256 of 400 of the complete genome.	Escherichia coli	35,669	12-Nov-98
rx00106	579	GB_EST15:AA494237	367	AA494237	ng83f04.s1 NCI_CGAP_Pr6 Homo sapiens cDNA clone IMAGE:941407 similar to SW:DYR_LACCA P00381 DIHYDROFOLATE REDUCTASE ;, mRNA sequence.	Homo sapiens	42,896	20-Aug-97
		GB_BA2:AF161327	2021	AF161327	Corynebacterium diptheriae histidine kinase ChrS (chrS) and response regulator ChrA (chrA) genes, complete cds.	Corynebacterium diphtheriae	40,210	9-Sep-99
		GB_PAT:AR041189	654	AR041189	Sequence 4 from patent US 5811286.	Unknown.	41,176	29-Sep-99
rx00115	1170	GB_PR4:AC007110	148336	AC007110	Homo sapiens chromosome 17, clone hRPK.472_J_18, complete sequence.	Homo sapiens	36,783	30-MAR- 1999
		GB_HTG3:AC008537	170030	AC008537	Homo sapiens chromosome 19 clone CIT-HSPC_490E21, *** SEQUENCING IN PROGRESS ***; 93 unordered pieces.	Homo sapiens	40,296	2-Sep-99
		GB_HTG3:AC008537	170030	AC008537	Homo sapiens chromosome 19 clone CIT-HSPC_490E21, *** SEQUENCING IN PROGRESS ***; 93 unordered pieces.	Homo sapiens	40,296	2-Sep-99

Table 4 (continued)

rxa00116	1284	GB_BA2:AF062345	16458	AF062345	Caulobacter crescentus Sst1 (sst1), S-layer protein subunit (rsaA), ABC transporter (rsaD), membrane forming unit (rsaE), putative GDP-mannose-4,6-dehydratase (lpsA), putative acetyltransferase (lpsB), putative perosamine synthetase (lpsC), putative mannose-6-phosphate isomerase (lpsD), putative mannose-6-phosphate isomerase (lpsE), outer membrane protein (rsaF), and putative perosamine transferase (lpsE) genes, complete cds. Sequence 6 from patent US 5500353.	Caulobacter crescentus	36,235	19-OCT-1999
		GB_PAT:118647	3300	118647		Unknown.	36,821	07-OCT-1996
		GB_GSS13:AQ44619	751	AQ446197	nbxb0062D16r CUGI Rice BAC Library Oryza sativa genomic clone	Oryza sativa	38,124	8-Apr-99
rxa00131	732	GB_BA1:MTY20B11	36330	Z95121	nbxb0062D16r, genomic survey sequence. Mycobacterium tuberculosis H37Rv complete genome; segment 139/162.	Mycobacterium tuberculosis	43,571	17-Jun-98
		GB_BA1:SAR7932	15176	AJ007932	Streptomyces argillaceus mithramycin biosynthetic genes.	Streptomyces argillaceus	41,116	15-Jun-99
		GB_BA1:MTY20B11	36330	Z95121	Mycobacterium tuberculosis H37Rv complete genome; segment 139/162.	Mycobacterium tuberculosis	39,726	17-Jun-98
rxa00132	1557	GB_BA1:MTY20B11	36330	Z95121	Mycobacterium tuberculosis H37Rv complete genome; segment 139/162.	Mycobacterium tuberculosis	36,788	17-Jun-98
		GB_IN2:TVU40872	1882	U40872	Trichomonas vaginalis S-adenosyl-L-homocysteine hydrolase gene, complete cds.	Trichomonas vaginalis	61,914	31-OCT-1996
		GB_HTG6:AC010706	169265	AC010706	Drosophila melanogaster chromosome X clone BACR36D15 (D887) RPL-98 36.D.15 map 13C-13E strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 74 unordered pieces.	Drosophila melanogaster	51,325	22-Nov-99
rxa00145	1059	GB_BA1:MTY2B12	20431	Z81011	Mycobacterium tuberculosis H37Rv complete genome; segment 61/162.	Mycobacterium tuberculosis	63,365	18-Jun-98
		GB_BA1:PSEPYRBX	2273	L19649	Pseudomonas aeruginosa aspartate transcarbamoylase (pyrB) and dihydroorotase-like (pyrX) genes, complete cds's.	Pseudomonas aeruginosa	56,080	26-Jul-93
		GB_BA1:LLPYRBDNA	1468	X84262	L. leichmannii pyrB gene.	Lactobacillus leichmannii	47,514	29-Apr-97
rxa00146	1464	GB_BA1:MTY2B12	20431	Z81011	Mycobacterium tuberculosis H37Rv complete genome; segment 61/162.	Mycobacterium tuberculosis	60,714	18-Jun-98
		GB_BA1:MTY154	13935	Z98209	Mycobacterium tuberculosis H37Rv complete genome; segment 121/162.	Mycobacterium tuberculosis	39,229	17-Jun-98
		GB_BA1:MSGY154	40221	AD000002	Mycobacterium tuberculosis sequence from clone y154.	Mycobacterium tuberculosis	36,618	03-DEC-1996
rxa00147	1302	GB_BA1:MTY2B12	20431	Z81011	Mycobacterium tuberculosis H37Rv complete genome; segment 61/162.	Mycobacterium tuberculosis	61,527	18-Jun-98
		GB_BA1:MSGB937C	38914	L78820	Mycobacterium leprae cosmid B937 DNA sequence.	Mycobacterium leprae	59,538	15-Jun-96
		GB_BA1:PAU81259	7285	U81259	Pseudomonas aeruginosa dihydrodipicolinate reductase (dapB) gene, partial cds, carbamoylphosphate synthetase small subunit (carA) and carbamoylphosphate synthetase large subunit (carB) genes, complete cds, and FisJ homolog (ftsJ) gene, partial cds.	Pseudomonas aeruginosa	55,396	23-DEC-1996
rxa00156	1233	GB_BA1:SC9B10	33320	AL009204	Streptomyces coelicolor cosmid 9B10.	Streptomyces coelicolor	52,666	10-Feb-99



Table 4 (continued)

GB_BA2:AF002133	15437	AF002133	Mycobacterium avium strain GIR10 transcriptional regulator (mav81) gene, partial cds, aconitase (acr), invasin 1 (inv1), invasin 2 (inv2), transcriptional regulator (moxR), ketoacyl-reductase (fabG), enoyl-reductase (inhA) and ferrochelatase (mav272) genes, complete cds.	Mycobacterium avium	54,191	26-MAR-1998
GB_BA1:D85417	7984	D85417	Propionibacterium freudenreichii hemY, hemH, hemB, hemX, hemR and hemL genes, complete cds.	Propionibacterium freudenreichii	46,667	6-Feb-99
GB_HTG3:AC008167	174223	AC008167	Homo sapiens clone NH0172013, *** SEQUENCING IN PROGRESS ***; 7 unordered pieces.	Homo sapiens	37,451	21-Aug-99
GB_HTG3:AC008167	174223	AC008167	Homo sapiens clone NH0172013, *** SEQUENCING IN PROGRESS ***; 7 unordered pieces.	Homo sapiens	37,451	21-Aug-99
GB_HTG4:AC010118	80605	AC010118	Drosophila melanogaster chromosome 3LJ62B1 clone RPC198-10D15, *** SEQUENCING IN PROGRESS ***; 51 unordered pieces.	Drosophila melanogaster	38,627	16-OCT-1999
GB_BA1:AB024708	8734	AB024708	Corynebacterium glutamicum gltB and gltD genes for glutamine 2-oxoglutarate aminotransferase large and small subunits, complete cds.	Corynebacterium glutamicum	92,113	13-MAR-1999
GB_BA1:AB024708	8734	AB024708	Corynebacterium glutamicum gltB and gltD genes for glutamine 2-oxoglutarate aminotransferase large and small subunits, complete cds.	Corynebacterium glutamicum	93,702	13-MAR-1999
GB_EST24:AI232702	528	AI232702	EST229390 Normalized rat kidney, Bento Soares Rattus sp. cDNA clone RKICF35 3' end, mRNA sequence.	Rattus sp.	34,221	31-Jan-99
GB_HTG2:HSDJ850E	117353	AL121758	Homo sapiens chromosome 20 clone RP5-850E9, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Homo sapiens	37,965	03-DEC-1999
GB_HTG2:HSDJ850E	117353	AL121758	Homo sapiens chromosome 20 clone RP5-850E9, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Homo sapiens	37,965	03-DEC-1999
GB_PR2:CNS01DSA	159400	AL121766	Human chromosome 14 DNA sequence *** IN PROGRESS *** BAC R-412H8 of RPC1-11 library from chromosome 14 of Homo sapiens (Human), complete sequence.	Homo sapiens	38,796	11-Nov-99
GB_HTG2:AC005079	110000	AC005079	Homo sapiens clone RG252P22, *** SEQUENCING IN PROGRESS ***; 3 unordered pieces.	Homo sapiens	38,227	22-Nov-98
GB_HTG2:AC005079	110000	AC005079	Homo sapiens clone RG252P22, *** SEQUENCING IN PROGRESS ***; 3 unordered pieces.	Homo sapiens	38,227	22-Nov-98
GB_HTG2:AC005079	110000	AC005079	Homo sapiens clone RG252P22, *** SEQUENCING IN PROGRESS ***; 3 unordered pieces.	Homo sapiens	38,227	22-Nov-98
GB_BA1:PPEA3NIF	19771	X99594	Plasmid pEA3 nitrogen fixation genes.	Enterobacter agglomerans	48,826	2-Aug-96
GB_BA2:AF128444	2477	AF128444	Rhodobacter capsulatus molybdenum cofactor biosynthetic gene cluster, partial sequence.	Rhodobacter capsulatus	40,135	22-MAR-1999
GB_HTG4:AC010111	138938	AC010111	Drosophila melanogaster chromosome 3L70C1 clone RPC198-9B18, *** SEQUENCING IN PROGRESS ***; 64 unordered pieces.	Drosophila melanogaster	39,527	16-OCT-1999
GB_BA2:AF124518	1758	AF124518	Corynebacterium glutamicum 3-dehydroquinase (aroD) and shikimate dehydrogenase (aroE) genes, complete cds.	Corynebacterium glutamicum	98,237	18-MAY-1999
GB_PR3:AC004593	150221	AC004593	Homo sapiens PAC clone DJ0964C11 from 7p14-p15, complete sequence.	Homo sapiens	36,616	18-Apr-98
GB_HTG2:AC006907	188972	AC006907	Caenorhabditis elegans clone Y76B12, *** SEQUENCING IN PROGRESS ***; 25 unordered pieces.	Caenorhabditis elegans	37,095	26-Feb-99
GB_BA1:CGLYSI	4232	X60312	C. glutamicum lysI gene for L-lysine permease.	Corynebacterium glutamicum	100,000	30-Jan-92

Table 4 (continued)

	GB_HTG1:PFMAL13P 192581	AL049180	Plasmodium falciparum chromosome 13 strain 3D7, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Plasmodium falciparum	34,947	11-Aug-99
	GB_HTG1:PFMAL13P 192581	AL049180	Plasmodium falciparum chromosome 13 strain 3D7, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Plasmodium falciparum	34,947	11-Aug-99
rx00262	1197	GB_IN2:EHU89655 3219	Entamoeba histolytica unconventional myosin IB mRNA, complete cds.	Entamoeba histolytica	36,496	23-MAY-1997
		GB_IN2:EHU89655 3219	Entamoeba histolytica unconventional myosin IB mRNA, complete cds.	Entamoeba histolytica	37,544	23-MAY-1997
rx00266	531	GB_RO:AF016190 2939	Mus musculus connexin-36 (Cx36) gene, complete cds.	Mus musculus	41,856	9-Feb-99
		EM_PAT:EO9719 3505	DNA encoding precursor protein of alkaline cellulase.	Bacillus sp.	34,741	08-OCT-1997 (Rel. 52, Created)
rx00278	1155	GB_PAT:EO2133 3494	gDNA encoding alkaline cellulase.	Bacillus sp.	34,741	29-Sep-97
		GB_IN1:CELK05F6 36912	Caenorhabditis elegans cosmid K05F6.	Caenorhabditis elegans	36,943	6-Jan-98
		GB_BA1:CGU43535 2531	Corynebacterium glutamicum multidrug resistance protein (cmr) gene, complete cds.	Corynebacterium glutamicum	36,658	9-Apr-97
rx00295	1125	GB_RO:RNU30789 3510	Rattus norvegicus clone N27 mRNA.	Rattus norvegicus	38,190	20-Aug-96
		GB_BA2:CGU31281 1614	Corynebacterium glutamicum biotin synthase (bioB) gene, complete cds.	Corynebacterium glutamicum	99,111	21-Nov-96
		GB_BA1:BRLBIOBA 1647	Brevibacterium flavum gene for biotin synthetase, complete cds.	Corynebacterium glutamicum	98,489	3-Feb-99
		GB_PAT:EO3937 1005	DNA sequence encoding Brevibacterium flavum biotin-synthase.	Corynebacterium glutamicum	98,207	29-Sep-97
rx00323	1461	GB_BA1:MTCY427 38110	Mycobacterium tuberculosis H37Rv complete genome; segment 99/162.	Mycobacterium tuberculosis	35,615	24-Jun-99
		GB_BA1:MSGB32CS 36404	Mycobacterium leprae cosmid B32 DNA sequence.	Mycobacterium leprae	60,917	15-Jun-96
		GB_BA1:MTCY427 38110	Mycobacterium tuberculosis H37Rv complete genome; segment 99/162.	Mycobacterium tuberculosis	44,606	24-Jun-99
rx00324	3258	GB_BA1:MSGB32CS 36404	Mycobacterium leprae cosmid B32 DNA sequence.	Mycobacterium leprae	52,516	15-Jun-96
		GB_BA1:MTCY427 38110	Mycobacterium tuberculosis H37Rv complete genome; segment 99/162.	Mycobacterium tuberculosis	38,079	24-Jun-99
rx00330	1566	GB_OM:BOVELA 3242	Bovine elastin a mRNA, complete cds.	Bos taurus	39,351	27-Apr-93
		GB_BA1:CGTHRC 3120	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2).	Corynebacterium glutamicum	99,808	17-Jun-97
		GB_PAT:IO9078 3146	Sequence 4 from Patent WO 8809819.	Unknown.	99,617	02-DEC-1994
		GB_BA1:BLTHRESY 1892	Brevibacterium lactofermentum; ATCC 13869; DNA (genomic);	Corynebacterium glutamicum	99,170	20-Sep-95
rx00335	1554	GB_BA1:CGGLNA 3686	Corynebacterium glutamicum glnA gene.	Corynebacterium glutamicum	100,000	28-Aug-97

Table 4 (continued)

GB_BA2:AF005635	1690	AF005635	Corynebacterium glutamicum glutamine synthetase (glnA) gene, complete cds.	Corynebacterium glutamicum	98,906	14-Jun-99
GB_BA1:MSGB27CS	38793	L78817	Mycobacterium leprae cosmid B27 DNA sequence.	Mycobacterium leprae	66,345	15-Jun-96
GB_EST27:AI455217	624	AI455217	LD21828.3prime LD Drosophila melanogaster embryo pOT2 Drosophila melanogaster cDNA clone LD21828 3prime, mRNA sequence.	Drosophila melanogaster	34,510	09-MAR-1999
GB_BA2:SSU30252	2891	U30252	Synechococcus PCC7942 nucleoside diphosphate kinase and ORF2 protein genes, complete cds, ORF1 protein gene, partial cds, and neutral site 1 for vector use.	Synechococcus PCC7942	37,084	29-OCT-1999
GB_EST21:AA911262	581	AA911262	oe75a02.s1 NCI CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1417418 3' similar to gb:A18757 UROKINASE PLASMINOGEN ACTIVATOR SURFACE RECEPTOR, GPI-ANCHORED (HUMAN); mRNA sequence.	Homo sapiens	37,500	21-Apr-98
GB_BA1:MLU15187	36138	U15187	Mycobacterium leprae cosmid L296.	Mycobacterium leprae	52,972	09-MAR-1995
GB_IN2:AC004373	72722	AC004373	Drosophila melanogaster DNA sequence (P1 DS05273 (D80)), complete sequence.	Drosophila melanogaster	46,341	17-Jul-98
GB_IN2:AF145653	3197	AF145653	Drosophila melanogaster clone GH08860 BcDNA.GH08860 (BcDNA.GH08860) mRNA, complete cds.	Drosophila melanogaster	49,471	14-Jun-99
GB_BA1:AB024708	8734	AB024708	Corynebacterium glutamicum gltB and gltD genes for glutamine 2-oxoglutarate aminotransferase large and small subunits, complete cds.	Corynebacterium glutamicum	96,556	13-MAR-1999
GB_BA1:MTCY1A6	37751	Z83864	Mycobacterium tuberculosis H37Rv complete genome; segment 159/162.	Mycobacterium tuberculosis	39,486	17-Jun-98
GB_BA1:SC3A3	15901	AL109849	Streptomyces coelicolor cosmid 3A3.	Streptomyces coelicolor A3(2)	37,946	16-Aug-99
GB_BA1:AB024708	8734	AB024708	Corynebacterium glutamicum gltB and gltD genes for glutamine 2-oxoglutarate aminotransferase large and small subunits, complete cds.	Corynebacterium glutamicum	99,374	13-MAR-1999
GB_BA1:MTCY1A6	37751	Z83864	Mycobacterium tuberculosis H37Rv complete genome; segment 159/162.	Mycobacterium tuberculosis	41,333	17-Jun-98
GB_BA1:SC3A3	15901	AL109849	Streptomyces coelicolor cosmid 3A3.	Streptomyces coelicolor A3(2)	37,554	16-Aug-99
GB_BA1:AB024708	8734	AB024708	Corynebacterium glutamicum gltB and gltD genes for glutamine 2-oxoglutarate aminotransferase large and small subunits, complete cds.	Corynebacterium glutamicum	99,312	13-MAR-1999
GB_BA1:MTCY1A6	37751	Z83864	Mycobacterium tuberculosis H37Rv complete genome; segment 159/162.	Mycobacterium tuberculosis	36,971	17-Jun-98
GB_BA1:SC3A3	15901	AL109849	Streptomyces coelicolor cosmid 3A3.	Streptomyces coelicolor A3(2)	37,905	16-Aug-99
GB_VI:SBVORFS	7568	M89923	Sugarcane bacilliform virus ORF 1,2, and 3 DNA, complete cds.	Sugarcane bacilliform virus	35,843	12-Jun-93
GB_EST37:AI967505	380	AI967505	Ljirpest03-215-c10 Ljirp Lambda HybriZap two-hybrid library Lotus japonicus cDNA clone LP215-03-c10 5' similar to 60S ribosomal protein L39, mRNA sequence.	Lotus japonicus	42,593	24-Aug-99
GB_IN1:CELK09H9	37881	AF043700	Caenorhabditis elegans cosmid K09H9.	Caenorhabditis elegans	34,295	22-Jan-98

Table 4 (continued)

rx00377	1245	GB_BA1:CCU13664	1678	U13664	Caulobacter crescentus uroporphyrinogen decarboxylase homolog (hemE) gene, partial cds.	Caulobacter crescentus	36,832	24-MAR-1995
		GB_PL1:ANSDGENE	1299	Y08866	A.nidulans sD gene.	Emericella nidulans	39,603	17-OCT-1996
rx00382	1425	GB_GSS4:AQ730303	483	AQ730303	HS_5505_B1_C04_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1081 Col=7 Row=F, genomic survey sequence.	Homo sapiens	36,728	15-Jul-99
		GB_BA1:PAHEML	4444	X82072	P.aeruginosa hemL gene.	Pseudomonas aeruginosa	54,175	18-DEC-1995
		GB_BA1:MTY25D10	40838	Z95558	Mycobacterium tuberculosis H37Rv complete genome; segment 28/162.	Mycobacterium tuberculosis	61,143	17-Jun-98
		GB_BA1:MSGY224	40051	AD000004	Mycobacterium tuberculosis sequence from clone y224.	Mycobacterium tuberculosis	61,143	03-DEC-1996
rx00383	1467	GB_BA1:MLCB1222	34714	AL049491	Mycobacterium leprae cosmid B1222.	Mycobacterium leprae	43,981	27-Aug-99
		GB_HTG2:AC006269	167171	AC006269	Homo sapiens chromosome 17 clone hRPK.515_E_23 map 17, *** SEQUENCING IN PROGRESS ***; 2 ordered pieces.	Homo sapiens	35,444	10-Jun-99
		GB_HTG2:AC007638	178053	AC007638	Homo sapiens chromosome 17 clone hRPK.515_O_17 map 17, *** SEQUENCING IN PROGRESS ***; 8 unordered pieces.	Homo sapiens	34,821	22-MAY-1999
rx00391	843	GB_EST38:AW01705	613	AW017053	EST272398 Schistosoma mansoni male, Phil LoVerde/Joel Merrick Schistosoma mansoni cDNA clone SMMAS14 5' end, mRNA sequence.	Schistosoma mansoni	40,472	10-Sep-99
		GB_PAT:AR065852	32207	AR065852	Sequence 20 from patent US 5849564.	Unknown.	38,586	29-Sep-99
		GB_VI:AF148805	28559	AF148805	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds.	Kaposi's sarcoma-associated herpesvirus	38,509	2-Aug-99
rx00393	1017	GB_BA1:MTY25D10	40838	Z95558	Mycobacterium tuberculosis H37Rv complete genome; segment 28/162.	Mycobacterium tuberculosis	36,308	17-Jun-98
		GB_BA1:MSGY224	40051	AD000004	Mycobacterium tuberculosis sequence from clone y224.	Mycobacterium tuberculosis	39,282	03-DEC-1996
rx00402	623	GB_BA1:MLB1306	7762	Y13803	Mycobacterium leprae cosmid B1306 DNA.	Mycobacterium leprae	39,228	24-Jun-97
		GB_BA2:AF052652	2096	AF052652	Corynebacterium glutamicum homoserine O-acetyltransferase (metA) gene, complete cds.	Corynebacterium glutamicum	99,672	19-MAR-1998
		GB_BA2:AF109162	4514	AF109162	Corynebacterium diphtheriae heme uptake locus, complete sequence.	Corynebacterium diphtheriae	40,830	8-Jun-99
		GB_BA2:AF092918	20758	AF092918	Pseudomonas alcaligenes outer membrane Xcp-secretion system gene cluster.	Pseudomonas alcaligenes	50,161	06-DEC-1998
rx00403	1254	GB_BA2:AF052652	2096	AF052652	Corynebacterium glutamicum homoserine O-acetyltransferase (metA) gene, complete cds.	Corynebacterium glutamicum	99,920	19-MAR-1998
		GB_BA1:MTV016	53662	AL021841	Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.	Mycobacterium tuberculosis	52,898	23-Jun-99
		GB_EST23:AI111288	750	AI111288	SWOvAMCAQ02A05SK Onchocerca volvulus adult male cDNA (SAW98MLW-OvAM) Onchocerca volvulus cDNA clone SWOvAMCAQ02A05 5', mRNA sequence.	Onchocerca volvulus	37,565	31-Aug-98

Table 4 (continued)

rx00405	613	GB_BA1:MTV016	53662	AL021841	Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.	Mycobacterium tuberculosis	57,259	23-Jun-99
		GB_PR4:AC005145	143678	AC005145	Homo sapiens Xp22-166-169 GSHB-523A23 (Genome Systems Human BAC library) complete sequence.	Homo sapiens	34,179	08-DEC-1998
		GB_BA1:MTV016	53662	AL021841	Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.	Mycobacterium tuberculosis	40,169	23-Jun-99
rx00420	1587	GB_BA1:MTY13D12	37085	Z80343	Mycobacterium tuberculosis H37Rv complete genome; segment 156/162.	Mycobacterium tuberculosis	62,031	17-Jun-98
		GB_BA1:MSGY126	37164	AD000012	Mycobacterium tuberculosis sequence from clone y126.	Mycobacterium tuberculosis	61,902	10-DEC-1996
		GB_BA1:MSGB971C	37566	L78821	Mycobacterium leprae cosmid B971 DNA sequence.	Mycobacterium leprae	39,651	15-Jun-96
rx00435	1296	GB_BA1:AFACBBTZ	2760	M68904	Alcaligenes eutrophus chromosomal transketolase (cbbTc) and phosphoglycolate phosphatase (cbbZc) genes, complete cds.	Ralstonia eutropha	38,677	27-Jul-94
		GB_HTG4:AC009541	169583	AC009541	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***; 25 unordered pieces.	Homo sapiens	36,335	12-OCT-1999
		GB_HTG4:AC009541	169583	AC009541	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***; 25 unordered pieces.	Homo sapiens	36,335	12-OCT-1999
rx00437	579	GB_PR4:AC005951	155450	AC005951	Homo sapiens chromosome 17, clone hRPK.372_K_20, complete sequence.	Homo sapiens	31,738	18-Nov-98
		GB_BA1:SC2A11	22789	AL031184	Streptomyces coelicolor cosmid 2A11.	Streptomyces coelicolor	43,262	5-Aug-98
		GB_PR4:AC005951	155450	AC005951	Homo sapiens chromosome 17, clone hRPK.372_K_20, complete sequence.	Homo sapiens	37,647	18-Nov-98
rx00439	591	GB_BA1:MTV016	53662	AL021841	Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.	Mycobacterium tuberculosis	37,088	23-Jun-99
		GB_PL2:AF167358	1022	AF167358	Rumex acetosa expansin (EXP3) gene, partial cds.	Rumex acetosa	46,538	17-Aug-99
		GB_HTG3:AC009120	269445	AC009120	Homo sapiens chromosome 16 clone RPC1-11_484E3, *** SEQUENCING IN PROGRESS ***; 34 unordered pieces.	Homo sapiens	43,276	3-Aug-99
rx00440	582	GB_BA2:SKZ86111	7860	Z86111	Streptomyces lividans rpsP, trmD, rplS, sipW, sipX, sipY, sipZ, mutT genes and 4 open reading frames.	Streptomyces lividans	43,080	27-OCT-1999
		GB_BA1:SC2E1	38962	AL023797	Streptomyces coelicolor cosmid 2E1.	Streptomyces coelicolor	42,931	4-Jun-98
		GB_BA1:SC2E1	38962	AL023797	Streptomyces coelicolor cosmid 2E1.	Streptomyces coelicolor	36,702	4-Jun-98
rx00441	1287	GB_PR2:HS173D1	117338	AL031984	Human DNA sequence from clone 173D1 on chromosome 1p36.21-36.33. Contains ESTs, STSs and GSSs, complete sequence.	Homo sapiens	38,027	23-Nov-99
		GB_HTG2:HSDJ719K	267114	AL109931	Homo sapiens chromosome X clone RP4-719K3 map q21.1-21.31, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Homo sapiens	34,521	03-DEC-1999
		GB_HTG2:HSDJ719K	267114	AL109931	Homo sapiens chromosome X clone RP4-719K3 map q21.1-21.31, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Homo sapiens	34,521	03-DEC-1999
rx00446	987	GB_BA1:SCD78	36224	AL034355	Streptomyces coelicolor cosmid D78.	Streptomyces coelicolor	56,410	26-Nov-98
		GB_HTG4:AC009367	226055	AC009367	Drosophila melanogaster chromosome 3L76A2 clone RPC198-48B15, *** SEQUENCING IN PROGRESS ***; 44 unordered pieces.	Drosophila melanogaster	34,959	16-OCT-1999
		GB_HTG4:AC009367	226055	AC009367	Drosophila melanogaster chromosome 3L76A2 clone RPC198-48B15, *** SEQUENCING IN PROGRESS ***; 44 unordered pieces.	Drosophila melanogaster	34,959	16-OCT-1999

Table 4 (continued)

rxa00448	1143	GB_PR3:AC003670	88945	AC003670	Homo sapiens 12q13.1 PAC RPC11-130F5 (Roswell Park Cancer Institute Human PAC library) complete sequence.	Homo sapiens	35,682	9-Jun-98
		GB_HTG2:AF029367	148676	AF029367	Homo sapiens chromosome 12 clone RPC1-1 130F5 map 12q13.1, *** SEQUENCING IN PROGRESS ***; 156 unordered pieces.	Homo sapiens	31,373	18-OCT-1997
		GB_HTG2:AF029367	148676	AF029367	Homo sapiens chromosome 12 clone RPC1-1 130F5 map 12q13.1, *** SEQUENCING IN PROGRESS ***; 156 unordered pieces.	Homo sapiens	31,373	18-OCT-1997
rxa00450	424	GB_HTG2:AC007824	133361	AC007824	Drosophila melanogaster chromosome 3 clone BACR02L16 (D715) RPCL-98 02.L.16 map 89E-90A strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 91 unordered pieces.	Drosophila melanogaster	40,000	2-Aug-99
		GB_HTG2:AC007824	133361	AC007824	Drosophila melanogaster chromosome 3 clone BACR02L16 (D715) RPCL-98 02.L.16 map 89E-90A strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 91 unordered pieces.	Drosophila melanogaster	40,000	2-Aug-99
		GB_EST35:AI818057	412	AI818057	wk14a08.x1 NCL_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2412278 3' similar to gb:Y00764 UBQUINOL-CYTOCHROME C REDUCTASE 11 KD PROTEIN (HUMAN); mRNA sequence.	Homo sapiens	35,714	24-Aug-99
rxa00461	975	GB_BA1:MLCB1779	43254	Z98271	Mycobacterium leprae cosmid B1779.	Mycobacterium leprae	39,308	8-Aug-97
		GB_IN1:DMC86E4	29352	AL021086	Drosophila melanogaster cosmid clone 86E4.	Drosophila melanogaster	37,487	27-Apr-99
		GB_GSS15:AQ64032	467	AQ640325	927P1-2H3.TP 927P1 Trypanosoma brucei genomic clone 927P1-2H3, genomic survey sequence.	Trypanosoma brucei	38,116	8-Jul-99
rxa00465								
rxa00487	1692	GB_BA1:BAGUAA	3866	Y10499	B. ammoniagenes guaA gene.	Corynebacterium ammoniagenes	74,259	8-Jan-98
		GB_BA2:U00015	42325	U00015	Mycobacterium leprae cosmid B1620.	Mycobacterium leprae	37,248	01-MAR-1994
		GB_BA1:MTCY78	33818	Z77165	Mycobacterium tuberculosis H37Rv complete genome; segment 145/162.	Mycobacterium tuberculosis	39,725	17-Jun-98
rxa00488	1641	GB_BA1:MTCY78	33818	Z77165	Mycobacterium tuberculosis H37Rv complete genome; segment 145/162.	Mycobacterium tuberculosis	39,451	17-Jun-98
		GB_BA2:U00015	42325	U00015	Mycobacterium leprae cosmid B1620.	Mycobacterium leprae	39,178	01-MAR-1994
rxa00489	1245	GB_BA1:SCAJ10601	4592	AJ010601	Streptomyces coelicolor A3(2) DNA for whiD and whiK loci.	Streptomyces coelicolor	60,835	17-Sep-98
		GB_BA2:U00015	42325	U00015	Mycobacterium leprae cosmid B1620.	Mycobacterium leprae	38,041	01-MAR-1994
		GB_HTG2:HS225E12	126464	AL031772	Homo sapiens chromosome 6 clone RP1-225E12 map q24, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Homo sapiens	36,756	03-DEC-1999
		GB_HTG2:HS225E12	126464	AL031772	Homo sapiens chromosome 6 clone RP1-225E12 map q24, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Homo sapiens	36,756	03-DEC-1999
rxa00533	1155	GB_BA1:CGLYS	2803	X57226	C. glutamicum lysC-alpha, lysC-beta and asd genes for aspartokinase-alpha and -beta subunits, and aspartate beta semialdehyde dehydrogenase, respectively (EC 2.7.2.4; EC 1.2.1.11).	Corynebacterium glutamicum	99,913	17-Feb-97

Table 4 (continued)

GB_BA1:CGCYSCAS	1591	X82928	C. glutamicum aspartate-semialdehyde dehydrogenase gene.	Corynebacterium glutamicum	99,221	17-Feb-97
GB_PAT:A07546	2112	A07546	Recombinant DNA fragment (PstI-XhoI).	synthetic construct	99,391	30-Jul-93
GB_BA1:CGLYS	2803	X57226	C. glutamicum lysC-alpha, lysC-beta and asd genes for aspartokinase-alpha and -beta subunits, and aspartate beta semialdehyde dehydrogenase, respectively (EC 2.7.2.4; EC 1.2.1.11).	Corynebacterium glutamicum	99,856	17-Feb-97
GB_BA1:CORASKD	2957	L16848	Corynebacterium flavum aspartokinase (ask), and aspartate-semialdehyde dehydrogenase (asd) genes, complete cds.	Corynebacterium flavesens	98,701	11-Jun-93
GB_PAT:E14514	1643	E14514	DNA encoding Brevibacterium aspartokinase.	Corynebacterium glutamicum	98,773	28-Jul-99
GB_BA1:CGLEUA	3492	X70959	C. glutamicum gene leuA for isopropylmalate synthase.	Corynebacterium glutamicum	100,000	10-Feb-99
GB_BA1:MTV025	121125	AL022121	Mycobacterium tuberculosis H37Rv complete genome; segment 155/162.	Mycobacterium tuberculosis	68,003	24-Jun-99
GB_BA1:MTU8526	2412	U88526	Mycobacterium tuberculosis putative alpha-isopropyl malate synthase (leuA) gene, complete cds.	Mycobacterium tuberculosis	68,185	26-Feb-97
GB_BA2:SCD25	41622	AL118514	Streptomyces coelicolor cosmid D25.	Streptomyces coelicolor A3(2)	63,187	21-Sep-99
GB_BA1:MTCY7H7A	10451	Z95618	Mycobacterium tuberculosis H37Rv complete genome; segment 39/162.	Mycobacterium tuberculosis	62,401	17-Jun-98
GB_BA1:MTU34956	2462	U34956	Mycobacterium tuberculosis phosphoribosylformylglycinamide synthase (purL) gene, complete cds.	Mycobacterium tuberculosis	62,205	28-Jan-97
GB_PAT:192052	2115	I92052	Sequence 19 from patent US 5726299.	Unknown.	98,359	01-DEC-1998
GB_BA1:MLCB5	38109	Z95151	Mycobacterium leprae cosmid B5.	Mycobacterium leprae	62,468	24-Jun-97
GB_BA1:MTCY369	36850	Z80226	Mycobacterium tuberculosis H37Rv complete genome; segment 36/162.	Mycobacterium tuberculosis	60,814	17-Jun-98
GB_BA1:BAPURF	1885	X91252	B. ammoniagenes purF gene.	Corynebacterium ammoniagenes	66,095	5-Jun-97
GB_BA1:MLU15182	40123	U15182	Mycobacterium leprae cosmid B2266.	Mycobacterium leprae	64,315	09-MAR-1995
GB_BA1:MTCY7H7A	10451	Z95618	Mycobacterium tuberculosis H37Rv complete genome; segment 39/162.	Mycobacterium tuberculosis	64,863	17-Jun-98
GB_PAT:AR016483	2104	AR016483	Sequence 1 from patent US 5776740.	Unknown.	98,810	05-DEC-1998
EM_PAT:E11273	2104	E11273	DNA encoding serine hydroxymethyl transferase.	Corynebacterium glutamicum	98,810	08-OCT-1997 (Rel. 52, Created)
GB_PAT:E12594	2104	E12594	DNA encoding serine hydroxymethyltransferase from Brevibacterium flavum.	Corynebacterium glutamicum	98,810	24-Jun-98
GB_PAT:E12594	2104	E12594	DNA encoding serine hydroxymethyltransferase from Brevibacterium flavum.	Corynebacterium glutamicum	99,368	24-Jun-98

Table 4 (continued)

	GB_PAT:AR016483	2104	AR016483	Sequence 1 from patent US 5776740.	Unknown.	99,368	05-DEC-1998
	EM_PAT:E11273	2104	E11273	DNA encoding serine hydroxymethyl transferase.	Corynebacterium glutamicum	99,368	08-OCT-1997 (Rel. 52, Created) 24-Jun-98
rx00581	GB_PAT:E12594	2104	E12594	DNA encoding serine hydroxymethyltransferase from Brevibacterium flavum.	Corynebacterium glutamicum	37,071	08-OCT-1997 (Rel. 52, Created) 05-DEC-1998
	EM_PAT:E11273	2104	E11273	DNA encoding serine hydroxymethyl transferase.	Corynebacterium glutamicum	37,071	08-OCT-1997 (Rel. 52, Created) 05-DEC-1998
	GB_PAT:AR016483	2104	AR016483	Sequence 1 from patent US 5776740.	Unknown.	37,071	05-DEC-1998
rx00584	GB_BA1:CORAHPS	2570	L07603	Corynebacterium glutamicum 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase gene, complete cds.	Corynebacterium glutamicum	98,236	26-Apr-93
	GB_BA1:AOPCZA361	37941	AJ223998	Amycolatopsis orientalis cosmid PCZA361.	Amycolatopsis orientalis	54,553	29-MAR-1999
rx00618	GB_BA1:D90714	14358	D90714	Escherichia coli genomic DNA. (16.8 - 17.1 min).	Escherichia coli	53,312	7-Feb-99
	GB_EST19:AA802737	280	AA802737	GM06236.5prime GM Drosophila melanogaster ovary BlueScript Drosophila melanogaster cDNA clone GM06236 5prime, mRNA sequence.	Drosophila melanogaster	39,928	25-Nov-98
	GB_EST28:AI534381	581	AI534381	SD07186.5prime SD Drosophila melanogaster Schneider L2 cell culture pOT2 Drosophila melanogaster cDNA clone SD07186 5prime similar to X89858. Anti FBgn0011558 PID:g927407 SPTREMBL:Q24240, mRNA sequence.	Drosophila melanogaster	41,136	18-MAR-1999
rx00619	GB_IN1:DMANILLIN	4029	X89858	D.melanogaster mRNA for anillin protein.	Drosophila melanogaster	34,398	8-Nov-95
	GB_BA1:MTCY369	36850	Z80226	Mycobacterium tuberculosis H37Rv complete genome; segment 36/162.	Mycobacterium tuberculosis	62,776	17-Jun-98
	GB_BA1:MLCB5	38109	Z95151	Mycobacterium leprae cosmid B5.	Mycobacterium leprae	61,831	24-Jun-97
	GB_PAT:A60305	1845	A60305	Sequence 5 from Patent WO9708323.	unidentified	61,785	06-MAR-1998
rx00620	GB_PL2:AF063247	1450	AF063247	Pneumocystis carinii f. sp. ratti enolase mRNA, complete cds.	Pneumocystis carinii f. sp. ratti	41,060	5-Jan-99
	GB_BA1:STMAPP	2069	M91546	Streptomyces lividans aminopeptidase P (PepP) gene, complete cds.	Streptomyces lividans	37,126	12-Jun-93
	GB_HTG3:AC008763	214575	AC008763	Homo sapiens chromosome 19 clone CITB-E1_3214H19, *** SEQUENCING IN PROGRESS ***, 21 unordered pieces.	Homo sapiens	40,020	3-Aug-99
rx00624	GB_IN1:CEY41E3	150641	Z95559	Caenorhabditis elegans cosmid Y41E3, complete sequence.	Caenorhabditis elegans	36,986	2-Sep-99
	GB_EST13:AA362167	372	AA362167	EST71561 Macrophage I Homo sapiens cDNA 5' end, mRNA sequence.	Homo sapiens	38,378	21-Apr-97
rx00626	GB_IN1:CEY41E3	150641	Z95559	Caenorhabditis elegans cosmid Y41E3, complete sequence.	Caenorhabditis elegans	37,694	2-Sep-99
	GB_BA1:MTCY369	36850	Z80226	Mycobacterium tuberculosis H37Rv complete genome; segment 36/162.	Mycobacterium tuberculosis	57,971	17-Jun-98
	GB_BA1:MLCB5	38109	Z95151	Mycobacterium leprae cosmid B5.	Mycobacterium leprae	58,806	24-Jun-97
	GB_BA1:MLU15187	36138	U15187	Mycobacterium leprae cosmid L296.	Mycobacterium leprae	38,007	09-MAR-1995



Table 4 (continued)

rx00632	795	GB_BA1:BRLBIOAD	2272	D14083	Brevibacterium flavum genes for 7,8-diaminopelargonic acid aminotransferase and dethiobiotin synthetase, complete cds.	Corynebacterium glutamicum	97,358	3-Feb-99
		GB_PAT:E04041	675	E04041	DNA sequence coding for dethiobiotinsynthetase.	Corynebacterium glutamicum	98,074	29-Sep-97
		GB_PAT:E04040	1272	E04040	DNA sequence coding for diamino pelargonic acid aminotransferase.	Corynebacterium glutamicum	93,814	29-Sep-97
rx00633	1392	GB_BA1:BRLBIOAD	2272	D14083	Brevibacterium flavum genes for 7,8-diaminopelargonic acid aminotransferase and dethiobiotin synthetase, complete cds.	Corynebacterium glutamicum	95,690	3-Feb-99
		GB_PAT:E04040	1272	E04040	DNA sequence coding for diamino pelargonic acid aminotransferase.	Corynebacterium glutamicum	95,755	29-Sep-97
		GB_BA2:EHU38519	1290	U38519	Erwinia herbicola adenosylmethionine-8-amino-7-oxononanoate transaminase	Erwinia herbicola	55,564	4-Nov-96
rx00688	666	GB_BA1:MTV041	28826	AL021958	(bioA) gene, complete cds.	Mycobacterium tuberculosis	60,030	17-Jun-98
		GB_BA1:BRLSECY	1516	D14162	Brevibacterium flavum gene for SecY protein (complete cds) and gene or adenylate kinase (partial cds).	Corynebacterium glutamicum	99,563	3-Feb-99
		GB_BA2:MBU77912	7163	U77912	Mycobacterium bovis MBE50a gene, partial cds; and MBE50b, MBE50c, preprotein translocase SecY subunit (secY), adenylate kinase (adk), methionine aminopeptidase (map), RNA polymerase ECF sigma factor (sigE50), MBE50d, and MBE50e genes, complete cds.	Mycobacterium bovis	60,030	27-Jan-99
rx00708	930	GB_BA2:AF157493	25454	AF157493	Zymomonas mobilis ZM4 fosmid clone 42D7, complete sequence.	Zymomonas mobilis	39,116	5-Jul-99
		GB_PAT:100836	1853	I00836	Sequence 1 from Patent US 4758514.	Unknown.	47,419	21-MAY-1993
		GB_PAT:E00311	1853	E00311	DNA coding of 2,5-diketogluconic acid reductase.	unidentified	47,419	29-Sep-97
rx00717	1083	GB_PAT:178753	1187	I78753	Sequence 9 from patent US 5693781.	Unknown.	37,814	3-Apr-98
		GB_PAT:192042	1187	I92042	Sequence 9 from patent US 5726299.	Unknown.	37,814	01-DEC-1998
		GB_BA1:MTCI125	37432	Z98268	Mycobacterium tuberculosis H37Rv complete genome; segment 76/162.	Mycobacterium tuberculosis	50,647	17-Jun-98
rx00718	831	GB_BA1:MTCI125	37432	Z98268	Mycobacterium tuberculosis H37Rv complete genome; segment 76/162.	Mycobacterium tuberculosis	55,228	17-Jun-98
		GB_BA1:MTCI125	37432	Z98268	Mycobacterium tuberculosis H37Rv complete genome; segment 76/162.	Mycobacterium tuberculosis	40,300	17-Jun-98
		GB_GSS12:AQ42075	671	AQ42075	RPCI-11-168G18.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-168G18, genomic survey sequence.	Homo sapiens	35,750	23-MAR-1999
rx00727	1035	GB_HTG3:AC008332	118545	AC008332	Drosophila melanogaster chromosome 2 clone BACR48D10 (D867) RPCI-98 48.D.10 map 34A-34A strain y; cn bw sp, *** SEQUENCING IN PROGRESS	Drosophila melanogaster	40,634	6-Aug-99
		GB_HTG3:AC008332	118545	AC008332	***, 78 unordered pieces.			
		GB_HTG3:AC008332	118545	AC008332	Drosophila melanogaster chromosome 2 clone BACR48D10 (D867) RPCI-98 48.D.10 map 34A-34A strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 78 unordered pieces.	Drosophila melanogaster	40,634	6-Aug-99

Table 4 (continued)

rx00766	966	GB_HTG3:AC008332	118545	AC008332	Drosophila melanogaster chromosome 2 clone BACR48D10 (D867) RPC1-98 48.D.10 map 34A-34A strain Y; cn bw sp. *** SEQUENCING IN PROGRESS***, 78 unordered pieces.	Drosophila melanogaster	33,888	6-Aug-99
		GB_HTG2:AC006789	83823	AC006789	Caenorhabditis elegans clone Y49F6, *** SEQUENCING IN PROGRESS ***	Caenorhabditis elegans	36,737	25-Feb-99
		GB_HTG2:AC006789	83823	AC006789	2 unordered pieces.			
		GB_BA1:D90810	20476	D90810	Caenorhabditis elegans clone Y49F6, *** SEQUENCING IN PROGRESS ***	Caenorhabditis elegans	36,737	25-Feb-99
		GB_BA1:MTV043	68848	AL022004	2 unordered pieces.			
rx00770	1293	GB_BA1:MLU15182	40123	U15182	E.coli genomic DNA, Kohara clone #319(37.4-37.8 min.).	Escherichia coli	36,526	29-MAY-1997
		GB_BA2:SCD25	41622	AL118514	Mycobacterium tuberculosis H37Rv complete genome; segment 40/162.	Mycobacterium tuberculosis	66,193	24-Jun-99
		GB_HTG1:CER08A5	51920	Z82281	Mycobacterium leprae cosmid B2266.	Mycobacterium leprae	61,443	09-MAR-1995
		GB_HTG1:CER08A5	51920	Z82281	Streptomyces coelicolor cosmid D25.	Streptomyces coelicolor	59,938	21-Sep-99
rx00779	1056	GB_PL2:AF078693	1492	AF078693	Caenorhabditis elegans chromosome V clone R08A5, *** SEQUENCING IN PROGRESS ***	Caenorhabditis elegans	64,896	14-OCT-1998
		GB_BA1:MTCY98	31225	Z83860	Caenorhabditis elegans chromosome V clone R08A5, *** SEQUENCING IN PROGRESS ***	Caenorhabditis elegans	64,896	14-OCT-1998
		GB_BA1:AVINIFREG	7099	M60090	Chlamydomonas reinhardtii putative O-acetylserine(thiol)lyase precursor (Crcys-1A) mRNA, nuclear gene encoding organellar protein, complete cds.	Chlamydomonas reinhardtii	57,970	3-Nov-99
rx00838	1023	GB_BA2:AF001780	6701	AF001780	Mycobacterium tuberculosis H37Rv complete genome; segment 103/162.	Mycobacterium tuberculosis	54,410	17-Jun-98
		GB_EST1:Z30506	329	Z30506	Azotobacter chroococcum nifU, nifS, nifV, nifP, nifH, nifW, nifZ and nifM genes, complete cds.	Azotobacter chroococcum	51,729	26-Apr-93
		GB_PL2:AC006258	110469	AC006258	Cyanothece PCC 8801 NifP (nifP), nitrogenase (nifB), FdxN (fdxN), NifS (nifS) and NifU (nifU) genes, complete cds, and NifH (nifH) gene, partial cds.	Cyanothece PCC8801	36,309	08-MAR-1999
		GB_EST37:AI998439	455	AI998439	ATTS2430 AC16H Arabidopsis thaliana cDNA clone TAI306 3', mRNA sequence.	Arabidopsis thaliana	44,308	11-MAR-1994
rx00863	867	GB_BA1:BLDAPAB	3572	Z21502	Arabidopsis thaliana BAC F18G18 from chromosome V near 60.5 cM, complete sequence.	Arabidopsis thaliana	35,571	28-DEC-1998
		GB_PAT:E16749	2001	E16749	clone 701545695, mRNA sequence.	Arabidopsis thaliana	36,044	8-Sep-99
		GB_PAT:E14520	2001	E14520	B.lactofermentum dapA and dapB genes for dihydrodipicolinate synthase and dihydrodipicolinate reductase.	Corynebacterium glutamicum	99,539	16-Aug-93
		GB_BA1:CGDAPB	1902	X67737	gDNA encoding dihydrodipicolinate synthase (DDPS).	Corynebacterium glutamicum	99,539	28-Jul-99
		GB_BA1:BLDAPAB	3572	Z21502	DNA encoding Brevibacterium dihydrodipicolinic acid synthase.	Corynebacterium glutamicum	99,539	28-Jul-99
rx00864	873	GB_BA1:CGDAPB	1902	X67737	B.lactofermentum dapA and dapB genes for dihydrodipicolinate synthase and dihydrodipicolinate reductase.	Corynebacterium glutamicum	99,885	16-Aug-93
		GB_BA1:CGDAPB	1902	X67737	C.glutamicum dapB gene for dihydrodipicolinate reductase.	Corynebacterium glutamicum	100,000	1-Apr-93

Table 4 (continued)

rx00865	1026	GB_PAT:E14520	2001	E14520	DNA encoding Brevibacterium dihydrodipicolinate synthase.	Corynebacterium glutamicum	100,000	28-Jul-99
		GB_BA1:BLDAPAB	3572	Z21502	B.lactofermentum dapA and dapB genes for dihydrodipicolinate synthase and dihydrodipicolinate reductase.	Corynebacterium glutamicum	100,000	16-Aug-93
		GB_PAT:E16752	1411	E16752	gDNA encoding dihydrodipicolinate reductase (DDPR).	Corynebacterium glutamicum	99,805	28-Jul-99
rx00867	650	GB_PAT:AR038113	1411	AR038113	Sequence 18 from patent US 5804414.	Unknown.	99,805	29-Sep-99
		GB_BA1:MTV002	56414	AL008967	Mycobacterium tuberculosis H37Rv complete genome; segment 122/162.	Mycobacterium tuberculosis	39,179	17-Jun-98
		GB_BA1:MLCB22	40281	Z98741	Mycobacterium leprae cosmid B22.	Mycobacterium leprae	39,482	22-Aug-97
		GB_BA1:SAU19858	2838	U19858	Streptomyces antibioticus guanosine pentaphosphate synthetase (gpsI) gene, complete cds.	Streptomyces antibioticus	69,706	25-OCT-1996
rx00873	779	GB_BA1:SCO001206	9184	AJ001206	Streptomyces coelicolor A3(2), glycogen metabolism cluster II.	Streptomyces coelicolor	63,415	29-MAR-1999
		GB_BA1:SCO001205	9589	AJ001205	Streptomyces coelicolor A3(2) glycogen metabolism clusterI.	Streptomyces coelicolor	61,617	29-MAR-1999
		GB_BA1:D78198	2304	D78198	Pimelobacter sp. DNA for trehalose synthase, complete cds.	Pimelobacter sp.	60,594	5-Feb-99
rx00884	1263	GB_BA1:MTCY253	41230	Z81368	Mycobacterium tuberculosis H37Rv complete genome; segment 106/162.	Mycobacterium tuberculosis	37,785	17-Jun-98
		GB_BA1:MSGY222	41156	AD000010	Mycobacterium tuberculosis sequence from clone y222.	Mycobacterium tuberculosis	38,006	03-DEC-1996
		GB_GSS15:AQ65460	468	AQ654600	Sheared DNA-1O14.TF Sheared DNA Trypanosoma brucei genomic clone	Trypanosoma brucei	33,974	22-Jun-99
rx00891	1102	GB_BA1:MTCI418B	11700	Z96071	Sheared DNA-1O14, genomic survey sequence. Mycobacterium tuberculosis H37Rv complete genome; segment 77/162.	Mycobacterium tuberculosis	63,297	18-Jun-98
		GB_BA1:SCO001206	9184	AJ001206	Streptomyces coelicolor A3(2), glycogen metabolism cluster II.	Streptomyces coelicolor	61,965	29-MAR-1999
		GB_BA1:SCO001205	9589	AJ001205	Streptomyces coelicolor A3(2) glycogen metabolism clusterI.	Streptomyces coelicolor	61,727	29-MAR-1999
rx00952	963	EM_PAT:E10963	3118	E10963	gDNA encoding tryptophan synthase.	Corynebacterium glutamicum	99,688	08-OCT-1997 (Rel. 52, Created)
		GB_BA1:BLTRP	7725	X04960	Brevibacterium lactofermentum tryptophan operon.	Corynebacterium glutamicum	98,847	10-Feb-99
rx00954	644	GB_PAT:E01688	7725	E01688	Genomic DNA of trp operon of prepibacterium latophelmentamn.	unidentified	98,428	29-Sep-97
		GB_PAT:E01375	7726	E01375	DNA sequence of tryptophan operon.	Corynebacterium glutamicum	98,758	29-Sep-97
		GB_PAT:E01688	7725	E01688	Genomic DNA of trp operon of prepibacterium latophelmentamn.	unidentified	98,758	29-Sep-97
		GB_BA1:BLTRP	7725	X04960	Brevibacterium lactofermentum tryptophan operon.	Corynebacterium glutamicum	98,758	10-Feb-99
rx00955	1545	GB_PAT:E01375	7726	E01375	DNA sequence of tryptophan operon.	Corynebacterium glutamicum	98,372	29-Sep-97

Table 4 (continued)

	GB_BA1:BLTRP	7725	X04960	Brevibacterium lactofermentum tryptophan operon.	Corynebacterium glutamicum	98,372	10-Feb-99
rx00956	GB_PAT:E01688	7725	E01688	Genomic DNA of trp operon of prepibacterium latophelmentam.	glutamicum	98,242	29-Sep-97
	EM_PAT:E10963	3118	E10963	gDNA encoding tryptophan synthase.	Corynebacterium glutamicum	98,949	08-OCT-1997 (Rel. 52, Created) 10-Feb-99
rx00957	GB_BA1:BLTRP	7725	X04960	Brevibacterium lactofermentum tryptophan operon.	Corynebacterium glutamicum	99,107	29-Sep-97
	GB_PAT:E01375	7726	E01375	DNA sequence of tryptophan operon.	Corynebacterium glutamicum	98,945	10-Feb-99
rx00958	GB_BA1:BLTRP	7725	X04960	Brevibacterium lactofermentum tryptophan operon.	Corynebacterium glutamicum	99,165	29-Sep-97
	GB_PAT:E01375	7726	E01375	DNA sequence of tryptophan operon.	Corynebacterium glutamicum	98,927	10-Feb-99
rx00970	GB_PAT:E01688	7725	E01688	Genomic DNA of trp operon of prepibacterium latophelmentam.	glutamicum	98,867	29-Sep-97
	GB_BA1:BLTRP	7725	X04960	Brevibacterium lactofermentum tryptophan operon.	Corynebacterium glutamicum	98,792	10-Feb-99
rx00972	GB_PAT:E01375	7726	E01375	DNA sequence of tryptophan operon.	Corynebacterium glutamicum	98,792	29-Sep-97
	GB_PAT:E01688	7725	E01688	Genomic DNA of trp operon of prepibacterium latophelmentam.	glutamicum	98,658	29-Sep-97
rx00972	GB_BA1:CGHOMTHR	3685	Y00546	Corynebacterium glutamicum hom-thrB genes for homoserine dehydrogenase and homoserine Kinase.	glutamicum	99,905	12-Sep-93
	GB_PAT:109077	3685	109077	Sequence 1 from Patent WO 8809819.	Unknown.	99,810	02-DEC-1994
rx00972	GB_PAT:E01358	2615	E01358	DNA encoding for homoserine dehydrogenase(HDH)and homoserine kinase(HK).	Corynebacterium glutamicum	97,524	29-Sep-97
	GB_PAT:E16755	3579	E16755	gDNA encoding diaminopimelate decarboxylase (DDC) and arginyl-tRNA synthase.	Corynebacterium glutamicum	99,931	28-Jul-99
rx00981	GB_PAT:AR038110	3579	AR038110	Sequence 15 from patent US 5804414.	glutamicum	99,931	29-Sep-99
	GB_PAT:E14508	3579	E14508	DNA encoding Brevibacterium diaminopimelic acid decarboxylase and arginyl-tRNA synthase.	Unknown.	99,931	28-Jul-99
rx00981	GB_OV:GGA245664	512	AJ245664	Gallus gallus partial mRNA for ATP-citrate lyase (ACL gene).	glutamicum	37,538	28-Sep-99
	GB_PL2:AC007887	159434	AC007887	Genomic sequence for Arabidopsis thaliana BAC F1504 from chromosome I, complete sequence.	Gallus gallus	37,600	04-OCT-1999
rx00989	GB_GSS1:CNS00RN W	542	AL087338	Arabidopsis thaliana genome survey sequence T7 end of BAC F14D7 of IGF library from strain Columbia of Arabidopsis thaliana, genomic survey sequence.	Arabidopsis thaliana	41,264	28-Jun-99
	GB_BA1:MTV008	63033	AL021246	Mycobacterium tuberculosis H37Rv complete genome; segment 108/162.	Mycobacterium tuberculosis	40,773	17-Jun-98
rx00989	GB_BA1:SCVALSFP	3619	Y13070	S.coelicolor valS, fpgs, ndk genes.	Streptomyces coelicolor	58,119	03-MAR-1998
	GB_BA1:MTV008	63033	AL021246	Mycobacterium tuberculosis H37Rv complete genome; segment 108/162.	Mycobacterium tuberculosis	38,167	17-Jun-98

Table 4 (continued)

ra00997	705	GB_BA2:CGU31225	1817	U31225	Corynebacterium glutamicum L-proline:NADP+ 5-oxido-reductase (proC) gene, complete cds.	Corynebacterium glutamicum	40,841	2-Aug-96
		GB_HTG1:CEY39C12	282838	AL009026	Caenorhabditis elegans chromosome IV clone Y39C12, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	36,416	28-OCT-1999
		GB_IN1:CEB0001	39416	Z69634	Caenorhabditis elegans cosmid B0001, complete sequence.	Caenorhabditis elegans	36,416	2-Sep-99
ra01019	1110	GB_HTG2:AC005052	144734	AC005052	Homo sapiens clone RG038K21, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.	Homo sapiens	39,172	12-Jun-98
		GB_HTG2:AC005052	144734	AC005052	Homo sapiens clone RG038K21, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.	Homo sapiens	39,172	12-Jun-98
		GB_GSS9:AQ171808	512	AQ171808	HS_3179_A1_G03_T7 CIT Approved Human Genomic Sperm Library D	Homo sapiens	34,661	17-OCT-1998
					Homo sapiens genomic clone Plate=3179 Col=5 Row=M, genomic survey sequence.			
ra01026	1782	GB_BA1:SC1C2	42210	AL031124	Streptomyces coelicolor cosmid 1C2.	Streptomyces coelicolor	68,275	15-Jan-99
		GB_BA1:ATLEUCD	2982	X84647	A teichomyceticus teuC and leuD genes.	Actinoplanes teichomyceticus	65,935	04-OCT-1995
		GB_BA1:MTV012	70287	AL021287	Mycobacterium tuberculosis H37Rv complete genome; segment 132/162.	Mycobacterium tuberculosis	40,454	23-Jun-99
ra01027	1131	GB_BA1:MLCB637	44882	Z99263	Mycobacterium leprae cosmid B637.	Mycobacterium leprae	38,636	17-Sep-97
		GB_BA1:MTCY349	43523	Z83018	Mycobacterium tuberculosis H37Rv complete genome; segment 131/162.	Mycobacterium tuberculosis	51,989	17-Jun-98
ra01073	954	GB_BA1:SPUNGUMUT X	1172	Z21702	S.pneumoniae ung gene and mutX genes encoding uracil-DNA glycosylase and 8-oxodGTP nucleoside triphosphatase.	Streptococcus pneumoniae	38,088	15-Jun-94
		GB_BA1:BACOUTB	1004	M15811	Bacillus subtilis outB gene encoding a sporulation protein, complete cds.	Bacillus subtilis	53,723	26-Apr-93
		GB_PR4:AC007938	167237	AC007938	Homo sapiens clone UWGC:djs201 from 7q31, complete sequence.	Homo sapiens	34,322	1-Jul-99
		GB_PL2:ATAC006282	92577	AC006282	Arabidopsis thaliana chromosome II BAC F13K3 genomic sequence, complete sequence.	Arabidopsis thaliana	36,181	13-MAR-1999
ra01079	2226	GB_BA2:AF112535	4363	AF112535	Corynebacterium glutamicum putative glutaredoxin NrdH (nrdH), NrdI (nrdI), and ribonucleotide reductase alpha-chain (nrdE) genes, complete cds.	Corynebacterium glutamicum	99,820	5-Aug-99
		GB_BA1:CANRDFGE N	6054	Y09572	Corynebacterium ammoniagenes nrdH, nrdI, nrdE, nrdF genes.	Corynebacterium ammoniagenes	75,966	18-Apr-98
		GB_BA1:MTV012	70287	AL021287	Mycobacterium tuberculosis H37Rv complete genome; segment 132/162.	Mycobacterium tuberculosis	38,296	23-Jun-99
ra01080	567	GB_BA2:AF112535	4363	AF112535	Corynebacterium glutamicum putative glutaredoxin NrdH (nrdH), NrdI (nrdI), and ribonucleotide reductase alpha-chain (nrdE) genes, complete cds.	Corynebacterium glutamicum	100,000	5-Aug-99
		GB_BA1:CANRDFGE N	6054	Y09572	Corynebacterium ammoniagenes nrdH, nrdI, nrdE, nrdF genes.	Corynebacterium ammoniagenes	65,511	18-Apr-98
		GB_BA1:STNRD	4894	X73226	S.typhimurium nrdEF operon.	Salmonella typhimurium	52,477	03-MAR-1997
ra01087	999	GB_IN2:AF063412	1093	AF063412	Limnadia lenticularis elongation factor 1-alpha mRNA, partial cds.	Limnadia lenticularis	43,750	29-MAR-1999
		GB_PR3:HS24M15	134539	Z94055	Human DNA sequence from PAC 24M15 on chromosome 1. Contains tenascin-R (restriclin), EST.	Homo sapiens	37,475	23-Nov-99
		GB_IN2:ARU85702	1240	U85702	Anathix ralla elongation factor-1 alpha (EF-1a) gene, partial cds.	Anathix ralla	37,319	16-Jul-97

Table 4 (continued)

rx01095	857	GB_BA1:MTCY01B2	35938	Z95554	Mycobacterium tuberculosis H37Rv complete genome; segment 72/162.	Mycobacterium tuberculosis	43,243	17-Jun-98
		GB_HTG5:AC011632	175917	AC011632	Homo sapiens clone RP11-3N13, WORKING DRAFT SEQUENCE, 9 unordered pieces.	Homo sapiens	36,471	19-Nov-99
		GB_HTG5:AC011632	175917	AC011632	Homo sapiens clone RP11-3N13, WORKING DRAFT SEQUENCE, 9 unordered pieces.	Homo sapiens	36,836	19-Nov-99
rx01097	477	GB_BA2:AF030405	774	AF030405	Corynebacterium glutamicum cyclase (hisF) gene, complete cds.	Corynebacterium glutamicum	100,000	13-Nov-97
		GB_BA2:AF030405	774	AF030405	Corynebacterium glutamicum cyclase (hisF) gene, complete cds.	Corynebacterium glutamicum	41,206	13-Nov-97
rx01098	897	GB_BA2:AF030405	774	AF030405	Corynebacterium glutamicum cyclase (hisF) gene, complete cds.	Corynebacterium glutamicum	97,933	13-Nov-97
		GB_BA1:MSGY223	42061	AD000019	Mycobacterium tuberculosis sequence from clone y223.	Mycobacterium tuberculosis	40,972	10-DEC-1996
rx01100	861	GB_BA1:MLCB1610	40055	AL049913	Mycobacterium leprae cosmid B1610.	Mycobacterium leprae	61,366	27-Aug-99
		GB_BA2:AF051846	738	AF051846	Corynebacterium glutamicum phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase (hisA) gene, complete cds.	Corynebacterium glutamicum	97,154	12-MAR-1998
rx01101	756	GB_BA2:AF060558	636	AF060558	Corynebacterium glutamicum glutamine amidotransferase (hisH) gene, complete cds.	Corynebacterium glutamicum	95,455	29-Apr-98
		GB_HTG1:HSDJ140A	221755	AL109917	Homo sapiens chromosome 1 clone RP1-140A9, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	30,523	23-Nov-99
		GB_BA2:AF060558	636	AF060558	Corynebacterium glutamicum glutamine amidotransferase (hisH) gene, complete cds.	Corynebacterium glutamicum	94,462	29-Apr-98
		GB_BA1:SC4G6	36917	AL096884	Streptomyces coelicolor cosmid 4G6.	Streptomyces coelicolor A3(2)	38,378	23-Jul-99
rx01104	729	GB_BA1:STMHISOPA	3981	M31628	S.coelicolor histidine biosynthesis operon encoding hisD, partial cds., and hisC, hisB, hisH, and hisA genes, complete cds.	Streptomyces coelicolor A3(2)	60,053	26-Apr-93
		GB_BA1:STMHISOPA	3981	M31628	S.coelicolor histidine biosynthesis operon encoding hisD, partial cds., and hisC, hisB, hisH, and hisA genes, complete cds.	Streptomyces coelicolor	58,333	26-Apr-93
		GB_BA1:SC4G6	36917	AL096884	Streptomyces coelicolor cosmid 4G6.	Streptomyces coelicolor A3(2)	39,045	23-Jul-99
rx01105	1221	GB_BA1:MTCY336	32437	Z95586	Mycobacterium tuberculosis H37Rv complete genome; segment 70/162.	Mycobacterium tuberculosis	60,384	24-Jun-99
		GB_BA1:MTCY336	32437	Z95586	Mycobacterium tuberculosis H37Rv complete genome; segment 70/162.	Mycobacterium tuberculosis	60,931	24-Jun-99
		GB_BA1:MSGY223	42061	AD000019	Mycobacterium tuberculosis sequence from clone y223.	Mycobacterium tuberculosis	36,851	10-DEC-1996
rx01106	1449	GB_BA1:MLCB1610	40055	AL049913	Mycobacterium leprae cosmid B1610.	Mycobacterium leprae	60,902	27-Aug-99
		GB_BA1:MSGY223	42061	AD000019	Mycobacterium tuberculosis sequence from clone y223.	Mycobacterium tuberculosis	37,233	10-DEC-1996

Table 4 (continued)

	GB_BA1:MSHISC	2298	X65542	M.smegmatis genes hisD and hisC for histidinol dehydrogenase and histidinol-Mycobacterium smegmatis phosphate aminotransferase, respectively.	60,111	30-Jun-93
	GB_BA1:MTCY336	32437	Z95586	Mycobacterium tuberculosis H37Rv complete genome; segment 70/162.	58,420	24-Jun-99
rx01145	GB_BA1:CORAIA	4705	L09232	Corynebacterium glutamicum acetohydroxy acid synthase (ilvB) and (ilvN) genes, and acetohydroxy acid isomeroreductase (ilvC) gene, complete cds.	100,000	23-Feb-95
	GB_BA1:BRLILVCA	1364	D14551	Brevibacterium flavum ilvC gene for acetohydroxy acid isomeroreductase, complete cds.	99,560	3-Feb-99
	GB_PAT:E08232	1017	E08232	DNA encoding acetohydroxy-acid isomeroreductase.	99,803	29-Sep-97
rx01162	GB_PAT:A60299	2869	A60299	Sequence 18 from Patent WO9706261.	38,675	06-MAR-1998
	GB_PR3:HS24E5	35506	Z82185	Human DNA sequence from Fosmid 24E5 on chromosome 22q11.2-qter contains parvalbumin, ESTs, STS.	36,204	23-Nov-99
	GB_PR3:AC005265	43900	AC005265	Homo sapiens chromosome 19, cosmid F19750, complete sequence.	38,363	6-Jul-98
rx01208	GB_HTG2:AC004965	323792	AC004965	Homo sapiens clone DJ1106H14, *** SEQUENCING IN PROGRESS ***	36,058	12-Jun-98
	GB_HTG2:AC004965	323792	AC004965	unordered pieces.		
	GB_PL2:TAU55859	2397	U55859	Homo sapiens clone DJ1106H14, *** SEQUENCING IN PROGRESS ***	36,058	12-Jun-98
rx01209	GB_HTG3:AC011469	113436	AC011469	unordered pieces.		
	GB_HTG3:AC011469	113436	AC011469	Triticum aestivum heat shock protein 80 mRNA, complete cds.	37,269	1-Feb-99
	GB_PL1:AB010077	77380	AB010077	Homo sapiens chromosome 19 clone CIT-HSPC_475D23, *** SEQUENCING IN PROGRESS ***	40,000	07-OCT-1999
	GB_HTG3:AC011469	113436	AC011469	IN PROGRESS ***	40,000	07-OCT-1999
rx01215	GB_PL1:AB010077	77380	AB010077	Homo sapiens chromosome 19 clone CIT-HSPC_475D23, *** SEQUENCING IN PROGRESS ***	36,803	20-Nov-99
	GB_BA1:MTCY10G2	38970	Z92539	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH19, complete sequence.		
	GB_IN1:LEIPRPP	1887	M76553	Mycobacterium tuberculosis H37Rv complete genome; segment 47/162.	37,047	17-Jun-98
	GB_HTG2:HSJ799D1	130149	AL050344	Leishmania donovani phosphoribosylpyrophosphate synthetase gene, complete cds.	50,738	7-Jun-93
rx01239	GB_BA1:MTCY48	35377	Z74020	Homo sapiens chromosome 1 clone RP4-799D16 map p34.3-36.1, *** SEQUENCING IN PROGRESS ***	38,135	29-Nov-99
	GB_PR2:AB029032	6377	AB029032	in unordered pieces.		
	GB_GSS9:AAQ107201	355	AQ107201	Mycobacterium tuberculosis H37Rv complete genome; segment 69/162.	38,139	17-Jun-98
	GB_PL2:F5O8	99923	AC005990	sequence.		
rx01253	GB_PL2:F5O8	99923	AC005990	Homo sapiens mRNA for KIAA1109 protein, partial cds.	39,394	4-Aug-99
	GB_PL2:F5O8	99923	AC005990	HS_3098_A1_C03_T7 CIT Approved Human Genomic Sperm Library D	41,408	28-Aug-98
	GB_IN1:CELC06G1	31205	U41014	Homo sapiens genomic clone Plate=3098 Col=5 Row=E, genomic survey sequence.		
	GB_PL2:F5O8	99923	AC005990	Arabidopsis thaliana chromosome 1 BAC F5O8 sequence, complete sequence.	36,118	23-DEC-1998
	GB_PL2:F5O8	99923	AC005990	Arabidopsis thaliana chromosome 1 BAC F5O8 sequence, complete sequence.	35,574	23-DEC-1998
	GB_IN1:CELC06G1	31205	U41014	Caenorhabditis elegans cosmid C06G1.	38,560	30-Nov-95

Table 4 (continued)

rx01321	1044	GB_GSS14:AQ51884 441	AQ518843	HS_5106_A1_D10_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=682 Col=19 Row=G, genomic survey sequence.	Homo sapiens	41,121	05-MAY-1999
		GB_HTG2:AC007473 194859	AC007473	Drosophila melanogaster chromosome 2 clone BACR38D12 (D590) RPCI-98 38.D.12 map 48A-48B strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 60 unordered pieces.	Drosophila melanogaster	40,634	2-Aug-99
		GB_HTG4:AC011696 115847	AC011696	Drosophila melanogaster chromosome 2 clone BACR35F01 (D1156) RPCI-98 35.F.1 map 48A-48C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 108 unordered pieces.	Drosophila melanogaster	38,290	26-OCT-1999
rx01352	706	GB_PL2:ATAC005167 83260	AC005167	Arabidopsis thaliana chromosome II BAC F12A24 genomic sequence, complete sequence.	Arabidopsis thaliana	34,311	15-OCT-1998
		GB_PL2:ATAC005825 97380	AC005825	Arabidopsis thaliana chromosome II BAC T24I21 genomic sequence, complete sequence.	Arabidopsis thaliana	34,311	12-Apr-99
		GB_HTG3:AC011150 127222	AC011150	Homo sapiens clone 4_K_17, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	37,722	01-OCT-1999
rx01360	259	GB_EST32:A1725583 728	A1725583	BNLGH112371 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (U85081) root hair defective 3 [Arabidopsis thaliana], mRNA sequence.	Gossypium hirsutum	38,492	11-Jun-99
		GB_PR2:HS227P17 82951	Z81007	Human DNA sequence from PAC Z27P17, between markers DXS6791 and DXS8038 on chromosome X contains CpG island, EST.	Homo sapiens	39,738	23-Nov-99
		GB_EST34:AV171099 173	AV171099	AV171099 Mus musculus head C57BL/6J 14, 17 day embryo Mus musculus cDNA clone 3200002M11, mRNA sequence.	Mus musculus	46,237	6-Jul-99
rx01361	629	GB_RO:AB008915S1 530	AB008915	Mus musculus mGp11 gene, exon 1.	Mus musculus	45,574	28-Sep-99
		GB_EST22:A1050532 293	A1050532	uc83d10.y1 Sugano mouse kidney mKia Mus musculus cDNA clone IMAGE:1432243 5' similar to TR:O35120 O35120 MGPI1P.; mRNA sequence.	Mus musculus	44,097	9-Jul-98
rx01381	944	GB_RO:AB008895 3062	AB008895	Mus musculus mRNA for mGp1p, complete cds.	Mus musculus	41,316	23-Nov-97
		GB_PL1:AB005237 87835	AB005237	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJJ3, complete sequence.	Arabidopsis thaliana	36,606	20-Nov-99
		GB_GSS5:AQ766840 491	AQ766840	HS_2026_A2_C09_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2026 Col=18 Row=E, genomic survey sequence.	Homo sapiens	37,916	28-Jul-99
		GB_BA1:MTV043 68848	AL022004	Mycobacterium tuberculosis H37Rv complete genome; segment 40/162.	Mycobacterium tuberculosis	37,419	24-Jun-99
rx01393	993	GB_BA1:CGLYSEG 2374	X96471	C.glutamicum lysE and lysG genes.	Corynebacterium glutamicum	34,831	24-Feb-97
		GB_BA1:SC5A7 40337	AL031107	Streptomyces coelicolor cosmid 5A7.	Streptomyces coelicolor	35,138	27-Jul-98
		GB_PR3:AC004054 112184	AC004054	Homo sapiens chromosome 4 clone B220G8 map 4q21, complete sequence.	Homo sapiens	37,277	9-Jul-98
rx01394	822	GB_BA1:CGLYSEG 2374	X96471	C.glutamicum lysE and lysG genes.	Corynebacterium glutamicum	100,000	24-Feb-97
		GB_GSS5:AQ769223 500	AQ769223	HS_3155_B2_G10_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3155 Col=20 Row=N, genomic survey sequence.	Homo sapiens	38,400	28-Jul-99



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the integrity of their genetic information. Typical mutator strains have mutations in the genes for the DNA repair system (*e.g.*, mutHLS, mutD, mutT, etc.; for reference, see Rupp, W.D. (1996) DNA repair mechanisms, in: *Escherichia coli* and *Salmonella*, p. 2277-2294, ASM: Washington.) Such strains are well known to those of ordinary skill in the art. The use of such strains is illustrated, for example, in Greener, A. and Callahan, M. (1994) *Strategies* 7: 32-34.

**Example 5: DNA Transfer Between *Escherichia coli* and *Corynebacterium glutamicum***

Several *Corynebacterium* and *Brevibacterium* species contain endogenous plasmids (as *e.g.*, pHM1519 or pBL1) which replicate autonomously (for review see, *e.g.*, Martin, J.F. *et al.* (1987) *Biotechnology*, 5:137-146). Shuttle vectors for *Escherichia coli* and *Corynebacterium glutamicum* can be readily constructed by using standard vectors for *E. coli* (Sambrook, J. *et al.* (1989), "Molecular Cloning: A Laboratory Manual", Cold Spring Harbor Laboratory Press or Ausubel, F.M. *et al.* (1994) "Current Protocols in Molecular Biology", John Wiley & Sons) to which a origin or replication for and a suitable marker from *Corynebacterium glutamicum* is added. Such origins of replication are preferably taken from endogenous plasmids isolated from *Corynebacterium* and *Brevibacterium* species. Of particular use as transformation markers for these species are genes for kanamycin resistance (such as those derived from the Tn5 or Tn903 transposons) or chloramphenicol (Winnacker, E.L. (1987) "From Genes to Clones — Introduction to Gene Technology, VCH, Weinheim). There are numerous examples in the literature of the construction of a wide variety of shuttle vectors which replicate in both *E. coli* and *C. glutamicum*, and which can be used for several purposes, including gene over-expression (for reference, see *e.g.*, Yoshihama, M. *et al.* (1985) *J. Bacteriol.* 162:591-597, Martin J.F. *et al.* (1987) *Biotechnology*, 5:137-146 and Eikmanns, B.J. *et al.* (1991) *Gene*, 102:93-98).

Using standard methods, it is possible to clone a gene of interest into one of the shuttle vectors described above and to introduce such a hybrid vectors into strains of *Corynebacterium glutamicum*. Transformation of *C. glutamicum* can be achieved by protoplast transformation (Kastsumata, R. *et al.* (1984) *J. Bacteriol.* 159:306-311), electroporation (Liebl, E. *et al.* (1989) *FEMS Microbiol. Letters*, 53:399-303) and in cases where special vectors are used, also by conjugation (as described *e.g.* in Schäfer, A *et al.*

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min incubation at -20°C, the DNA was collected by centrifugation (13,000 rpm, Biofuge Fresco, Heraeus, Hanau, Germany). The DNA pellet was dissolved in TE-buffer. DNA prepared by this procedure could be used for all purposes, including southern blotting or construction of genomic libraries.

5

**Example 2: Construction of genomic libraries in *Escherichia coli* of *Corynebacterium glutamicum* ATCC13032.**

Using DNA prepared as described in Example 1, cosmid and plasmid libraries were constructed according to known and well established methods (see e.g., Sambrook, J. et al. 10 (1989) "Molecular Cloning : A Laboratory Manual", Cold Spring Harbor Laboratory Press, or Ausubel, F.M. et al. (1994) "Current Protocols in Molecular Biology", John Wiley & Sons.)

Any plasmid or cosmid could be used. Of particular use were the plasmids pBR322 (Sutcliffe, J.G. (1979) *Proc. Natl. Acad. Sci. USA*, 75:3737-3741); pACYC177 (Change & 15 Cohen (1978) *J. Bacteriol* 134:1141-1156), plasmids of the pBS series (pBSSK+, pBSSK- and others; Stratagene, LaJolla, USA), or cosmids as SuperCos1 (Stratagene, LaJolla, USA) or Lorist6 (Gibson, T.J., Rosenthal A. and Waterson, R.H. (1987) *Gene* 53:283-286. Gene libraries specifically for use in *C. glutamicum* may be constructed using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

20

**Example 3: DNA Sequencing and Computational Functional Analysis**

Genomic libraries as described in Example 2 were used for DNA sequencing according to standard methods, in particular by the chain termination method using ABI377 sequencing machines (see e.g., Fleischman, R.D. et al. (1995) "Whole-genome 25 Random Sequencing and Assembly of Haemophilus Influenzae Rd., *Science*, 269:496-512). Sequencing primers with the following nucleotide sequences were used: 5'-GGAAACAGTATGACCATG-3' or 5'-GTAAAACGACGGCCAGT-3'.

**Example 4: *In vivo* Mutagenesis**

30 *In vivo* mutagenesis of *Corynebacterium glutamicum* can be performed by passage of plasmid (or other vector) DNA through *E. coli* or other microorganisms (e.g. *Bacillus* spp. or yeasts such as *Saccharomyces cerevisiae*) which are impaired in their capabilities to maintain

### Exemplification

#### **Example 1: Preparation of total genomic DNA of *Corynebacterium glutamicum* ATCC 13032**

- 5 A culture of *Corynebacterium glutamicum* (ATCC 13032) was grown overnight at 30°C with vigorous shaking in BHI medium (Difco). The cells were harvested by centrifugation, the supernatant was discarded and the cells were resuspended in 5 ml buffer-I (5% of the original volume of the culture — all indicated volumes have been calculated for 100 ml of culture volume). Composition of buffer-I: 140.34 g/l sucrose,
- 10 2.46 g/l  $\text{MgSO}_4 \times 7\text{H}_2\text{O}$ , 10 ml/l  $\text{KH}_2\text{PO}_4$  solution (100 g/l, adjusted to pH 6.7 with KOH), 50 ml/l M12 concentrate (10 g/l  $(\text{NH}_4)_2\text{SO}_4$ , 1 g/l NaCl, 2 g/l  $\text{MgSO}_4 \times 7\text{H}_2\text{O}$ , 0.2 g/l  $\text{CaCl}_2$ , 0.5 g/l yeast extract (Difco), 10 ml/l trace-elements-mix (200 mg/l  $\text{FeSO}_4 \times \text{H}_2\text{O}$ , 10 mg/l  $\text{ZnSO}_4 \times 7\text{H}_2\text{O}$ , 3 mg/l  $\text{MnCl}_2 \times 4\text{H}_2\text{O}$ , 30 mg/l  $\text{H}_3\text{BO}_3$ , 20 mg/l  $\text{CoCl}_2 \times 6\text{H}_2\text{O}$ , 1 mg/l  $\text{NiCl}_2 \times 6\text{H}_2\text{O}$ , 3 mg/l  $\text{Na}_2\text{MoO}_4 \times 2\text{H}_2\text{O}$ , 500 mg/l complexing agent
- 15 (EDTA or critic acid), 100 ml/l vitamins-mix (0.2 mg/l biotin, 0.2 mg/l folic acid, 20 mg/l p-amino benzoic acid, 20 mg/l riboflavin, 40 mg/l ca-panthothenate, 140 mg/l nicotinic acid, 40 mg/l pyridoxole hydrochloride, 200 mg/l myo-inositol). Lysozyme was added to the suspension to a final concentration of 2.5 mg/ml. After an approximately 4 h incubation at 37°C, the cell wall was degraded and the resulting
- 20 protoplasts are harvested by centrifugation. The pellet was washed once with 5 ml buffer-I and once with 5 ml TE-buffer (10 mM Tris-HCl, 1 mM EDTA, pH 8). The pellet was resuspended in 4 ml TE-buffer and 0.5 ml SDS solution (10%) and 0.5 ml NaCl solution (5 M) are added. After adding of proteinase K to a final concentration of 200 µg/ml, the suspension is incubated for ca. 18 h at 37°C. The DNA was purified by
- 25 extraction with phenol, phenol-chloroform-isoamylalcohol and chloroform-isoamylalcohol using standard procedures. Then, the DNA was precipitated by adding 1/50 volume of 3 M sodium acetate and 2 volumes of ethanol, followed by a 30 min incubation at -20°C and a 30 min centrifugation at 12,000 rpm in a high speed centrifuge using a SS34 rotor (Sorvall). The DNA was dissolved in 1 ml TE-buffer containing 20
- 30 µg/ml RNaseA and dialysed at 4°C against 1000 ml TE-buffer for at least 3 hours. During this time, the buffer was exchanged 3 times. To aliquots of 0.4 ml of the dialysed DNA solution, 0.4 ml of 2 M LiCl and 0.8 ml of ethanol are added. After a 30



Table 4 (continued)

	GB_HTG2:AC008223	130212	AC008223	Drosophila melanogaster chromosome 3 clone BACR16118 (D815) RPCI-98 16.1.18 map 95A-95A strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 101 unordered pieces.	Drosophila melanogaster	32,757	2-Aug-99
	GB_BA1:MTCY71	42729	Z92771	Mycobacterium tuberculosis H37Rv complete genome; segment 141/162.	Mycobacterium tuberculosis	37,838	10-Feb-99
rx02758	GB_HTG5:AC011678	171967	AC011678	Homo sapiens clone 14_B_7, *** SEQUENCING IN PROGRESS ***; 20 unordered pieces.	Homo sapiens	35,331	5-Nov-99
	GB_HTG5:AC011678	171967	AC011678	Homo sapiens clone 14_B_7, *** SEQUENCING IN PROGRESS ***; 20 unordered pieces.	Homo sapiens	33,807	5-Nov-99
	GB_BA2:AF064070	23183	AF064070	Burkholderia pseudomallei putative dihydroorotase (pyrC) gene, partial cds; putative 1-acyl-sn-glycerol-3-phosphate acyltransferase (plsC), putative diadenosine tetraphosphatase (apaH), complete cds; type II O-antigen biosynthesis gene cluster, complete sequence; putative undecaprenyl phosphate N-acetylglucosaminyltransferase, and putative UDP-glucose 4-epimerase genes, complete cds; and putative galactosyl transferase gene, partial cds.	Burkholderia pseudomallei	36,929	20-Jan-99
rx02771	GB_BA2:AF038651	4077	AF038651	Corynebacterium glutamicum dipeptide-binding protein (dciAE) gene, partial cds; adenine phosphoribosyltransferase (apt) and GTP pyrophosphokinase (rel) genes, complete cds; and unknown gene.	Corynebacterium glutamicum	99,852	14-Sep-98
	GB_IN1:CELT19B4	37121	U80438	Caenorhabditis elegans cosmid T19B4.	Caenorhabditis elegans	43,836	04-DEC-1996
	GB_EST36:AV193572	360	AV193572	AV193572 Yuji Kohara unpublished cDNA: Strain N2 hermaphrodite embryo Caenorhabditis elegans cDNA clone yk618h8 5', mRNA sequence.	Caenorhabditis elegans	48,588	22-Jul-99
rx02772	GB_BA2:AF038651	4077	AF038651	Corynebacterium glutamicum dipeptide-binding protein (dciAE) gene, partial cds; adenine phosphoribosyltransferase (apt) and GTP pyrophosphokinase (rel) genes, complete cds; and unknown gene.	Corynebacterium glutamicum	99,914	14-Sep-98
	GB_BA1:MTCY227	35946	Z77724	Mycobacterium tuberculosis H37Rv complete genome; segment 114/162.	Mycobacterium tuberculosis	38,339	17-Jun-98
	GB_BA1:U00011	40429	U00011	Mycobacterium leprae cosmid B1177.	Mycobacterium leprae	38,996	01-MAR-1994
rx02790	GB_BA1:MTCY159	33818	Z83863	Mycobacterium tuberculosis H37Rv complete genome; segment 111/162.	Mycobacterium tuberculosis	37,640	17-Jun-98
	GB_PR4:AC006581	172931	AC006581	Homo sapiens 12p21 BAC RPC111-259018 (Roswell Park Cancer Institute Human BAC Library) complete sequence.	Homo sapiens	37,906	3-Jun-99
	GB_PR4:AC006581	172931	AC006581	Homo sapiens 12p21 BAC RPC111-259018 (Roswell Park Cancer Institute Human BAC Library) complete sequence.	Homo sapiens	35,280	3-Jun-99
rx02791	GB_BA1:MTCY159	33818	Z83863	Mycobacterium tuberculosis H37Rv complete genome; segment 111/162.	Mycobacterium tuberculosis	39,765	17-Jun-98
	GB_OV:CHKCEK2	3694	M35195	Chicken tyrosine kinase (cek2) mRNA, complete cds.	Gallus gallus	38,937	28-Apr-93
	GB_BA1:MSASDASK	5037	Z17372	M.smegmatis asd, ask-alpha, and ask-beta genes.	Mycobacterium smegmatis	38,495	9-Aug-94
rx02802	GB_EST24:A1223401	169	A1223401	qq48g01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838448 3' similar to WP:C25D7.8 CE08394.; mRNA sequence.	Homo sapiens	40,828	27-OCT-1998

Table 4 (continued)

rx02629	708	GB_VI:BRSMGP	462	M86652	Bovine respiratory syncytial virus membrane glycoprotein mRNA, complete cds.	Bovine respiratory syncytial 37,013 virus	28-Apr-93
		GB_VI:BRSMGP	462	M86652	Bovine respiratory syncytial virus membrane glycoprotein mRNA, complete cds.	Bovine respiratory syncytial 37,013 virus	28-Apr-93
rx02645	1953	GB_PAT:A45577	1925	A45577	Sequence 1 from Patent WO9519442.	Corynebacterium glutamicum	07-MAR-1997
		GB_PAT:A45581	1925	A45581	Sequence 5 from Patent WO9519442.	Corynebacterium glutamicum	07-MAR-1997
		GB_BA1:CORILVA	1925	L01508	Corynebacterium glutamicum threonine dehydratase (livA) gene, complete cds.	Corynebacterium glutamicum	26-Apr-93
rx02646	1392	GB_BA1:CORILVA	1925	L01508	Corynebacterium glutamicum threonine dehydratase (livA) gene, complete cds.	Corynebacterium glutamicum	26-Apr-93
		GB_PAT:A45585	1925	A45585	Sequence 9 from Patent WO9519442.	Corynebacterium glutamicum	07-MAR-1997
		GB_PAT:A45583	1925	A45583	Sequence 7 from Patent WO9519442.	Corynebacterium glutamicum	07-MAR-1997
rx02648	1326	GB_OV:ICTCNC	2049	M83111	Ictalurus punctatus cyclic nucleotide-gated channel RNA sequence.	Ictalurus punctatus	24-MAY-1993
		GB_EST11:AA265464	345	AA265464	mx91c06.r1 Soares mouse NML Mus musculus cDNA clone IMAGE:693706 5', mRNA sequence.	Mus musculus	20-MAR-1997
		GB_GSS8:AQ006950	480	AQ006950	CIT-HSP-2294E14, TR CIT-HSP Homo sapiens genomic clone 2294E14, genomic survey sequence.	Homo sapiens	27-Jun-98
rx02653							
rx02687	1068	GB_BA1:CORPHEA	1088	M13774	C.glutamicum pheA gene encoding prephenate dehydratase, complete cds.	Corynebacterium glutamicum	26-Apr-93
		GB_PAT:E04483	948	E04483	DNA encoding prephenate dehydratase.	Corynebacterium glutamicum	29-Sep-97
		GB_PAT:E06110	948	E06110	DNA encoding prephenate dehydratase.	Corynebacterium glutamicum	29-Sep-97
rx02717	1005	GB_PL1:HVCH4H	59748	Y14573	Hordeum vulgare DNA for chromosome 4H.	Hordeum vulgare	25-MAR-1999
		GB_PR2:HS310H5	29718	Z69705	Human DNA sequence from cosmid 310H5 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains EST and CpG island.	Homo sapiens	22-Nov-99
		GB_PR3:AC004754	39188	AC004754	Homo sapiens chromosome 16, cosmid clone RT286 (LANL), complete sequence.	Homo sapiens	28-MAY-1998
rx02754	1461	GB_HTG2:AC008223	130212	AC008223	Drosophila melanogaster chromosome 3 clone BACR16118 (DB15) RPCI-98 16.1.18 map 95A-95A strain Y; cn bw sp, *** SEQUENCING IN PROGRESS***, 101 unordered pieces.	Drosophila melanogaster	2-Aug-99

Table 4 (continued)

αa02517	570	GB_BA1:MTV007	32806	AL021184	Mycobacterium tuberculosis H37Rv complete genome; segment 64/162.	Mycobacterium tuberculosis	61,335	17-Jun-98
		GB_BA1:MLCL536	36224	Z99125	Mycobacterium leprae cosmid L536.	Mycobacterium leprae	37,018	04-DEC-1998
		GB_BA1:U00013	35881	U00013	Mycobacterium leprae cosmid B1496.	Mycobacterium leprae	37,018	01-MAR-1994
αa02532	1170	GB_BA1:SCC22	22115	AL096839	Streptomyces coelicolor cosmid C22.	Streptomyces coelicolor	37,071	12-Jul-99
		GB_OV:AF137219	831	AF137219	Amia calva mixed lineage leukemia-like protein (Mli) gene, partial cds.	Amia calva	36,853	7-Sep-99
		GB_EST30:AI645057	301	AI645057	vs52a10.y1 Stratagene mouse Tcell 937311 Mus musculus cDNA clone IMAGE:1149882 5', mRNA sequence.	Mus musculus	41,860	29-Apr-99
		GB_EST20:AA822595	429	AA822595	vs52a10.r1 Stratagene mouse Tcell 937311 Mus musculus cDNA clone IMAGE:1149882 5', mRNA sequence.	Mus musculus	42,353	17-Feb-98
αa02536	879	GB_HTG2:AF130866	118874	AF130866	Homo sapiens chromosome 8 clone PAC 172N13 map 8q24, *** SEQUENCING IN PROGRESS ***. In unordered pieces.	Homo sapiens	40,754	21-MAR-1999
		GB_HTG2:AF130866	118874	AF130866	Homo sapiens chromosome 8 clone PAC 172N13 map 8q24, *** SEQUENCING IN PROGRESS ***. In unordered pieces.	Homo sapiens	40,754	21-MAR-1999
		GB_PL1:ATT12J5	84499	AL035522	Arabidopsis thaliana DNA chromosome 4, BAC clone T12J5 (ESSAll project), Arabidopsis thaliana		35,063	24-Feb-99
αa02550	1434	GB_BA1:MTCY279	9150	Z97991	Mycobacterium tuberculosis H37Rv complete genome; segment 17/162.	Mycobacterium tuberculosis	37,773	17-Jun-98
		GB_BA1:MSG81970C	39399	L78815	Mycobacterium leprae cosmid B1970 DNA sequence.	Mycobacterium leprae	39,024	15-Jun-96
αa02559	1026	GB_BA2:SC2H4	25970	AL031514	Streptomyces coelicolor cosmid 2H4.	Streptomyces coelicolor A3(2)	37,906	19-OCT-1999
		GB_BA1:MTV004	69350	AL009198	Mycobacterium tuberculosis H37Rv complete genome; segment 144/162.	Mycobacterium tuberculosis	47,358	18-Jun-98
		GB_PAT:I28684	5100	I28684	Sequence 1 from patent US 5573915.	Unknown.	39,138	6-Feb-97
		GB_BA1:MTU27357	5100	U27357	Mycobacterium tuberculosis cyclopropane mycolic acid synthase (cma1) gene, complete cds.	Mycobacterium tuberculosis	39,138	26-Sep-95
αa02622	1683	GB_BA2:AE001780	11997	AE001780	Thermotoga maritima section 92 of 136 of the complete genome.	Thermotoga maritima	44,914	2-Jun-99
		GB_OV:AF064564	49254	AF064564	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds.	Fugu rubripes	39,732	17-Aug-99
		GB_OV:AF064564	49254	AF064564	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds.	Fugu rubripes	36,703	17-Aug-99
αa02623	714	GB_GSS5:AQ818728	444	AQ818728	HS_5268_A1_G09_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=844 Col=17 Row=M, genomic survey sequence.	Homo sapiens	38,801	26-Aug-99
		GB_HTG5:AC011083	198586	AC011083	Homo sapiens chromosome 9 clone RP11-111M7 map 9, WORKING DRAFT SEQUENCE, 51 unordered pieces.	Homo sapiens	35,714	19-Nov-99
		GB_GSS6:AQ826948	544	AQ826948	HS_5014_A2_C12_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=590 Col=24 Row=E, genomic survey sequence.	Homo sapiens	39,146	27-Aug-99

rx02458	1413	GB_EST1:T05804	406	T05804	EST03693 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBDG63 similar to EST containing Alu repeat, mRNA sequence.	Homo sapiens	37,915	30-Jun-93
		GB_PL1:AB006699	77363	AB006699	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDJ22, complete sequence.	Arabidopsis thaliana	35,526	20-Nov-99
		GB_BA2:AF114233	1852	AF114233	Corynebacterium glutamicum 5-enolpyruvylshikimate 3-phosphate synthase (aroA) gene, complete cds.	Corynebacterium glutamicum	100,000	7-Feb-99
		GB_EST37:AW013061	578	AW013061	ODT-0033 Winter flounder ovary Pleuronectes americanus cDNA clone ODT-0033 5' similar to FRUCTOSE-BISPHOSPHATE ALDOLASE B (LIVER), mRNA sequence.	Pleuronectes americanus	39,175	10-Sep-99
rx02469	1554	GB_GSS15:AQ65002	728	AQ650027	Sheared DNA-5L2.TF Sheared DNA Trypanosoma brucei genomic clone Sheared DNA-5L2, genomic survey sequence.	Trypanosoma brucei	39,281	22-Jun-99
		GB_BA1:MTCY359	36021	Z83859	Mycobacterium tuberculosis H37Rv complete genome; segment 84/162.	Mycobacterium tuberculosis	39,634	17-Jun-98
		GB_BA1:MLCB1788	39228	AL008609	Mycobacterium leprae cosmid B1788.	Mycobacterium leprae	59,343	27-Aug-99
		GB_BA1:SCAJ10601	4692	AJ010601	Streptomyces coelicolor A3(2) DNA for whiD and whiK loci.	Streptomyces coelicolor	48,899	17-Sep-98
rx02497	1050	GB_BA2:CGU31224	422	U31224	Corynebacterium glutamicum (ppx) gene, partial cds.	Corynebacterium glutamicum	96,445	2-Aug-96
		GB_BA1:MTCY20G9	37218	Z77162	Mycobacterium tuberculosis H37Rv complete genome; segment 25/162.	Mycobacterium tuberculosis	59,429	17-Jun-98
		GB_BA1:SCE7	16911	AL049819	Streptomyces coelicolor cosmid E7.	Streptomyces coelicolor	39,510	10-MAY-1999
rx02499	933	GB_BA2:CGU31225	1817	U31225	Corynebacterium glutamicum L-proline:NADP+ 5-oxido-reductase (proC) gene, complete cds.	Corynebacterium glutamicum	97,749	2-Aug-96
		GB_BA1:NG17PILA	1920	X13965	Neisseria gonorrhoeae pila gene.	Neisseria gonorrhoeae	43,249	30-Sep-93
		GB_HTG2:AC007984	129715	AC007984	Drosophila melanogaster chromosome 3 clone BACR05C10 (D781) RPCI-98 05.C.10 map 97D-97E strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 87 unordered pieces.	Drosophila melanogaster	33,406	2-Aug-99
rx02501	1188	GB_BA1:MTCY20G9	37218	Z77162	Mycobacterium tuberculosis H37Rv complete genome; segment 25/162.	Mycobacterium tuberculosis	39,357	17-Jun-98
		GB_BA1:U00018	42991	U00018	Mycobacterium leprae cosmid B2168.	Mycobacterium leprae	51,768	01-MAR-1994
rx02503	522	GB_VI:HE1CG	152261	X14112	Herpes simplex virus (HSV) type 1 complete genome.	human herpesvirus 1	39,378	17-Apr-97
		GB_PR3:AC005328	35414	AC005328	Homo sapiens chromosome 19, cosmid R26660, complete sequence.	Homo sapiens	39,922	28-Jul-98
		GB_PR3:AC005545	43514	AC005545	Homo sapiens chromosome 19, cosmid R26634, complete sequence.	Homo sapiens	39,922	3-Sep-98
		GB_PR3:AC005328	35414	AC005328	Homo sapiens chromosome 19, cosmid R26660, complete sequence.	Homo sapiens	34,911	28-Jul-98
rx02504	681	GB_BA1:MTCY20G9	37218	Z77162	Mycobacterium tuberculosis H37Rv complete genome; segment 25/162.	Mycobacterium tuberculosis	54,940	17-Jun-98
		GB_PR3:AC005328	35414	AC005328	Homo sapiens chromosome 19, cosmid R26660, complete sequence.	Homo sapiens	41,265	28-Jul-98
		GB_PR3:AC005545	43514	AC005545	Homo sapiens chromosome 19, cosmid R26634, complete sequence.	Homo sapiens	41,265	3-Sep-98
rx02516	1386	GB_BA1:MLCL536	36224	Z99125	Mycobacterium leprae cosmid L536.	Mycobacterium leprae	37,723	04-DEC-1998
		GB_BA1:U00013	35881	U00013	Mycobacterium leprae cosmid B1496.	Mycobacterium leprae	37,723	01-MAR-1994



Table 4 (continued)

rx02345	1320	GB_BA1:BAPURKE	2582	X91189	B. ammoniagenes purK and purE genes.	Corynebacterium ammoniagenes	61,731	14-Jan-97
		GB_BA1:MTCY71	42729	Z92771	Mycobacterium tuberculosis H37Rv complete genome; segment 141/162.	Mycobacterium tuberculosis	39,624	10-Feb-99
		GB_BA1:MTCY71	42729	Z92771	Mycobacterium tuberculosis H37Rv complete genome; segment 141/162.	Mycobacterium tuberculosis	39,847	10-Feb-99
rx02350	618	GB_BA1:BAPURKE	2582	X91189	B. ammoniagenes purK and purE genes.	Corynebacterium ammoniagenes	64,286	14-Jan-97
		GB_PL1:SC130KBXV	129528	X94335	S. cerevisiae 130kb DNA fragment from chromosome XV.	Saccharomyces cerevisiae	36,617	15-Jul-97
		GB_PL1:SCXVORFS	50984	X90518	S. cerevisiae DNA of 51 Kb from chromosome XV right arm.	Saccharomyces cerevisiae	36,617	1-Nov-95
rx02373	1038	GB_PAT:E00311	1853	E00311	DNA coding of 2,5-diketogluconic acid reductase.	unidentified	56,123	29-Sep-97
		GB_PAT:106030	1853	I06030	Sequence 4 from Patent EP 0305608.	Unknown.	56,220	02-DEC-1994
		GB_PAT:100836	1853	I00836	Sequence 1 from Patent US 4758514.	Unknown.	56,220	21-MAY-1993
rx02375	1350	GB_BA2:CGU31230	3005	U31230	Corynebacterium glutamicum Obg protein homolog gene, partial cds, gamma glutamyl kinase (proB) gene, complete cds, and (unkdh) gene, complete cds.	Corynebacterium glutamicum	99,332	2-Aug-96
		GB_HTG3:AC009946	169072	AC009946	Homo sapiens clone NH0012C17, *** SEQUENCING IN PROGRESS ***; 1 unordered pieces.	Homo sapiens	36,115	8-Sep-99
		GB_HTG3:AC009946	169072	AC009946	Homo sapiens clone NH0012C17, *** SEQUENCING IN PROGRESS ***; 1 unordered pieces.	Homo sapiens	36,115	8-Sep-99
rx02380	777	GB_BA1:MTCY253	41230	Z81368	Mycobacterium tuberculosis H37Rv complete genome; segment 106/162.	Mycobacterium tuberculosis	38,088	17-Jun-98
		GB_HTG4:AC010658	120754	AC010658	Drosophila melanogaster chromosome 3L75C1 clone RPC198-3B20, *** SEQUENCING IN PROGRESS ***; 78 unordered pieces.	Drosophila melanogaster	35,817	16-OCT-1999
		GB_HTG4:AC010658	120754	AC010658	Drosophila melanogaster chromosome 3L75C1 clone RPC198-3B20, *** SEQUENCING IN PROGRESS ***; 78 unordered pieces.	Drosophila melanogaster	35,817	16-OCT-1999
rx02382	1419	GB_BA1:CGPROAGE	1783	X82929	C. glutamicum proA gene.	Corynebacterium glutamicum	98,802	23-Jan-97
		GB_BA1:MTCY428	26914	Z81451	Mycobacterium tuberculosis H37Rv complete genome; segment 107/162.	Mycobacterium tuberculosis	38,054	17-Jun-98
		GB_BA2:CGU31230	3005	U31230	Corynebacterium glutamicum Obg protein homolog gene, partial cds, gamma glutamyl kinase (proB) gene, complete cds, and (unkdh) gene, complete cds.	Corynebacterium glutamicum	98,529	2-Aug-96
rx02400	693	GB_BA1:CGACEA	2427	X75504	C. glutamicum aceA gene and thix genes (partial).	Corynebacterium glutamicum	100,000	9-Sep-94
		GB_PAT:186191	2135	I86191	Sequence 3 from patent US 5700661.	Unknown.	100,000	10-Jun-98
		GB_PAT:113693	2135	I13693	Sequence 3 from patent US 5439822.	Unknown.	100,000	26-Sep-95
rx02432	1098	GB_GSS15:AQ60684	574	AQ606842	HS_5404_B2_E07_TTA RPC1-11 Human Male BAC Library Homo sapiens genomic clone Plate=980 Col=14 Row=J, genomic survey sequence.	Homo sapiens	39,716	10-Jun-99

Table 4 (continued)

GB_EST23:AI128623	363	AI128623	qa62c01.s1 Soares_fetal_heart_NbrH19W Homo sapiens cDNA clone IMAGE:1691328 3', mRNA sequence.	Homo sapiens	37,017	05-OCT-1998
GB_PL2:ATAC007019	102335	AC007019	Arabidopsis thaliana chromosome II BAC F7D8 genomic sequence, complete sequence.	Arabidopsis thaliana	33,988	16-MAR-1999
GB_BA2:AF116184	540	AF116184	Corynebacterium glutamicum L-aspartate-alpha-decarboxylase precursor (panD) gene, complete cds.	Corynebacterium glutamicum	100,000	02-MAY-1999
GB_GSS9:AA164310	507	AQ164310	HS_2171_A2_E01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2171 Col=2 Row=I, genomic survey sequence.	Homo sapiens	37,278	16-OCT-1998
GB_VI:MH68TKH	4557	X93468	Murine herpesvirus type 68 thymidine kinase and glycoprotein H genes.	murine herpesvirus 68	40,288	3-Sep-96
GB_HTG4:AC006091	176878	AC006091	Drosophila melanogaster chromosome 3 clone BACR48G05 (D475) RPCI-98 48.G.5 map 91F1-91F13 strain y; cn bw sp. *** SEQUENCING IN PROGRESS *** 4 unordered pieces.	Drosophila melanogaster	36,454	27-OCT-1999
GB_HTG4:AC006091	176878	AC006091	Drosophila melanogaster chromosome 3 clone BACR48G05 (D475) RPCI-98 48.G.5 map 91F1-91F13 strain y; cn bw sp. *** SEQUENCING IN PROGRESS *** 4 unordered pieces.	Drosophila melanogaster	36,454	27-OCT-1999
GB_BA2:RRU65510	16259	U65510	Rhodospirillum rubrum CO-induced hydrogenase operon (cooM, cooK, cooL, cooX, cooU, cooH) genes, iron sulfur protein (cooF) gene, carbon monoxide dehydrogenase (cooS) gene, carbon monoxide dehydrogenase accessory proteins (cooC, cooT, cooJ) genes, putative transcriptional activator (cooA) gene, nicotinate-nucleotide pyrophosphorylase (nadC) gene, complete cds, L-aspartate oxidase (nadB) gene, and alkyl hydroperoxide reductase (ahpC) gene, partial cds.	Rhodospirillum rubrum	37,828	9-Apr-97
GB_BA1:MSGY224	40051	AD000004	Mycobacterium tuberculosis sequence from clone y224.	Mycobacterium tuberculosis	49,418	03-DEC-1996
GB_BA1:MTY25D10	40838	Z95558	Mycobacterium tuberculosis H37Rv complete genome; segment 28/162.	Mycobacterium tuberculosis	49,360	17-Jun-98
GB_BA1:MSGY224	40051	AD000004	Mycobacterium tuberculosis sequence from clone y224.	Mycobacterium tuberculosis	38,150	03-DEC-1996
GB_HTG3:AC011348	111083	AC011348	Homo sapiens chromosome 5 clone CIT-HSPC_303E13, *** SEQUENCING IN PROGRESS *** 3 ordered pieces.	Homo sapiens	35,821	06-OCT-1999
GB_HTG3:AC011348	111083	AC011348	Homo sapiens chromosome 5 clone CIT-HSPC_303E13, *** SEQUENCING IN PROGRESS *** 3 ordered pieces.	Homo sapiens	35,821	06-OCT-1999
GB_HTG3:AC011412	89234	AC011412	Homo sapiens chromosome 5 clone CIT978SKB_81K21, *** SEQUENCING IN PROGRESS *** 3 ordered pieces.	Homo sapiens	36,181	06-OCT-1999
GB_BA1:MSGY224	40051	AD000004	Mycobacterium tuberculosis sequence from clone y224.	Mycobacterium tuberculosis	37,792	03-DEC-1996
GB_BA1:MTY25D10	40838	Z95558	Mycobacterium tuberculosis H37Rv complete genome; segment 28/162.	Mycobacterium tuberculosis	37,792	17-Jun-98
GB_EST23:AI117213	476	AI117213	ub83h02.r1 Soares 2NbMT Mus musculus cDNA clone IMAGE:1395123 5', mRNA sequence.	Mus musculus	35,084	2-Sep-98

**Table 4 (continued)**

Table 4 (continued)

948	948	GB_PR4:AC006236	127593	AC006236	Homo sapiens chromosome 17, clone hCIT.162_E_12, complete sequence.	Homo sapiens	37,191	29-DEC-1998
		GB_BA1:MSGY154	40221	AD000002	Mycobacterium tuberculosis sequence from clone y154.	Mycobacterium tuberculosis	53,541	03-DEC-1996
		GB_BA1:MTCY154	13935	Z98209	Mycobacterium tuberculosis H37Rv complete genome; segment 121/162.	Mycobacterium tuberculosis	40,407	17-Jun-98
		GB_BA1:U00019	36033	U00019	Mycobacterium leprae cosmid B2235.	Mycobacterium leprae	40,541	01-MAR-1994
		GB_BA1:MSGB937C	38914	L78820	Mycobacterium leprae cosmid B937 DNA sequence.	Mycobacterium leprae	66,027	15-Jun-96
		GB_BA1:MTCY2B12	20431	Z81011	Mycobacterium tuberculosis H37Rv complete genome; segment 61/162.	Mycobacterium tuberculosis	71,723	18-Jun-98
		GB_BA2:U01072	4393	U01072	Mycobacterium bovis BCG orotidine-5'-monophosphate decarboxylase (uraA) gene.	Mycobacterium bovis	67,101	22-DEC-1993
		GB_BA1:MSU91572	960	U91572	Mycobacterium smegmatis carbamoyl phosphate synthetase (pyrAB) gene, partial cds and orotidine 5'-monophosphate decarboxylase (pyrF) gene, complete cds.	Mycobacterium smegmatis	60,870	22-MAR-1997
		GB_HTG3:AC009364	192791	AC009364	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***; 57 unordered pieces.	Homo sapiens	37,994	1-Sep-99
		GB_HTG3:AC009364	192791	AC009364	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***; 57 unordered pieces.	Homo sapiens	37,994	1-Sep-99
		GB_BA1:MTCY21B4	39150	Z80108	Mycobacterium tuberculosis H37Rv complete genome; segment 62/162.	Mycobacterium tuberculosis	55,844	23-Jun-98
		GB_BA2:AF077324	5228	AF077324	Rhodococcus equi strain 103 plasmid RE-VP1 fragment f.	Rhodococcus equi	41,185	5-Nov-98
		GB_EST22:AU017763	586	AU017763	AU017763 Mouse two-cell stage embryo cDNA Mus musculus cDNA clone J0744A04 3', mRNA sequence.	Mus musculus	38,616	19-OCT-1998
		GB_BA1:MTCY21B4	39150	Z80108	Mycobacterium tuberculosis H37Rv complete genome; segment 62/162.	Mycobacterium tuberculosis	56,282	23-Jun-98
		GB_HTG3:AC010745	193862	AC010745	Homo sapiens clone NH0549D18, *** SEQUENCING IN PROGRESS ***; 30 unordered pieces.	Homo sapiens	36,772	21-Sep-99
		GB_HTG3:AC010745	193862	AC010745	Homo sapiens clone NH0549D18, *** SEQUENCING IN PROGRESS ***; 30 unordered pieces.	Homo sapiens	36,772	21-Sep-99
		EM_PAT:E09855	1239	E09855	gDNA encoding S-adenosylmethionine synthetase.	Corynebacterium glutamicum	99,515	07-OCT-1997 (Rel. 52, Created)
		GB_PAT:A37831	5392	A37831	Sequence 1 from Patent WO9408014.	Streptomyces pristinaespiralis	63,568	05-MAR-1997
		GB_BA2:AF117274	2303	AF117274	Streptomyces spectabilis flavoprotein homolog Dfp (dfp) gene, partial cds; and Streptomyces spectabilis S-adenosylmethionine synthetase (metK) gene, complete cds.	Streptomyces spectabilis	65,000	31-MAR-1999
		EM_BA1:AB003693	5589	AB003693	Corynebacterium ammoniagenes DNA for rib operon, complete cds.	Corynebacterium ammoniagenes	52,909	03-OCT-1997 (Rel. 52, Created)

Table 4 (continued)

GB_BA2:AF048764	1437	AF048764	Corynebacterium glutamicum argininosuccinate lyase (argH) gene, complete cds.	Corynebacterium glutamicum	87,561	1-Jul-98
GB_BA1:MTCY06H11	38000	Z85982	Mycobacterium tuberculosis H37Rv complete genome; segment 73/162.	Mycobacterium tuberculosis	64,732	17-Jun-98
GB_BA1:MTCY31	37630	Z73101	Mycobacterium tuberculosis H37Rv complete genome; segment 41/162.	Mycobacterium tuberculosis	36,998	17-Jun-98
GB_BA1:CGGLTG	3013	X66112	C-glutamicum glt gene for citrate synthase and ORF.	Corynebacterium glutamicum	39,910	17-Feb-95
GB_PL2:PGU65399	2700	U65399	Basidiomycete CECT 20197 phenoloxidase (pox1) gene, complete cds.	basidiomycete CECT 20197	38,474	19-Jul-97
GB_PR3:AC002468	115888	AC002468	Human Chromosome 15q26.1 PAC clone pDJ417d7, complete sequence.	Homo sapiens	35,941	16-Sep-98
GB_BA1:MSGB1970C	39399	L78815	Mycobacterium leprae cosmid B1970 DNA sequence.	Mycobacterium leprae	40,286	15-Jun-96
GB_PR3:AC002468	115888	AC002468	Human Chromosome 15q26.1 PAC clone pDJ417d7, complete sequence.	Homo sapiens	33,689	16-Sep-98
GB_BA1:BRLASPA	1987	D25316	Brevibacterium flavum aspA gene for aspartase, complete cds.	Corynebacterium glutamicum	99,353	6-Feb-99
GB_PAT:E04307	1581	E04307	DNA encoding Brevibacterium flavum aspartase.	Corynebacterium glutamicum	99,367	29-Sep-97
GB_BA1:ECOUW93	338534	U14003	Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes.	Escherichia coli	37,651	17-Apr-96
GB_BA2:AF050166	840	AF050166	Corynebacterium glutamicum ATP phosphoribosyltransferase (hisG) gene, complete cds.	Corynebacterium glutamicum	98,214	5-Jan-99
GB_BA1:BRLASPA	1987	D25316	Brevibacterium flavum aspA gene for aspartase, complete cds.	Corynebacterium glutamicum	93,805	6-Feb-99
GB_PAT:E08649	188	E08649	DNA encoding part of aspartase from coryneform bacteria.	Corynebacterium glutamicum	100,000	29-Sep-97
GB_BA2:AF086704	264	AF086704	Corynebacterium glutamicum phosphoribosyl-ATP-pyrophosphohydrolase (hisE) gene, complete cds.	Corynebacterium glutamicum	100,000	8-Feb-99
GB_BA1:EAY17145	6019	Y17145	Eubacterium acidaminophilum grdR, grdI, grdH genes and partial ldc, grdT genes.	Eubacterium acidaminophilum	39,075	5-Aug-98
GB_STS:G01195	332	G01195	fruit fly STS Dm1930 clone DS06959 T7.	Drosophila melanogaster	35,542	28-Feb-95
GB_BA1:MTCY261	27322	Z97559	Mycobacterium tuberculosis H37Rv complete genome; segment 95/162.	Mycobacterium tuberculosis	33,938	17-Jun-98
GB_BA1:MLCB2533	40245	AL035310	Mycobacterium leprae cosmid B2533.	Mycobacterium leprae	65,517	27-Aug-99
GB_BA1:U00017	42157	U00017	Mycobacterium leprae cosmid B2126.	Mycobacterium leprae	36,770	01-MAR-1994
GB_BA1:U00017	42157	U00017	Mycobacterium leprae cosmid B2126.	Mycobacterium leprae	38,674	01-MAR-1994
GB_BA1:MLCB2533	40245	AL035310	Mycobacterium leprae cosmid B2533.	Mycobacterium leprae	65,465	27-Aug-99
GB_BA1:MTCY261	27322	Z97559	Mycobacterium tuberculosis H37Rv complete genome; segment 95/162.	Mycobacterium tuberculosis	37,577	17-Jun-98
GB_BA1:U00017	42157	U00017	Mycobacterium leprae cosmid B2126.	Mycobacterium leprae	59,823	01-MAR-1994
GB_BA1:AP000063	185300	AP000063	Aeropyrum pernix genomic DNA, section 617.	Aeropyrum pernix	39,442	22-Jun-99

Table 4 (continued)

GB_BA1:CGARGCJB D	4355	X86157	C.glutamicum argC, argJ, argB, argD, and argF genes.	Corynebacterium glutamicum	100,000	25-Jul-96
GB_BA2:AE001816	10007	AE001816	Thermotoga maritima section 128 of 136 of the complete genome.	Thermotoga maritima	50,238	2-Jun-99
GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	99,612	1-Jul-98
GB_BA1:CGARGCJB D	4355	X86157	C.glutamicum argC, argJ, argB, argD, and argF genes.	Corynebacterium glutamicum	99,612	25-Jul-96
GB_BA1:MTCY06H11	38000	Z85982	Mycobacterium tuberculosis H37Rv complete genome; segment 73/162.	Mycobacterium tuberculosis	57,278	17-Jun-98
GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	100,000	1-Jul-98
GB_BA2:AF031518	2045	AF031518	Corynebacterium glutamicum ornithine carbamoyltransferase (argF) gene, complete cds.	Corynebacterium glutamicum	99,898	5-Jan-99
GB_BA1:CGARGCJB D	4355	X86157	C.glutamicum argC, argJ, argB, argD, and argF genes.	Corynebacterium glutamicum	100,000	25-Jul-96
GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	99,843	1-Jul-98
GB_BA2:AF031518	2045	AF031518	Corynebacterium glutamicum ornithine carbamoyltransferase (argF) gene, complete cds.	Corynebacterium glutamicum	88,679	5-Jan-99
GB_BA2:AF041436	516	AF041436	Corynebacterium glutamicum arginine repressor (argR) gene, complete cds.	Corynebacterium glutamicum	100,000	5-Jan-99
GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	99,774	1-Jul-98
GB_BA2:AF030520	1206	AF030520	Corynebacterium glutamicum argininosuccinate synthetase (argG) gene, complete cds.	Corynebacterium glutamicum	99,834	19-Nov-97
GB_BA1:SCARGGH	1909	Z49111	S.clavuligerus argG gene and argH gene (partial).	Streptomyces clavuligerus	65,913	22-Apr-96
GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	88,524	1-Jul-98

Table 4 (continued)

rxa02136	645	GB_PL2:ATAC005819	57752	AC005819	Arabidopsis thaliana chromosome II BAC T3A4 genomic sequence, complete sequence.	Arabidopsis thaliana	34,123	3-Nov-98
		GB_PL2:F15K9	71097	AC005278	Arabidopsis thaliana chromosome 1 BAC F15K9 sequence, complete sequence.	Arabidopsis thaliana	31,260	7-Nov-98
rx02139	1962	GB_PL2:U89959	106973	U89959	Arabidopsis thaliana BAC T7123, complete sequence.	Arabidopsis thaliana	34,281	26-Jun-98
		GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	62,904	17-Jun-98
		GB_BA1:MSGB1554C	36548	L78814	Mycobacterium leprae cosmid B1554 DNA sequence.	Mycobacterium leprae	36,648	15-Jun-96
		GB_BA1:MSGB1551C	36548	L78813	Mycobacterium leprae cosmid B1551 DNA sequence.	Mycobacterium leprae	36,648	15-Jun-96
rx02153	903	GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	99,104	1-Jul-98
		GB_BA1:AF005242	1044	AF005242	Corynebacterium glutamicum N-acetylglutamate-5-semialdehyde dehydrogenase (argC) gene, complete cds.	Corynebacterium glutamicum	99,224	2-Jul-97
		GB_BA1:CGARGCJB	4355	X86157	C. glutamicum argC, argJ, argB, argD, and argF genes.	Corynebacterium glutamicum	100,000	25-Jul-96
rx02154	414	GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	98,551	1-Jul-98
		GB_BA1:AF005242	1044	AF005242	Corynebacterium glutamicum N-acetylglutamate-5-semialdehyde dehydrogenase (argC) gene, complete cds.	Corynebacterium glutamicum	98,477	2-Jul-97
		GB_BA1:CGARGCJB	4355	X86157	C. glutamicum argC, argJ, argB, argD, and argF genes.	Corynebacterium glutamicum	100,000	25-Jul-96
rx02155	1287	GB_BA1:CGARGCJB	4355	X86157	C. glutamicum argC, argJ, argB, argD, and argF genes.	Corynebacterium glutamicum	99,767	25-Jul-96
		GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	99,378	1-Jul-98
		GB_BA1:MSGB1133C	42106	L78811	Mycobacterium leprae cosmid B1133 DNA sequence.	Mycobacterium leprae	55,504	15-Jun-96
rx02156	1074	GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	100,000	1-Jul-98

Table 4 (continued)

rx02085	2358	GB_BA1:MTCY22G8	22550	Z95585	Mycobacterium tuberculosis H37Rv complete genome; segment 49/162.	Mycobacterium tuberculosis	38,442	17-Jun-98
		GB_BA1:MLCB33	42224	Z94723	Mycobacterium leprae cosmid B33.	Mycobacterium leprae	56,486	24-Jun-97
		GB_BA1:ECOUW85	91414	M87049	E. coli genomic sequence of the region from 84.5 to 86.5 minutes.	Escherichia coli	52,127	29-MAY-1995
rx02093	927	GB_EST14:AA448146	452	AA448146	zw82h01.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782737	Homo sapiens	34,163	4-Jun-97
		GB_EST17:AA641937	444	AA641937	5', mRNA sequence.			
		GB_PR3:AC003074	143029	AC003074	ns18b10.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1183963	Homo sapiens	35,586	27-OCT-1997
rx02106	1179	GB_BA1:SC1A6	37620	AL023496	Human PAC clone DJ0596009 from 7p15, complete sequence.	Homo sapiens	31,917	6-Nov-97
		GB_PR4:AC005553	179651	AC005553	Streptomyces coelicolor cosmid 1A6.	Streptomyces coelicolor	35,818	13-Jan-99
		GB_EST3:R49746	397	R49746	Homo sapiens chromosome 17, clone hRPK.112_J_9, complete sequence.	Homo sapiens	34,274	31-DEC-1998
		GB_BA1:SC6G10	36734	AL049497	yg71g10.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:38768 5' similar to gb:V00567 BETA-2-MICROGLOBULIN PRECURSOR (HUMAN);, mRNA sequence.	Homo sapiens	41,162	18-MAY-1995
rx02111	1407	GB_BA1:U00010	41171	U00010	Streptomyces coelicolor cosmid 6G10.	Streptomyces coelicolor	50,791	24-MAR-1999
		GB_BA1:MTCY336	32437	Z95586	Mycobacterium leprae cosmid B1170.	Mycobacterium leprae	37,563	01-MAR-1994
rx02112	960	GB_HTG3:AC010579	157658	AC010579	Mycobacterium tuberculosis H37Rv complete genome; segment 70/162.	Mycobacterium tuberculosis	39,504	24-Jun-99
		GB_GSS3:B09839	1191	B09839	Drosophila melanogaster chromosome 3 clone BACR09D08 (D1101) RPCI-98	Drosophila melanogaster	37,909	24-Sep-99
		GB_HTG3:AC010579	157658	AC010579	09.D.8 map 96F-96F strain y; cn bw sp. *** SEQUENCING IN PROGRESS			
		GB_BA1:SCSECYDN	6154	X83011	***, 121 unordered pieces.			
rx02134	1044	GB_EST32:AI731596	568	AI731596	T12A12-Sp6 TAMU Arabidopsis thaliana genomic clone T12A12, genomic survey sequence.	Arabidopsis thaliana	37,843	14-MAY-1997
		GB_BA1:SCSECYDN	6154	X83011	Drosophila melanogaster chromosome 3 clone BACR09D08 (D1101) RPCI-98	Drosophila melanogaster	37,909	24-Sep-99
		GB_EST32:AI731596	568	AI731596	09.D.8 map 96F-96F strain y; cn bw sp. *** SEQUENCING IN PROGRESS			
		GB_BA1:SCSECYDN	6154	X83011	***, 121 unordered pieces.			
		GB_EST32:AI731596	568	AI731596	S. coelicolor secY locus DNA.	Streptomyces coelicolor	36,533	02-MAR-1998
		GB_BA1:SCSECYDN	6154	X83011	BNLGH10185 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (AC004005) putative ribosomal protein L7 [Arabidopsis thaliana], mRNA sequence.	Gossypium hirsutum	33,451	11-Jun-99
		GB_PR3:HS525L6	168111	AL023807	S. coelicolor secY locus DNA.	Streptomyces coelicolor	36,756	02-MAR-1998
rx02135	1197	GB_PL2:ATF21P8	85785	AL022347	Human DNA sequence from clone RP3-525L6 on chromosome 6p22.3-23	Homo sapiens	34,365	23-Nov-99
		GB_PL2:U89959	106973	U89959	Contains CA repeat, STSs, GSSs and a CpG Island, complete sequence.			
		GB_PL2:U89959	106973	U89959	Arabidopsis thaliana DNA chromosome 4, BAC clone F21P8 (ESSA project).	Arabidopsis thaliana	34,325	9-Jun-99
		GB_PL2:U89959	106973	U89959	Arabidopsis thaliana BAC T7123, complete sequence.	Arabidopsis thaliana	33,874	26-Jun-98



Table 4 (continued)

950	GB_BA1:CGPAN	1228	AF050168	Corynebacterium ammoniagenes subunit (nrdF) gene, complete cds.	Corynebacterium ammoniagenes	72,082	23-Apr-98
950	GB_BA1:CGPAN	2164	X96580	C.glutamicum panB, panC & xylB genes.	Corynebacterium glutamicum	100,000	11-MAY-1999
936	GB_PL1:AP000423	154478	AP000423	Arabidopsis thaliana chloroplast genomic DNA, complete sequence, strain:Columbia.	Chloroplast Arabidopsis thaliana	35,917	15-Sep-99
936	GB_PL1:AP000423	154478	AP000423	Arabidopsis thaliana chloroplast genomic DNA, complete sequence, strain:Columbia.	Chloroplast Arabidopsis thaliana	33,925	15-Sep-99
936	GB_BA1:CGPAN	2164	X96580	C.glutamicum panB, panC & xylB genes.	Corynebacterium glutamicum	100,000	11-MAY-1999
936	GB_BA1:XCUC33548	8429	U33548	Xanthomonas campestris hrpB pathogenicity locus proteins HrpB1, HrpB2, HrpB3, HrpB4, HrpB5, HrpB6, HrpB7, HrpB8, HrpA1, and ORF62 genes, complete cds.	Xanthomonas campestris pv. vesicatoria	38,749	19-Sep-96
1059	GB_BA1:XANHRPB6	1329	M99174	Xanthomonas campestris hrpB6 gene, complete cds.	Xanthomonas campestris	39,305	14-Sep-93
1059	GB_IN2:CFU43371	1060	U43371	Crithidia fasciculata inosine-uridine preferring nucleoside hydrolase (IUNH) gene, complete cds.	Crithidia fasciculata	61,417	18-Jun-96
1230	GB_BA2:AE001467	11601	AE001467	Helicobacter pylori, strain J99 section 28 of 132 of the complete genome.	Helicobacter pylori J99	38,560	20-Jan-99
1230	GB_RO:AF175967	3492	AF175967	Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds.	Mus musculus	40,275	26-Sep-99
1230	GB_BA1:CGDAPE	1966	X81379	C.glutamicum dapE gene and orf2.	Corynebacterium glutamicum	100,000	8-Aug-95
859	GB_BA1:CGDNAARO	2612	X85965	C.glutamicum ORF3 and aroP gene.	Corynebacterium glutamicum	38,889	30-Nov-97
859	GB_BA1:APU47055	6469	U47055	Anabaena PCC7120 nitrogen fixation proteins (nifE, nifN, nifX, nifW) genes, complete cds, and nitrogenase (nifK) and hesA genes, partial cds.	Anabaena PCC7120	36,647	17-Feb-96
859	GB_BA1:MTIC364	29540	Z93777	Mycobacterium tuberculosis H37Rv complete genome; segment 52/162.	Mycobacterium tuberculosis	59,415	17-Jun-98
859	GB_BA1:MSGB1912C	38503	L01536	M. leprae genomic dna sequence, cosmid b1912.	Mycobacterium leprae	57,093	14-Jun-96
859	GB_BA1:MLU15180	38675	U15180	Mycobacterium leprae cosmid B1756.	Mycobacterium leprae	57,210	09-MAR-1995
1464	GB_BA1:CGGDHA	2037	X72855	C.glutamicum GDHA gene.	Corynebacterium glutamicum	99,317	24-MAY-1993
1464	GB_BA1:CGGDH	2037	X59404	Corynebacterium glutamicum, gdh gen for glutamate dehydrogenase.	Corynebacterium glutamicum	94,387	30-Jul-99
1464	GB_BA1:PAE18494	1628	Y18494	Pseudomonas aeruginosa gdhA gene, strain PAC1.	Pseudomonas aeruginosa	62,247	6-Feb-99

Table 4 (continued)

rx01807	915	GB_BA1:AP000063 GB_HTG4:AC010694	185300 115857	AP000063 AC010694	Aeropyrum pernix genomic DNA, section 6/7. Drosophila melanogaster clone RPC198-6H2, *** SEQUENCING IN PROGRESS ***, 75 unordered pieces.	Aeropyrum pernix Drosophila melanogaster	40,067 35,450	22-Jun-99 16-OCT-1999
rx01821	401	GB_HTG4:AC010694 GB_BA1:CGL007732	115857 4460	AC010694 AJ007732	Drosophila melanogaster clone RPC198-6H2, *** SEQUENCING IN PROGRESS ***, 75 unordered pieces. Corynebacterium glutamicum 3' ppc gene, secG gene, amt gene, ocd gene and 5' soxA gene.	Drosophila melanogaster Corynebacterium glutamicum	35,450 100,000	16-OCT-1999 7-Jan-99
rx01835	654	GB_RO:RATALGL GB_OV:APIGY2 GB_EST30:A1629479	7601 1381 353	M24108 X78272 A1629479	Rattus norvegicus (clone A2U42) alpha2u globulin gene, exons 1-7. Anas platyrhynchos (Super M) IgY upslon heavy chain gene, exon 2. 486101D10.x1 486 - leaf primordia cDNA library from Hake lab Zea mays cDNA, mRNA sequence.	Rattus norvegicus Anas platyrhynchos Zea mays	38,692 36,962 38,109	15-DEC-1994 15-Feb-99 26-Apr-99
rx01850	1470	GB_STS:G48245 GB_GSS3:B49052 GB_BA2:ECOUW67_0 GB_BA2:AE000392 GB_BA2:U32715	515 515 10345 13136	G48245 B49052 U18997	SHGC-62915 Human Homo sapiens STS genomic, sequence tagged site. RPC111-4112.TV RPC1-11 Homo sapiens genomic clone RPC1-11-4112, genomic survey sequence. Escherichia coli K-12 chromosomal region from 67.4 to 76.0 minutes.	Homo sapiens Homo sapiens Escherichia coli	37,021 37,021 37,196	26-MAR-1999 8-Apr-99 U18997
rx01878	1002	GB_HTG1:CEY64F11 GB_HTG1:CEY64F11 GB_HTG1:CEY64F11 GB_HTG1:CEY64F11	177748 177748 177748 177748	Z99776 Z99776 Z99776 Z99776	Caenorhabditis elegans chromosome IV clone Y64F11, *** SEQUENCING IN PROGRESS ***, in unordered pieces. Caenorhabditis elegans chromosome IV clone Y64F11, *** SEQUENCING IN PROGRESS ***, in unordered pieces. Caenorhabditis elegans chromosome IV clone Y64F11, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans Caenorhabditis elegans Caenorhabditis elegans	37,564 37,564 37,576	14-OCT-1998 14-OCT-1998 14-OCT-1998
rx01892	852	GB_BA1:MTCY274 GB_BA1:MLCB250 GB_BA1:MSGB1529C	39991 40603 36985	Z74024 Z97369 L78824	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162. Mycobacterium leprae cosmid B250. Mycobacterium leprae cosmid B1529 DNA sequence.	Mycobacterium tuberculosis Mycobacterium leprae Mycobacterium leprae	35,910 64,260 64,260	19-Jun-98 27-Aug-99 15-Jun-96
rx01894	978	GB_BA1:MTCY274 GB_IN1:CELF46H5 GB_HTG3:AC009204	39991 38886 115633	Z74024 U41543 AC009204	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162. Caenorhabditis elegans cosmid F46H5. Drosophila melanogaster chromosome 2 clone BACR03E19 (D1033) RPC1-98 03.E.19 map 36E-37C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 94 unordered pieces.	Mycobacterium tuberculosis Caenorhabditis elegans Drosophila melanogaster	37,229 38,525 31,579	19-Jun-98 29-Nov-96 18-Aug-99
rx01920	1125	GB_BA2:AF112536 GB_BA1:CANRDFGE	1798 6054	AF112536 Y09572	Corynebacterium glutamicum ribonucleotide reductase beta-chain (nrdF) gene, complete cds. Corynebacterium ammoniagenes nrdH, nrdI, nrdE, nrdF genes.	Corynebacterium glutamicum Corynebacterium ammoniagenes	99,733 70,321	5-Aug-99 18-Apr-98

Table 4 (continued)

rx01699	693	GB_BA1:MSG8937C	38914	L78820	Mycobacterium leprae cosmid B937 DNA sequence.	Mycobacterium leprae	62,780	15-Jun-96
		GB_BA2:AF124600	4115	AF124600	Corynebacterium glutamicum chorismate synthase (aroC), shikimate kinase (aroK), and 3-dehydroquinase synthase (aroB) genes, complete cds; and putative cytoplasmic peptidase (pepQ) gene, partial cds.	Corynebacterium glutamicum	100,000	04-MAY-1999
		GB_BA2:AF016585	41097	AF016585	Streptomyces caelestis cytochrome P-450 hydroxylase homolog (nidi) gene, partial cds; polyketide synthase modules 1 through 7 (nida) genes, complete cds; and N-methyltransferase homolog gene, partial cds.	Streptomyces caelestis	40,260	07-DEC-1997
		GB_EST9:C19712	399	C19712	C19712 Rice panicle at ripening stage Oryza sativa cDNA clone E10821_1A, mRNA sequence.	Oryza sativa	45,425	24-OCT-1996
rx01712	805	GB_EST21:AA952466	278	AA952466	TENS1404 T. cruzi epimastigote normalized cDNA Library Trypanosoma cruzi cDNA clone 1404 5', mRNA sequence.	Trypanosoma cruzi	40,876	29-OCT-1998
		GB_EST21:AA952466	278	AA952466	TENS1404 T. cruzi epimastigote normalized cDNA Library Trypanosoma cruzi cDNA clone 1404 5', mRNA sequence.	Trypanosoma cruzi	41,367	29-OCT-1998
rx01719	684	GB_HTG1:HSDJ534K	154416	AL109925	Homo sapiens chromosome 1 clone RP4-534K7, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	35,651	23-Nov-99
		GB_HTG1:HSDJ534K	154416	AL109925	Homo sapiens chromosome 1 clone RP4-534K7, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	35,651	23-Nov-99
		GB_EST27:AI447108	431	AI447108	mq91e08.x1 Stratagene mouse heart (#937316) Mus musculus cDNA clone IMAGE:586118 3', mRNA sequence.	Mus musculus	39,671	09-MAR-1999
rx01720	1332	GB_PR4:AC006322	179640	AC006322	Homo sapiens PAC clone DJ1060B11 from 7q11.23-q21.1, complete sequence.	Homo sapiens	35,817	18-MAR-1999
		GB_PL2:TM018A10	106184	AF013294	Arabidopsis thaliana BAC TM018A10.	Arabidopsis thaliana	35,698	12-Jul-97
		GB_PR4:AC006322	179640	AC006322	Homo sapiens PAC clone DJ1060B11 from 7q11.23-q21.1, complete sequence.	Homo sapiens	37,243	18-MAR-1999
rx01746	876	GB_EST3:R46227	443	R46227	y952a03.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:36000 3', mRNA sequence.	Homo sapiens	42,812	22-MAY-1995
		GB_EST3:R46227	443	R46227	y952a03.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:36000 3', mRNA sequence.	Homo sapiens	42,655	22-MAY-1995
rx01747	1167	GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	59,294	17-Jun-98
		GB_BA1:MLC822	40281	Z98741	Mycobacterium leprae cosmid B22.	Mycobacterium leprae	57,584	22-Aug-97
		GB_BA1:SC5F7	40024	AL096872	Streptomyces coelicolor cosmid 5F7.	Streptomyces coelicolor A3(2)	61,810	22-Jul-99
rx01757	924	GB_EST21:AA918454	416	AA918454	om38c02.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1543298 3' similar to WP:F28F8.3 CE09757 SMALL NUCLEAR RIBONUCLEOPROTEIN E.; mRNA sequence.	Homo sapiens	39,655	23-Jun-98
		GB_EST4:H34042	345	H34042	EST110563 Rat PC-12 cells, NGF-treated (9 days) Rattus sp. cDNA clone RPNB181 5' end, mRNA sequence.	Rattus sp.	35,942	2-Apr-98
		GB_EST20:AA899038	450	AA899038	NCP6G8T7 Peritrichal Neurospora crassa cDNA clone NP6G8 3' end, mRNA sequence.	Neurospora crassa	40,000	12-Apr-98

Table 4 (continued)

rx01617	795	GB_BA1:MLCB1351	38936	Z95117	Mycobacterium leprae cosmid B1351.	Mycobacterium leprae	36,756	24-Jun-97
		GB_PR2:HSMTM0	217657	AL034384	Human chromosome Xq28, cosmid clones 7H3, 14D7, C1230, 11E7, F1096, A12197, 12G8, A09100; complete sequence bases 1..217657.	Homo sapiens	40,811	5-Jul-99
		GB_PR2:HS13D10	153147	AL021407	Homo sapiens DNA sequence from PAC 13D10 on chromosome 6p22.3-23. Contains CpG island.	Homo sapiens	38,768	23-Nov-99
		GB_PR2:HSMTM0	217657	AL034384	Human chromosome Xq28, cosmid clones 7H3, 14D7, C1230, 11E7, F1096, A12197, 12G8, A09100; complete sequence bases 1..217657.	Homo sapiens	39,018	5-Jul-99
rx01657	723	GB_BA1:MTCY1A10	25949	Z95387	Mycobacterium tuberculosis H37Rv complete genome; segment 117/162.	Mycobacterium tuberculosis	40,656	17-Jun-98
		GB_EST6:D79278	392	D79278	HUM213D06B Human aorta polyA+ (TFujiwara) Homo sapiens cDNA clone GEN-213D06 5', mRNA sequence.	Homo sapiens	44,262	9-Feb-96
		GB_BA2:AF129925	10243	AF129925	Thiobacillus ferrooxidans carboxysome operon, complete cds.	Thiobacillus ferrooxidans	40,709	17-MAY-1999
rx01660	675	GB_BA1:MTV013	11364	AL021309	Mycobacterium tuberculosis H37Rv complete genome; segment 134/162.	Mycobacterium tuberculosis	40,986	17-Jun-98
		GB_RO:MMFV1	6480	X97719	M.musculus retrovirus restriction gene Fv1.	Mus musculus	35,364	29-Aug-96
		GB_PAT:A67508	6480	A67508	Sequence 1 from Patent WO9743410.	Mus musculus	35,364	05-MAY-1999
rx01678	651	GB_VI:TVU95309	600	U95309	Tula virus O64 nucleocapsid protein gene, partial cds.	Tula virus	41,894	28-OCT-1997
		GB_VI:TVU95303	600	U95303	Tula virus O52 nucleocapsid protein gene, partial cds.	Tula virus	41,712	28-OCT-1997
		GB_VI:TVU95302	600	U95302	Tula virus O24 nucleocapsid protein gene, partial cds.	Tula virus	39,576	28-OCT-1997
rx01679	1359	GB_EST5:H91843	362	H91843	ys81e01.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:221208 3' similar to gb:X63749_rna1 GUANINE NUCLEOTIDE-BINDING PROTEIN G(T), ALPHA-1 (HUMAN);, mRNA sequence.	Homo sapiens	39,157	29-Nov-95
		GB_STS:G26925	362	G26925	human STS SHGC-30023, sequence tagged site.	Homo sapiens	39,157	14-Jun-96
		GB_PL2:AF139451	1202	AF139451	Gossypium robinsonii CeiA2 pseudogene, partial sequence.	Gossypium robinsonii	38,910	1-Jun-99
rx01690	1224	GB_BA1:SC1C2	42210	AL031124	Streptomyces coelicolor cosmid 1C2.	Streptomyces coelicolor	60,644	15-Jan-99
		GB_EST22:A1064232	493	A1064232	GH04563.5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH04563 5prime, mRNA sequence.	Drosophila melanogaster	38,037	24-Nov-98
		GB_IN2:AF117896	1020	AF117896	Drosophila melanogaster neuropeptide F (npf) gene, complete cds.	Drosophila melanogaster	36,122	2-Jul-99
rx01692	873	GB_BA2:AF067123	1034	AF067123	Lactobacillus reuteri cobalamin biosynthesis protein J (cblJ) gene, partial cds; and uroporphyrin-III C-methyltransferase (sumT) gene, complete cds.	Lactobacillus reuteri	48,079	3-Jun-98
		GB_RO:RATNFHPEP	3085	M37227	Rat heavy neurofilament (NF-H) polypeptide, partial cds.	Rattus norvegicus	37,093	27-Apr-93
		GB_RO:RSNFH	3085	X13804	Rat mRNA for heavy neurofilament polypeptide NF-H C-terminus.	Rattus sp.	37,093	14-Jul-95
rx01698	1353	GB_BA2:AF124600	4115	AF124600	Corynebacterium glutamicum chorismate synthase (aroC), shikimate kinase (aroK), and 3-dehydroquinate synthase (aroB) genes, complete cds; and putative cytoplasmic peptidase (pepQ) gene, partial cds.	Corynebacterium glutamicum	100,000	04-MAY-1999
		GB_BA1:MTCY159	33818	Z83863	Mycobacterium tuberculosis H37Rv complete genome; segment 111/162.	Mycobacterium tuberculosis	36,323	17-Jun-98

Table 4 (continued)

rx01514	711	GB_BA1:MTY15C10	33050	Z95436	Mycobacterium tuberculosis H37Rv complete genome; segment 154/162.	Mycobacterium tuberculosis	40,086	17-Jun-98
		GB_BA1:MTY7H7B	24244	Z95557	Mycobacterium tuberculosis H37Rv complete genome; segment 153/162.	Mycobacterium tuberculosis	43,343	18-Jun-98
		GB_BA1:MLCB2548	38916	AL023093	Mycobacterium leprae cosmid B2548.	Mycobacterium leprae	38,177	27-Aug-99
		GB_PL1:EGGTPCHI	242	Z49757	E. gracilis mRNA for GTP cyclohydrolase I (core region).	Euglena gracilis	64,876	20-OCT-1995
rx01515	975	GB_BA1:ECOUW93	338534	U14003	Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes.	Escherichia coli	38,943	17-Apr-96
		GB_BA1:ECOUW93	338534	U14003	Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes.	Escherichia coli	37,500	17-Apr-96
		GB_BA1:MTCY49	39430	Z73966	Mycobacterium tuberculosis H37Rv complete genome; segment 93/162.	Mycobacterium tuberculosis	38,010	24-Jun-99
rx01516	513	GB_IN1:DME238847	5419	AJ238847	Drosophila melanogaster mRNA for drosophila dodeca-satellite protein 1 (DDP-1).	Drosophila melanogaster	36,346	13-Aug-99
		GB_HTG3:AC009210	103814	AC009210	Drosophila melanogaster chromosome 2 clone BACR01105 (D1054) RPL-98 01.1.6 map 55D-55D strain y; cn bw sp. *** SEQUENCING IN PROGRESS ***. 86 unordered pieces.	Drosophila melanogaster	37,897	20-Aug-99
rx01517	600	GB_IN2:AF132179	4842	AF132179	Drosophila melanogaster clone LD21677 unknown mRNA.	Drosophila melanogaster	36,149	3-Jun-99
		GB_PL2:F6H8	82596	AF178045	Arabidopsis thaliana BAC F6H8.	Arabidopsis thaliana	35,846	19-Aug-99
		GB_PL2:AF038831	647	AF038831	Sorosporium saponariae internal transcribed spacer 1, 5.8S ribosomal RNA gene; and internal transcribed spacer 2, complete sequence.	Sorosporium saponariae	40,566	13-Apr-99
		GB_PL2:ATAC005957	108355	AC005957	Arabidopsis thaliana chromosome II BAC T15J14 genomic sequence, complete sequence.	Arabidopsis thaliana	38,095	7-Jan-99
rx01521	921	GB_BA1:ANANIFBH	5936	J05111	Anabaena sp. (clone ANH20.1) nitrogen fixation operon nifB, fdxN, nifS, nifU, and nifH genes, complete cds.	Anabaena sp.	38,206	26-Apr-93
		GB_PR2:AC002461	197273	AC002461	Human BAC clone RG204116 from 7q31, complete sequence.	Homo sapiens	36,623	20-Aug-97
		GB_PR2:AC002461	197273	AC002461	Human BAC clone RG204116 from 7q31, complete sequence.	Homo sapiens	34,719	20-Aug-97
rx01528	651	GB_RO:MM437P9	165901	AL049866	Mus musculus chromosome X, clone 437P9.	Mus musculus	37,500	29-Jun-99
		GB_PR3:AC005740	186780	AC005740	Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.	Homo sapiens	37,031	01-OCT-1998
		GB_PR3:AC005740	186780	AC005740	Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.	Homo sapiens	38,035	01-OCT-1998
rx01551	1998	GB_BA1:MTY22G10	35420	Z84724	Mycobacterium tuberculosis H37Rv complete genome; segment 21/162.	Mycobacterium tuberculosis	38,371	17-Jun-98
		GB_BA2:ECOUW89	176195	U00006	E. coli chromosomal region from 89.2 to 92.8 minutes.	Escherichia coli	38,064	17-DEC-1993
rx01561	1053	GB_BA1:SCQ11	15441	AL098823	Streptomyces coelicolor cosmid Q11.	Streptomyces coelicolor	60,775	8-Jul-99
		GB_IN1:CEY62H9A	47396	AL032630	Caenorhabditis elegans cosmid Y62H9A, complete sequence.	Caenorhabditis elegans	38,514	2-Sep-99
		GB_PR4:HSU51003	3202	U51003	Homo sapiens DLX-2 (DLX-2) gene, complete cds.	Homo sapiens	37,730	07-DEC-1999
rx01599	1785	GB_OM:PIGDAO1	395	M18444	Pig D-amino acid oxidase (DAO) gene, exon 1.	Sus scrofa	39,340	27-Apr-93
		GB_BA1:MTCH125	37432	Z98268	Mycobacterium tuberculosis H37Rv complete genome; segment 76/162.	Mycobacterium tuberculosis	63,300	17-Jun-98
		GB_BA1:U00021	39193	U00021	Mycobacterium leprae cosmid L247.	Mycobacterium leprae	36,756	29-Sep-94



What is claimed:

1. An isolated nucleic acid molecule from *Corynebacterium glutamicum* encoding a  
5 metabolic pathway protein, or a portion thereof, provided that the nucleic acid  
molecule does not consist of any of the F-designated genes set forth in Table 1.
2. The isolated nucleic acid molecule of claim 1, wherein said metabolic pathway  
protein is selected from the group consisting of proteins involved in the metabolism  
10 of an amino acid, a vitamin, a cofactor, a nutraceutical, a nucleotide, a nucleoside, or  
trehalose.
3. An isolated *Corynebacterium glutamicum* nucleic acid molecule selected from the  
group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the  
15 Sequence Listing, or a portion thereof, provided that the nucleic acid molecule does  
not consist of any of the F-designated genes set forth in Table 1.
4. An isolated nucleic acid molecule which encodes a polypeptide sequence selected  
from the group consisting of those sequences set forth as even-numbered SEQ ID  
20 NOs of the Sequence Listing, provided that the nucleic acid molecule does not  
consist of any of the F-designated genes set forth in Table 1.
5. An isolated nucleic acid molecule which encodes a naturally occurring allelic variant  
of a polypeptide selected from the group of amino acid sequences consisting of those  
25 sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing,  
provided that the nucleic acid molecule does not consist of any of the F-designated  
genes set forth in Table 1.
6. An isolated nucleic acid molecule comprising a nucleotide sequence which is at least  
30 50% homologous to a nucleotide sequence selected from the group consisting of  
those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, or

**Equivalents**

Those of ordinary skill in the art will recognize, or will be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the

5 following claims.



1451-1463). Other separation techniques may also be utilized for protein separation, such as capillary gel electrophoresis; such techniques are well known in the art.

Proteins separated by these methodologies can be visualized by standard techniques, such as by staining or labeling. Suitable stains are known in the art, and  
5 include Coomassie Brilliant Blue, silver stain, or fluorescent dyes such as Sypro Ruby (Molecular Probes). The inclusion of radioactively labeled amino acids or other protein precursors (*e.g.*,  $^{35}\text{S}$ -methionine,  $^{35}\text{S}$ -cysteine,  $^{14}\text{C}$ -labelled amino acids,  $^{15}\text{N}$ -amino acids,  $^{15}\text{NO}_3$  or  $^{15}\text{NH}_4^+$  or  $^{13}\text{C}$ -labelled amino acids) in the medium of *C. glutamicum* permits the labeling of proteins from these cells prior to their separation. Similarly,  
10 fluorescent labels may be employed. These labeled proteins can be extracted, isolated and separated according to the previously described techniques.

Proteins visualized by these techniques can be further analyzed by measuring the amount of dye or label used. The amount of a given protein can be determined quantitatively using, for example, optical methods and can be compared to the amount  
15 of other proteins in the same gel or in other gels. Comparisons of proteins on gels can be made, for example, by optical comparison, by spectroscopy, by image scanning and analysis of gels, or through the use of photographic films and screens. Such techniques are well-known in the art.

To determine the identity of any given protein, direct sequencing or other  
20 standard techniques may be employed. For example, N- and/or C-terminal amino acid sequencing (such as Edman degradation) may be used, as may mass spectrometry (in particular MALDI or ESI techniques (*see, e.g.,* Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192)). The protein sequences provided herein can be used for the identification of *C. glutamicum* proteins by these techniques.

25 The information obtained by these methods can be used to compare patterns of protein presence, activity, or modification between different samples from various biological conditions (*e.g.*, different organisms, time points of fermentation, media conditions, or different biotopes, among others). Data obtained from such experiments alone, or in combination with other techniques, can be used for various applications,  
30 such as to compare the behavior of various organisms in a given (*e.g.*, metabolic) situation, to increase the productivity of strains which produce fine chemicals or to increase the efficiency of the production of fine chemicals.

described in Schena, M. *et al.* (1995) *supra*) and fluorescent labels may be detected, for example, by the method of Shalon *et al.* (1996) *Genome Research* 6: 639-645).

The application of the sequences of the invention to DNA microarray technology, as described above, permits comparative analyses of different strains of *C. glutamicum* or other Corynebacteria. For example, studies of inter-strain variations based on individual transcript profiles and the identification of genes that are important for specific and/or desired strain properties such as pathogenicity, productivity and stress tolerance are facilitated by nucleic acid array methodologies. Also, comparisons of the profile of expression of genes of the invention during the course of a fermentation reaction are possible using nucleic acid array technology.

### **Example 13: Analysis of the Dynamics of Cellular Protein Populations (Proteomics)**

The genes, compositions, and methods of the invention may be applied to study the interactions and dynamics of populations of proteins, termed 'proteomics'. Protein populations of interest include, but are not limited to, the total protein population of *C. glutamicum* (*e.g.*, in comparison with the protein populations of other organisms), those proteins which are active under specific environmental or metabolic conditions (*e.g.*, during fermentation, at high or low temperature, or at high or low pH), or those proteins which are active during specific phases of growth and development.

Protein populations can be analyzed by various well-known techniques, such as gel electrophoresis. Cellular proteins may be obtained, for example, by lysis or extraction, and may be separated from one another using a variety of electrophoretic techniques. Sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) separates proteins largely on the basis of their molecular weight. Isoelectric focusing polyacrylamide gel electrophoresis (IEF-PAGE) separates proteins by their isoelectric point (which reflects not only the amino acid sequence but also posttranslational modifications of the protein). Another, more preferred method of protein analysis is the consecutive combination of both IEF-PAGE and SDS-PAGE, known as 2-D-gel electrophoresis (described, for example, in Hermann *et al.* (1998) *Electrophoresis* 19: 3217-3221; Fountoulakis *et al.* (1998) *Electrophoresis* 19: 1193-1202; Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192; Antelmann *et al.* (1997) *Electrophoresis* 18:

may be used to monitor and measure the individual signal intensities of the hybridized molecules at defined regions. This methodology allows the simultaneous quantification of the relative or absolute amount of all or selected nucleic acids in the applied nucleic acid sample or mixture. DNA microarrays, therefore, permit an analysis of the  
5 expression of multiple (as many as 6800 or more) nucleic acids in parallel (see, *e.g.*, Schena, M. (1996) *BioEssays* 18(5): 427-431).

The sequences of the invention may be used to design oligonucleotide primers which are able to amplify defined regions of one or more *C. glutamicum* genes by a nucleic acid amplification reaction such as the polymerase chain reaction. The choice  
10 and design of the 5' or 3' oligonucleotide primers or of appropriate linkers allows the covalent attachment of the resulting PCR products to the surface of a support medium described above (and also described, for example, Schena, M. *et al.* (1995) *Science* 270: 467-470).

Nucleic acid microarrays may also be constructed by *in situ* oligonucleotide  
15 synthesis as described by Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367. By photolithographic methods, precisely defined regions of the matrix are exposed to light. Protective groups which are photolabile are thereby activated and undergo nucleotide addition, whereas regions that are masked from light do not undergo any modification. Subsequent cycles of protection and light activation permit the  
20 synthesis of different oligonucleotides at defined positions. Small, defined regions of the genes of the invention may be synthesized on microarrays by solid phase oligonucleotide synthesis.

The nucleic acid molecules of the invention present in a sample or mixture of nucleotides may be hybridized to the microarrays. These nucleic acid molecules can be  
25 labeled according to standard methods. In brief, nucleic acid molecules (*e.g.*, mRNA molecules or DNA molecules) are labeled by the incorporation of isotopically or fluorescently labeled nucleotides, *e.g.*, during reverse transcription or DNA synthesis. Hybridization of labeled nucleic acids to microarrays is described (*e.g.*, in Schena, M. *et al.* (1995) *supra*; Wodicka, L. *et al.* (1997), *supra*; and DeSaizieu A. *et al.* (1998),  
30 *supra*). The detection and quantification of the hybridized molecule are tailored to the specific incorporated label. Radioactive labels can be detected, for example, as

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were compared to genes present in Genbank in a three-step process. In a first step, a BLASTN analysis (*e.g.*, a local alignment analysis) was performed for each of the sequences of the invention against the nucleotide sequences present in Genbank, and the top 500 hits were retained for further analysis. A subsequent FASTA search (*e.g.*, a  
5 combined local and global alignment analysis, in which limited regions of the sequences are aligned) was performed on these 500 hits. Each gene sequence of the invention was subsequently globally aligned to each of the top three FASTA hits, using the GAP program in the GCG software package (using standard parameters). In order to obtain correct results, the length of the sequences extracted from Genbank were adjusted to the  
10 length of the query sequences by methods well-known in the art. The results of this analysis are set forth in Table 4. The resulting data is identical to that which would have been obtained had a GAP (global) analysis alone been performed on each of the genes of the invention in comparison with each of the references in Genbank, but required significantly reduced computational time as compared to such a database-wide GAP  
15 (global) analysis. Sequences of the invention for which no alignments above the cutoff values were obtained are indicated on Table 4 by the absence of alignment information. It will further be understood by one of ordinary skill in the art that the GAP alignment homology percentages set forth in Table 4 under the heading "% homology (GAP)" are listed in the European numerical format, wherein a ',' represents a decimal point. For  
20 example, a value of "40,345" in this column represents "40.345%".

**Example 12: Construction and Operation of DNA Microarrays**

The sequences of the invention may additionally be used in the construction and application of DNA microarrays (the design, methodology, and uses of DNA arrays are  
25 well known in the art, and are described, for example, in Schena, M. *et al.* (1995) *Science* 270: 467-470; Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367; DeSaizieu, A. *et al.* (1998) *Nature Biotechnology* 16: 45-48; and DeRisi, J.L. *et al.* (1997) *Science* 278: 680-686).

DNA microarrays are solid or flexible supports consisting of nitrocellulose,  
30 nylon, glass, silicone, or other materials. Nucleic acid molecules may be attached to the surface in an ordered manner. After appropriate labeling, other nucleic acids or nucleic acid mixtures can be hybridized to the immobilized nucleic acid molecules, and the label

90:5873-77. Such an algorithm is incorporated into the NBLAST and XBLAST programs (version 2.0) of Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to MP nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to MP protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.*, (1997) *Nucleic Acids Res.* 25(17):3389-3402. When utilizing BLAST and Gapped BLAST programs, one of ordinary skill in the art will know how to optimize the parameters of the program (*e.g.*, XBLAST and NBLAST) for the specific sequence being analyzed.

Another example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Meyers and Miller ((1988) *Comput. Appl. Biosci.* 4: 11-17). Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. Additional algorithms for sequence analysis are known in the art, and include ADVANCE and ADAM. described in Torelli and Robotti (1994) *Comput. Appl. Biosci.* 10:3-5; and FASTA, described in Pearson and Lipman (1988) *P.N.A.S.* 85:2444-8.

The percent homology between two amino acid sequences can also be accomplished using the GAP program in the GCG software package (available at <http://www.gcg.com>), using either a Blosum 62 matrix or a PAM250 matrix, and a gap weight of 12, 10, 8, 6, or 4 and a length weight of 2, 3, or 4. The percent homology between two nucleic acid sequences can be accomplished using the GAP program in the GCG software package, using standard parameters, such as a gap weight of 50 and a length weight of 3.

A comparative analysis of the gene sequences of the invention with those present in Genbank has been performed using techniques known in the art (see, *e.g.*, Bexevanis and Ouellette, eds. (1998) *Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins.* John Wiley and Sons: New York). The gene sequences of the invention

cells, then the cells are removed from the culture by low-speed centrifugation, and the supernate fraction is retained for further purification.

The supernatant fraction from either purification method is subjected to chromatography with a suitable resin, in which the desired molecule is either retained on a chromatography resin while many of the impurities in the sample are not, or where the impurities are retained by the resin while the sample is not. Such chromatography steps may be repeated as necessary, using the same or different chromatography resins. One of ordinary skill in the art would be well-versed in the selection of appropriate chromatography resins and in their most efficacious application for a particular molecule to be purified. The purified product may be concentrated by filtration or ultrafiltration, and stored at a temperature at which the stability of the product is maximized.

There are a wide array of purification methods known to the art and the preceding method of purification is not meant to be limiting. Such purification techniques are described, for example, in Bailey, J.E. & Ollis, D.F. *Biochemical Engineering Fundamentals*, McGraw-Hill: New York (1986).

The identity and purity of the isolated compounds may be assessed by techniques standard in the art. These include high-performance liquid chromatography (HPLC), spectroscopic methods, staining methods, thin layer chromatography, NIRS, enzymatic assay, or microbiologically. Such analysis methods are reviewed in: Patek *et al.* (1994) *Appl. Environ. Microbiol.* 60: 133-140; Malakhova *et al.* (1996) *Biotehnologiya* 11: 27-32; and Schmidt *et al.* (1998) *Bioprocess Engineer.* 19: 67-70. *Ulmann's Encyclopedia of Industrial Chemistry*, (1996) vol. A27, VCH: Weinheim, p. 89-90, p. 521-540, p. 540-547, p. 559-566, 575-581 and p. 581-587; Michal, G. (1999) *Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology*, John Wiley and Sons; Fallon, A. *et al.* (1987) *Applications of HPLC in Biochemistry in: Laboratory Techniques in Biochemistry and Molecular Biology*, vol. 17.

#### **Example 11: Analysis of the Gene Sequences of the Invention**

The comparison of sequences and determination of percent homology between two sequences are art-known techniques, and can be accomplished using a mathematical algorithm, such as the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci. USA* 87:2264-68, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. USA*

Ullman, Encyclopedia of Industrial Chemistry, vol. A2, p. 89-90 and p. 443-613, VCH: Weinheim (1985); Fallon, A. *et al.*, (1987) "Applications of HPLC in Biochemistry" in: Laboratory Techniques in Biochemistry and Molecular Biology, vol. 17; Rehm *et al.* (1993) Biotechnology, vol. 3, Chapter III: "Product recovery and purification", page 5 469-714, VCH: Weinheim; Belter, P.A. *et al.* (1988) Bioseparations: downstream processing for biotechnology, John Wiley and Sons; Kennedy, J.F. and Cabral, J.M.S. (1992) Recovery processes for biological materials, John Wiley and Sons; Shaeiwitz, J.A. and Henry, J.D. (1988) Biochemical separations, in: Ulmann's Encyclopedia of Industrial Chemistry, vol. B3, Chapter 11, page 1-27, VCH: Weinheim; and Dechow, 10 F.J. (1989) Separation and purification techniques in biotechnology, Noyes Publications.)

In addition to the measurement of the final product of fermentation, it is also possible to analyze other components of the metabolic pathways utilized for the production of the desired compound, such as intermediates and side-products, to 15 determine the overall efficiency of production of the compound. Analysis methods include measurements of nutrient levels in the medium (*e.g.*, sugars, hydrocarbons, nitrogen sources, phosphate, and other ions), measurements of biomass composition and growth, analysis of the production of common metabolites of biosynthetic pathways, and measurement of gasses produced during fermentation. Standard methods for these 20 measurements are outlined in Applied Microbial Physiology, A Practical Approach, P.M. Rhodes and P.F. Stanbury, eds., IRL Press, p. 103-129; 131-163; and 165-192 (ISBN: 0199635773) and references cited therein.

#### **Example 10: Purification of the Desired Product from *C. glutamicum* Culture**

25 Recovery of the desired product from the *C. glutamicum* cells or supernatant of the above-described culture can be performed by various methods well known in the art. If the desired product is not secreted from the cells, the cells can be harvested from the culture by low-speed centrifugation, the cells can be lysed by standard techniques, such as mechanical force or sonication. The cellular debris is removed by centrifugation, and 30 the supernatant fraction containing the soluble proteins is retained for further purification of the desired compound. If the product is secreted from the *C. glutamicum*

found, for example, in the following references: Dixon, M., and Webb, E.C., (1979) *Enzymes*. Longmans: London; Fersht, (1985) *Enzyme Structure and Mechanism*. Freeman: New York; Walsh, (1979) *Enzymatic Reaction Mechanisms*. Freeman: San Francisco; Price, N.C., Stevens, L. (1982) *Fundamentals of Enzymology*. Oxford Univ. Press: Oxford; Boyer, P.D., ed. (1983) *The Enzymes*, 3<sup>rd</sup> ed. Academic Press: New York; Bisswanger, H., (1994) *Enzymkinetik*, 2<sup>nd</sup> ed. VCH: Weinheim (ISBN 3527300325); Bergmeyer, H.U., Bergmeyer, J., Graßl, M., eds. (1983-1986) *Methods of Enzymatic Analysis*, 3<sup>rd</sup> ed., vol. I-XII, Verlag Chemie: Weinheim; and Ullmann's *Encyclopedia of Industrial Chemistry* (1987) vol. A9, "Enzymes". VCH: Weinheim, p. 352-363.

The activity of proteins which bind to DNA can be measured by several well-established methods, such as DNA band-shift assays (also called gel retardation assays). The effect of such proteins on the expression of other molecules can be measured using reporter gene assays (such as that described in Kolmar, H. *et al.* (1995) *EMBO J.* 14: 3895-3904 and references cited therein). Reporter gene test systems are well known and established for applications in both pro- and eukaryotic cells, using enzymes such as beta-galactosidase, green fluorescent protein, and several others.

The determination of activity of membrane-transport proteins can be performed according to techniques such as those described in Gennis, R.B. (1989) "Pores, Channels and Transporters", in *Biomembranes, Molecular Structure and Function*, Springer: Heidelberg, p. 85-137; 199-234; and 270-322.

#### **Example 9: Analysis of Impact of Mutant Protein on the Production of the Desired Product**

The effect of the genetic modification in *C. glutamicum* on production of a desired compound (such as an amino acid) can be assessed by growing the modified microorganism under suitable conditions (such as those described above) and analyzing the medium and/or the cellular component for increased production of the desired product (*i.e.*, an amino acid). Such analysis techniques are well known to one of ordinary skill in the art, and include spectroscopy, thin layer chromatography, staining methods of various kinds, enzymatic and microbiological methods, and analytical chromatography such as high performance liquid chromatography (see, for example,



is also possible to maintain a constant culture pH through the addition of NaOH or NH<sub>4</sub>OH during growth. If complex medium components such as yeast extract are utilized, the necessity for additional buffers may be reduced, due to the fact that many complex compounds have high buffer capacities. If a fermentor is utilized for culturing the micro-organisms, the pH can also be controlled using gaseous ammonia.

The incubation time is usually in a range from several hours to several days. This time is selected in order to permit the maximal amount of product to accumulate in the broth. The disclosed growth experiments can be carried out in a variety of vessels, such as microtiter plates, glass tubes, glass flasks or glass or metal fermentors of different sizes.

For screening a large number of clones, the microorganisms should be cultured in microtiter plates, glass tubes or shake flasks, either with or without baffles. Preferably 100 ml shake flasks are used, filled with 10% (by volume) of the required growth medium. The flasks should be shaken on a rotary shaker (amplitude 25 mm) using a speed-range of 100 – 300 rpm. Evaporation losses can be diminished by the maintenance of a humid atmosphere; alternatively, a mathematical correction for evaporation losses should be performed.

If genetically modified clones are tested, an unmodified control clone or a control clone containing the basic plasmid without any insert should also be tested. The medium is inoculated to an OD<sub>600</sub> of 0.5 – 1.5 using cells grown on agar plates, such as CM plates (10 g/l glucose, 2,5 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l agar, pH 6.8 with 2M NaOH) that had been incubated at 30°C. Inoculation of the media is accomplished by either introduction of a saline suspension of *C. glutamicum* cells from CM plates or addition of a liquid preculture of this bacterium.

25

#### **Example 8 – *In vitro* Analysis of the Function of Mutant Proteins**

The determination of activities and kinetic parameters of enzymes is well established in the art. Experiments to determine the activity of any given altered enzyme must be tailored to the specific activity of the wild-type enzyme, which is well within the ability of one of ordinary skill in the art. Overviews about enzymes in general, as well as specific details concerning structure, kinetics, principles, methods, applications and examples for the determination of many enzyme activities may be

advantageous to supply mixtures of different carbon sources. Other possible carbon sources are alcohols and organic acids, such as methanol, ethanol, acetic acid or lactic acid. Nitrogen sources are usually organic or inorganic nitrogen compounds, or materials which contain these compounds. Exemplary nitrogen sources include ammonia gas or  
5 ammonia salts, such as  $\text{NH}_4\text{Cl}$  or  $(\text{NH}_4)_2\text{SO}_4$ ,  $\text{NH}_4\text{OH}$ , nitrates, urea, amino acids or complex nitrogen sources like corn steep liquor, soy bean flour, soy bean protein, yeast extract, meat extract and others.

Inorganic salt compounds which may be included in the media include the chloride-, phosphorous- or sulfate- salts of calcium, magnesium, sodium, cobalt,  
10 molybdenum, potassium, manganese, zinc, copper and iron. Chelating compounds can be added to the medium to keep the metal ions in solution. Particularly useful chelating compounds include dihydroxyphenols, like catechol or protocatechuate, or organic acids, such as citric acid. It is typical for the media to also contain other growth factors, such as vitamins or growth promoters, examples of which include biotin, riboflavin, thiamin, folic  
15 acid, nicotinic acid, pantothenate and pyridoxin. Growth factors and salts frequently originate from complex media components such as yeast extract, molasses, corn steep liquor and others. The exact composition of the media compounds depends strongly on the immediate experiment and is individually decided for each specific case. Information about media optimization is available in the textbook "Applied Microbiol. Physiology, A  
20 Practical Approach (*eds.* P.M. Rhodes, P.F. Stanbury, IRL Press (1997) pp. 53-73, ISBN 0 19 963577 3). It is also possible to select growth media from commercial suppliers, like standard 1 (Merck) or BHI (grain heart infusion, DIFCO) or others.

All medium components are sterilized, either by heat (20 minutes at 1.5 bar and 121°C) or by sterile filtration. The components can either be sterilized together or, if  
25 necessary, separately. All media components can be present at the beginning of growth, or they can optionally be added continuously or batchwise.

Culture conditions are defined separately for each experiment. The temperature should be in a range between 15°C and 45°C. The temperature can be kept constant or can be altered during the experiment. The pH of the medium should be in the range of 5 to  
30 8.5, preferably around 7.0, and can be maintained by the addition of buffers to the media. An exemplary buffer for this purpose is a potassium phosphate buffer. Synthetic buffers such as MOPS, HEPES, ACES and others can alternatively or simultaneously be used. It

(1988) Current Protocols in Molecular Biology, Wiley: New York), in which a primer designed to bind to the gene of interest is labeled with a detectable tag (usually radioactive or chemiluminescent), such that when the total RNA of a culture of the organism is extracted, run on gel, transferred to a stable matrix and incubated with this probe, the binding and quantity of binding of the probe indicates the presence and also the quantity of mRNA for this gene. This information is evidence of the degree of transcription of the mutant gene. Total cellular RNA can be prepared from *Corynebacterium glutamicum* by several methods, all well-known in the art, such as that described in Bormann, E.R. *et al.* (1992) *Mol. Microbiol.* 6: 317-326.

10 To assess the presence or relative quantity of protein translated from this mRNA, standard techniques, such as a Western blot, may be employed (see, for example, Ausubel *et al.* (1988) Current Protocols in Molecular Biology, Wiley: New York). In this process, total cellular proteins are extracted, separated by gel electrophoresis, transferred to a matrix such as nitrocellulose, and incubated with a probe, such as an antibody, which  
15 specifically binds to the desired protein. This probe is generally tagged with a chemiluminescent or colorimetric label which may be readily detected. The presence and quantity of label observed indicates the presence and quantity of the desired mutant protein present in the cell.

#### 20 **Example 7: Growth of Genetically Modified *Corynebacterium glutamicum* — Media and Culture Conditions**

Genetically modified *Corynebacteria* are cultured in synthetic or natural growth media. A number of different growth media for *Corynebacteria* are both well-known and readily available (Lieb *et al.* (1989) *Appl. Microbiol. Biotechnol.*, 32:205-210; von der  
25 Osten *et al.* (1998) *Biotechnology Letters*, 11:11-16; Patent DE 4,120,867; Liebl (1992) "The Genus *Corynebacterium*, in: The Prokaryotes, Volume II, Balows, A. *et al.*, eds. Springer-Verlag). These media consist of one or more carbon sources, nitrogen sources, inorganic salts, vitamins and trace elements. Preferred carbon sources are sugars, such as  
mono-, di-, or polysaccharides. For example, glucose, fructose, mannose, galactose,  
30 ribose, sorbose, ribulose, lactose, maltose, sucrose, raffinose, starch or cellulose serve as very good carbon sources. It is also possible to supply sugar to the media via complex compounds such as molasses or other by-products from sugar refinement. It can also be

(1990) *J. Bacteriol.* 172:1663-1666). It is also possible to transfer the shuttle vectors for *C. glutamicum* to *E. coli* by preparing plasmid DNA from *C. glutamicum* (using standard methods well-known in the art) and transforming it into *E. coli*. This transformation step can be performed using standard methods, but it is advantageous to use an Mcr-deficient  
5 *E. coli* strain, such as NM522 (Gough & Murray (1983) *J. Mol. Biol.* 166:1-19).

Genes may be overexpressed in *C. glutamicum* strains using plasmids which comprise pCG1 (U.S. Patent No. 4,617,267) or fragments thereof, and optionally the gene for kanamycin resistance from TN903 (Grindley, N.D. and Joyce, C.M. (1980) *Proc. Natl. Acad. Sci. USA* 77(12): 7176-7180). In addition, genes may be  
10 overexpressed in *C. glutamicum* strains using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

Aside from the use of replicative plasmids, gene overexpression can also be achieved by integration into the genome. Genomic integration in *C. glutamicum* or other *Corynebacterium* or *Brevibacterium* species may be accomplished by well-known  
15 methods, such as homologous recombination with genomic region(s), restriction endonuclease mediated integration (REMI) (see, e.g., DE Patent 19823834), or through the use of transposons. It is also possible to modulate the activity of a gene of interest by modifying the regulatory regions (e.g., a promoter, a repressor, and/or an enhancer) by sequence modification, insertion, or deletion using site-directed methods (such as  
20 homologous recombination) or methods based on random events (such as transposon mutagenesis or REMI). Nucleic acid sequences which function as transcriptional terminators may also be inserted 3' to the coding region of one or more genes of the invention; such terminators are well-known in the art and are described, for example, in Winnacker, E.L. (1987) *From Genes to Clones – Introduction to Gene Technology*. VCH:  
25 Weinheim.

#### **Example 6: Assessment of the Expression of the Mutant Protein**

Observations of the activity of a mutated protein in a transformed host cell rely on the fact that the mutant protein is expressed in a similar fashion and in a similar quantity  
30 to that of the wild-type protein. A useful method to ascertain the level of transcription of the mutant gene (an indicator of the amount of mRNA available for translation to the gene product) is to perform a Northern blot (for reference see, for example, Ausubel *et al.*

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<210> 7

<211> 792

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(769)

<223> RXC02390

<400> 7

```

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ggccgcgagg atctcgtagc tcgcttcgag tcataggccg gtg gag tgg acc gct 115
                               Val Glu Trp Thr Ala
                               1 5

ttt ggc acc ctg att ctg ctc aat ttg gtg ggc agt tta tcc ccg ggg 163
Phe Gly Thr Leu Ile Leu Leu Asn Leu Val Gly Ser Leu Ser Pro Gly
                               10 15 20

cct gat acc ttt ttc ctc ctc cgc tta gcc acc cgc tcc aga gcg cac 211
Pro Asp Thr Phe Phe Leu Leu Arg Leu Ala Thr Arg Ser Arg Ala His
                               25 30 35

gcg atc gct ggc gtc gcc ggc atc gtc acc gga ctc acg gtg tgg gtg 259
Ala Ile Ala Gly Val Ala Gly Ile Val Thr Gly Leu Thr Val Trp Val
                               40 45 50

acg ctg acg gtc gtg gga gca gcg gcg ctg ctc acc act tat ccg tcg 307
Thr Leu Thr Val Val Gly Ala Ala Leu Leu Thr Thr Tyr Pro Ser
                               55 60 65

att ctc gga atc atc cag ctc gtc ggc ggc acg tac cta agc ttc att 355
Ile Leu Gly Ile Ile Gln Leu Val Gly Gly Thr Tyr Leu Ser Phe Ile
                               70 75 80 85

ggg tac aag ttg ctg cgc tcg gcg tcg aga gag ctt atc gac gcc cgc 403
Gly Tyr Lys Leu Leu Arg Ser Ala Ser Arg Glu Leu Ile Asp Ala Arg
                               90 95 100

cag ttc cgt ttc aac gcc gat gcc cga cct atc ccg gat gcg gta gaa 451
Gln Phe Arg Phe Asn Ala Asp Ala Arg Pro Ile Pro Asp Ala Val Glu
                               105 110 115

gca ctg gga acc cgc act cag gta tat cga caa ggt ttg gcc acc aac 499
Ala Leu Gly Thr Arg Thr Gln Val Tyr Arg Gln Gly Leu Ala Thr Asn
                               120 125 130

ctg tca aac cct aaa gtt gtc atg tac ttc gcg gca att ctg gct ccg 547
Leu Ser Asn Pro Lys Val Val Met Tyr Phe Ala Ala Ile Leu Ala Pro
                               135 140 145

ttg atg cca gcg cac cca tca ccg gtg ctg gcg ttc tct atc atc gtg 595
Leu Met Pro Ala His Pro Ser Pro Val Leu Ala Phe Ser Ile Ile Val
                               150 155 160 165

```

His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg  
                     85                    90                    95  
 Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val  
                     100                    105                    110  
 Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe  
                     115                    120                    125  
 Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala  
                     130                    135                    140  
 Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr  
                     145                    150                    155                    160  
 His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg  
                     165                    170                    175  
 Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro  
                     180                    185                    190  
 Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys  
                     195                    200                    205  
 Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala  
                     210                    215                    220  
 Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly  
                     225                    230                    235                    240  
 Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys  
                     245                    250                    255  
 Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe  
                     260                    265                    270  
 Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe  
                     275                    280                    285  
 Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala  
                     290                    295                    300  
 Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly  
                     305                    310                    315                    320  
 Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala  
                     325                    330                    335  
 Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile  
                     340                    345                    350  
 Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu  
                     355                    360                    365  
 Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile  
                     370                    375                    380  
 Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala  
                     385                    390                    395                    400

acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc  
1027  
Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile  
295 300 305

gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc  
1075  
Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser  
310 315 320 325

ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag  
1123  
Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys  
330 335 340

gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct  
1171  
Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala  
345 350 355

cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa  
1219  
Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu  
360 365 370

gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca  
1267  
Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala  
375 380 385

gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa  
1315  
Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu  
390 395 400 405

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1330  
Phe Lys Glu Arg Gly  
410

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<213> Corynebacterium glutamicum

<400> 6  
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1 5 10 15

Gly Ser Val Gln Ala Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp  
20 25 30

Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro  
35 40 45

Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly  
50 55 60

Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly  
65 70 75 80

gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac	307
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp	
55 60 65	
atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga	355
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg	
70 75 80 85	
tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac	403
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn	
90 95 100	
ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg	451
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val	
105 110 115	
tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc	499
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly	
120 125 130	
gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga	547
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly	
135 140 145	
cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga	595
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Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile  
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cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259  
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Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly  
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Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly  
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His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg  
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Ala Leu Ala Asp Ala Gly Leu Gly Glu Gly Thr Ala Lys Val Cys Val			
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## SEQUENCE LISTING

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```

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modifications from the sequence set forth as odd-numbered SEQ ID NOs of the Sequence Listings.

38. A host cell comprising a nucleic acid molecule selected from the group consisting of  
5 the nucleic acid molecules set forth as odd-numbered SEQ ID NOs of the Sequence Listing, wherein the regulatory region of the nucleic acid molecule is modified relative to the wild-type regulatory region of the molecule.



31. The method of claim 25, wherein said fine chemical is selected from the group consisting of: organic acids, nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols,  
5 carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.
32. The method of claim 25, wherein said fine chemical is an amino acid.
33. The method of claim 32, wherein said amino acid is drawn from the group consisting  
10 of: lysine, glutamate, glutamine, alanine, aspartate, glycine, serine, threonine, methionine, cysteine, valine, leucine, isoleucine, arginine, proline, histidine, tyrosine, phenylalanine, and tryptophan.
34. A method for producing a fine chemical, comprising culturing a cell whose genomic  
15 DNA has been altered by the inclusion of a nucleic acid molecule of any one of claims 1-9.
35. A method for diagnosing the presence or activity of *Corynebacterium diphtheriae* in a subject, comprising detecting the presence of one or more of SEQ ID NOs 1  
20 through 1156 of the Sequence Listing in the subject, provided that the sequences are not or are not encoded by any of the F-designated sequences set forth in Table 1, thereby diagnosing the presence or activity of *Corynebacterium diphtheriae* in the subject.
- 25 36. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth as odd-numbered SEQ ID NOs of the Sequence Listing, wherein the nucleic acid molecule is disrupted.
- 30 37. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth as odd-numbered SEQ ID NOs in the Sequence Listing, wherein the nucleic acid molecule comprises one or more nucleic acid

24. An isolated polypeptide comprising an amino acid sequence which is at least 50% homologous to an amino acid sequence selected from the group consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing,  
5 provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.
25. A method for producing a fine chemical, comprising culturing a cell containing a vector of claim 12 such that the fine chemical is produced.  
10
26. The method of claim 25, wherein said method further comprises the step of recovering the fine chemical from said culture.
27. The method of claim 25, wherein said method further comprises the step of  
15 transfecting said cell with the vector of claim 11 to result in a cell containing said vector.
28. The method of claim 25, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium*.  
20
29. The method of claim 25, wherein said cell is selected from the group consisting of: *Corynebacterium glutamicum*, *Corynebacterium herculis*, *Corynebacterium lilium*, *Corynebacterium acetoacidophilum*, *Corynebacterium acetoglutamicum*, *Corynebacterium acetophilum*, *Corynebacterium ammoniagenes*, *Corynebacterium fujiokense*, *Corynebacterium nitrilophilus*, *Brevibacterium ammoniagenes*,  
25 *Brevibacterium butanicum*, *Brevibacterium divaricatum*, *Brevibacterium flavum*, *Brevibacterium healii*, *Brevibacterium ketoglutamicum*, *Brevibacterium ketosoreductum*, *Brevibacterium lactofermentum*, *Brevibacterium linens*, *Brevibacterium paraffinolyticum*, and those strains set forth in Table 3.
30. The method of claim 25, wherein expression of the nucleic acid molecule from said vector results in modulation of production of said fine chemical.  
30

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bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.

17. A method of producing a polypeptide comprising culturing the host cell of claim 12  
5 in an appropriate culture medium to, thereby, produce the polypeptide.

18. An isolated metabolic pathway polypeptide from *Corynebacterium glutamicum*, or a portion thereof.

10 19. The protein of claim 18, wherein said polypeptide is selected from the group of metabolic pathway proteins which participate in the metabolism of an amino acid, a vitamin, a cofactor, a nutraceutical, a nucleotide, a nucleoside, or trehalose.

20. An isolated polypeptide comprising an amino acid sequence selected from the group  
15 consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.

21. An isolated polypeptide comprising a naturally occurring allelic variant of a  
20 polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, or a portion thereof, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.

25 22. The isolated polypeptide of any of claims 18-21, further comprising heterologous amino acid sequences.

23. An isolated polypeptide which is encoded by a nucleic acid molecule comprising a  
nucleotide sequence which is at least 50% homologous to a nucleic acid selected  
30 from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, provided that the nucleic acid molecule does not consist of any of the F-designated nucleic acid molecules set forth in Table 1.

a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

7. An isolated nucleic acid molecule comprising a fragment of at least 15 nucleotides  
5 of a nucleic acid comprising a nucleotide sequence selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
- 10 8. An isolated nucleic acid molecule which hybridizes to the nucleic acid molecule of any one of claims 1-7 under stringent conditions.
9. An isolated nucleic acid molecule comprising the nucleic acid molecule of any one of claims 1-8 or a portion thereof and a nucleotide sequence encoding a heterologous  
15 polypeptide.
10. A vector comprising the nucleic acid molecule of any one of claims 1-9.
11. The vector of claim 10, which is an expression vector.
- 20 12. A host cell transfected with the expression vector of claim 11.
13. The host cell of claim 12, wherein said cell is a microorganism.
- 25 14. The host cell of claim 13, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium*.
15. The host cell of claim 12, wherein the expression of said nucleic acid molecule results in the modulation in production of a fine chemical from said cell.
- 30 16. The host cell of claim 15, wherein said fine chemical is selected from the group consisting of: organic acids, nonproteinogenic amino acids, purine and pyrimidine

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 55 60 65

gag tgg tac aaa gac gcc gtt ttc tac gaa gtg ctg gtt cgt gcc ttc 355  
 Glu Trp Tyr Lys Asp Ala Val Phe Tyr Glu Val Leu Val Arg Ala Phe  
 70 75 80 85

tac gat cca gaa ggc aac gga gtc gga tcg ttg aaa ggc ctg acc gaa 403  
 Tyr Asp Pro Glu Gly Asn Gly Val Gly Ser Leu Lys Gly Leu Thr Glu  
 90 95 100

aaa ctg gat tac atc cag tgg ctc ggc gtg gat tgc att tgg atc cca 451  
 Lys Leu Asp Tyr Ile Gln Trp Leu Gly Val Asp Cys Ile Trp Ile Pro  
 105 110 115

ccg ttt tat gat tcc cca ctg cgc gac ggc ggt tac gat atc cgc aac 499

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                180                185                190
atg agc aaa tat cct cag gca gtc tcg ctt gat ttg cgt gaa ttt gca 624
Met Ser Lys Tyr Pro Gln Ala Val Ser Leu Asp Leu Arg Glu Phe Ala
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gga cac acc cct cga gag atg tcg ggc ggg cag ctg ttc cct acc att 672
Gly His Thr Pro Arg Glu Met Ser Gly Gly Gln Leu Phe Pro Thr Ile
                210                215                220

gct gaa cgg gag tgg att gtc act tta gcc cct cac gga ttc ttc tgg 720
Ala Glu Arg Glu Trp Ile Val Thr Leu Ala Pro His Gly Phe Phe Trp
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ttt gat ctc acc gcc gat gaa aag gac gat atg gaa tgagcattgg 766
Phe Asp Leu Thr Ala Asp Glu Lys Asp Asp Met Glu
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ccaacacatc atc 779

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<213> Corynebacterium glutamicum

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Ser Glu Pro Arg Met Arg Ala Asn Val Gly Ile Arg Arg Arg Leu Ser
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Pro Leu Leu Glu Gly Asp Arg Asn Gln Leu Glu Leu Leu His Gly Leu
                50                55                60

Leu Leu Ser Leu Pro Gly Ser Pro Val Leu Tyr Tyr Gly Asp Glu Ile
                65                70                75                80

Gly Met Gly Asp Asn Ile Trp Leu His Asp Arg Asp Gly Val Arg Thr
                85                90                95

Pro Met Gln Trp Ser Asn Asp Arg Asn Gly Gly Phe Ser Lys Ala Asp
                100                105                110

Pro Glu Arg Leu Tyr Leu Pro Ala Ile Gln Asn Asp Gln Tyr Gly Tyr
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Ala Gln Val Asn Val Glu Ser Gln Leu Asn Arg Glu Asn Ser Leu Leu
                130                135                140

Arg Trp Leu Arg Asn Gln Ile Leu Ile Arg Lys Gln Tyr Arg Ala Phe
                145                150                155                160

Gly Ala Gly Thr Tyr Arg Glu Val Ser Ser Thr Asn Glu Ser Val Leu
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Thr Phe Leu Arg Glu His Lys Gly Gln Thr Ile Leu Cys Val Asn Asn

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Ser Gly

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 <223> RXA00873

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gaa atg gtc tcc gat gag gaa cgc agc tac atg tac tcc caa ttc gcc 96  
 Glu Met Val Ser Asp Glu Glu Arg Ser Tyr Met Tyr Ser Gln Phe Ala  
                   20                  25                  30

tcc gaa cct cgc atg cgc gcc aac gta gga atc cgc agg cgc ctt tcc 144  
 Ser Glu Pro Arg Met Arg Ala Asn Val Gly Ile Arg Arg Arg Leu Ser  
           35                  40                  45

cca ctg ctt gaa ggc gac cgc aac cag ctg gaa ctc ctt cac ggt ttg 192  
 Pro Leu Leu Glu Gly Asp Arg Asn Gln Leu Glu Leu Leu His Gly Leu  
   50                  55                  60

ttg ctg tct cta cct ggc tca ccc gtg ttg tat tac ggt gat gaa att 240  
 Leu Leu Ser Leu Pro Gly Ser Pro Val Leu Tyr Tyr Gly Asp Glu Ile  
 -65                  70                  75                  80

ggc atg ggc gac aat atc tgg ctc cac gac cgc gac gga gtg cgc acc 288  
 Gly Met Gly Asp Asn Ile Trp Leu His Asp Arg Asp Gly Val Arg Thr  
                   85                  90                  95

ccc atg cag tgg tcc aac gac cgc aac ggt ggt ttc tcc aaa gct gat 336  
 Pro Met Gln Trp Ser Asn Asp Arg Asn Gly Gly Phe Ser Lys Ala Asp  
           100                  105                  110

cct gaa cgc ctg tac ctt cca gcg atc caa aat gat caa tac ggc tac 384  
 Pro Glu Arg Leu Tyr Leu Pro Ala Ile Gln Asn Asp Gln Tyr Gly Tyr  
           115                  120                  125

gcc caa gta aac gtg gaa agc caa ctc aac cgc gaa aac tcc ctg ctg 432  
 Ala Gln Val Asn Val Glu Ser Gln Leu Asn Arg Glu Asn Ser Leu Leu  
   130                  135                  140

cgc tgg ctc cga aac caa atc ctt atc cgc aag cag tac cgc gca ttt 480  
 Arg Trp Leu Arg Asn Gln Ile Leu Ile Arg Lys Gln Tyr Arg Ala Phe  
 145                  150                  155                  160

ggt gcc gga acc tac cgt gaa gtg tcc tcc acc aat gag tca gtg ttg 528  
 Gly Ala Gly Thr Tyr Arg Glu Val Ser Ser Thr Asn Glu Ser Val Leu  
                   165                  170                  175

aca ttt tta cga gaa cac aag ggc caa acc att ttg tgt gtc aac aac 576  
 Thr Phe Leu Arg Glu His Lys Gly Gln Thr Ile Leu Cys Val Asn Asn

Phe Phe Leu His Ile Pro Phe Pro Ser Pro Asp Leu Phe Arg Gln Leu  
 165 170 175  
 Pro Trp Arg Glu Glu Ile Val Arg Gly Met Leu Gly Ala Asp Leu Val  
 180 185 190  
 Gly Phe His Leu Val Gln Asn Ala Glu Asn Phe Leu Ala Leu Thr Gln  
 195 200 205  
 Gln Val Ala Gly Thr Ala Gly Ser His Val Gly Gln Pro Asp Thr Leu  
 210 215 220  
 Gln Val Ser Gly Glu Ala Leu Val Arg Glu Ile Gly Ala His Val Glu  
 225 230 235 240  
 Thr Ala Asp Gly Arg Arg Val Ser Val Gly Ala Phe Pro Ile Ser Ile  
 245 250 255  
 Asp Val Glu Met Phe Gly Glu Ala Ser Lys Ser Ala Val Leu Asp Leu  
 260 265 270  
 Leu Lys Thr Leu Asp Glu Pro Glu Thr Val Phe Leu Gly Val Asp Arg  
 275 280 285  
 Leu Asp Tyr Thr Lys Gly Ile Leu Gln Arg Leu Leu Ala Phe Glu Glu  
 290 295 300  
 Leu Leu Glu Ser Gly Ala Leu Glu Ala Asp Lys Ala Val Leu Leu Gln  
 305 310 315 320  
 Val Ala Thr Pro Ser Arg Glu Arg Ile Asp His Tyr Arg Val Ser Arg  
 325 330 335  
 Ser Gln Val Glu Glu Ala Val Gly Arg Ile Asn Gly Arg Phe Gly Arg  
 340 345 350  
 Met Gly Arg Pro Val Val His Tyr Leu His Arg Ser Leu Ser Lys Asn  
 355 360 365  
 Asp Leu Gln Val Leu Tyr Thr Ala Ala Asp Val Met Leu Val Thr Pro  
 370 375 380  
 Phe Lys Asp Gly Met Asn Leu Val Ala Lys Glu Phe Val Ala Asn His  
 385 390 395 400  
 Arg Asp Gly Thr Gly Ala Leu Val Leu Ser Glu Phe Ala Gly Ala Ala  
 405 410 415  
 Thr Glu Leu Thr Gly Ala Tyr Leu Cys Asn Pro Phe Asp Val Glu Ser  
 420 425 430  
 Ile Lys Arg Gln Met Val Ala Ala Val His Asp Leu Lys His Asn Pro  
 435 440 445  
 Glu Ser Ala Ala Thr Arg Met Lys Thr Asn Ser Glu Gln Val Tyr Thr  
 450 455 460  
 His Asp Val Asn Val Trp Ala Asn Ser Phe Leu Asp Cys Leu Ala Gln  
 465 470 475 480



gct ttg gtg ctg tcc gaa ttt gcc ggc gcg gcc act gag ctg acc ggt  
1363

Ala Leu Val Leu Ser Glu Phe Ala Gly Ala Ala Thr Glu Leu Thr Gly  
410 415 420

gcg tat tta tgc aac cca ttt gat gtg gaa tcc atc aaa cgg caa atg  
1411

Ala Tyr Leu Cys Asn Pro Phe Asp Val Glu Ser Ile Lys Arg Gln Met  
425 430 435

gtg gca gct gtc cat gat ttg aag cac aat ccg gaa tct gcg gca acg  
1459

Val Ala Ala Val His Asp Leu Lys His Asn Pro Glu Ser Ala Ala Thr  
440 445 450

cga atg aaa acg aac agc gag cag gtc tat acc cac gac gtc aac gtg  
1507

Arg Met Lys Thr Asn Ser Glu Gln Val Tyr Thr His Asp Val Asn Val  
455 460 465

tgg gct aat agt ttc ctg gat tgt ttg gca cag tcg gga  
1546

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<212> PRT

<213> *Corynebacterium glutamicum*

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Gly Gly Leu Val Thr Gly Leu Ser Pro Val Leu Glu Gln His Arg Gly  
35 40 45

Cys Trp Val Gly Trp Pro Gly Thr Val Asp Val Ala Pro Glu Pro Phe  
50 55 60

Arg Thr Asp Thr Gly Val Leu Leu His Pro Val Val Leu Thr Ala Ser  
65 70 75 80

Asp Tyr Glu Gly Phe Tyr Glu Gly Phe Ser Asn Ala Thr Leu Trp Pro  
85 90 95

Leu Phe His Asp Leu Ile Val Thr Pro Val Tyr Asn Thr Asp Trp Trp  
100 105 110

His Ala Phe Arg Glu Val Asn Leu Lys Phe Ala Glu Ala Val Ser Gln  
115 120 125

Val Ala Ala His Gly Ala Thr Val Trp Val Gln Asp Tyr Gln Leu Leu  
130 135 140

Leu Val Pro Gly Ile Leu Arg Gln Met Arg Pro Asp Leu Lys Ile Gly  
145 150 155 160

caa aac gca gaa aac ttc ctt gcg tta acc cag cag gtt gcc ggc act 739  
 Gln Asn Ala Glu Asn Phe Leu Ala Leu Thr Gln Gln Val Ala Gly Thr  
 200 205 210

gcc ggg tct cat gtg ggt cag ccg gac acc ttg cag gtc agt ggt gaa 787  
 Ala Gly Ser His Val Gly Gln Pro Asp Thr Leu Gln Val Ser Gly Glu  
 215 220 225

gca ttg gtg cgt gag att ggc gct cat gtt gaa acc gct gac gga agg 835  
 Ala Leu Val Arg Glu Ile Gly Ala His Val Glu Thr Ala Asp Gly Arg  
 230 235 240 245

cga gtt agc gtc ggg gcg ttc ccg atc tcg att gat gtt gaa atg ttt 883  
 Arg Val Ser Val Gly Ala Phe Pro Ile Ser Ile Asp Val Glu Met Phe  
 250 255 260

ggg gag gcg tcg aaa agc gcc gtt ctt gat ctt tta aaa acg ctc gac 931  
 Gly Glu Ala Ser Lys Ser Ala Val Leu Asp Leu Leu Lys Thr Leu Asp  
 265 270 275

gag ccg gaa acc gta ttc ctg ggc gtt gac cga ctg gac tac acc aag 979  
 Glu Pro Glu Thr Val Phe Leu Gly Val Asp Arg Leu Asp Tyr Thr Lys  
 280 285 290

ggc att ttg cag cgc ctg ctt gcg ttt gag gaa ctg ctg gaa tcc ggc  
 1027  
 Gly Ile Leu Gln Arg Leu Leu Ala Phe Glu Glu Leu Leu Glu Ser Gly  
 295 300 305

gcg ttg gag gcc gac aaa gct gtg ttg ctg cag gtc gcg acg cct tcg  
 1075  
 Ala Leu Glu Ala Asp Lys Ala Val Leu Leu Gln Val Ala Thr Pro Ser  
 310 315 320 325

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 1123  
 Arg Glu Arg Ile Asp His Tyr Arg Val Ser Arg Ser Gln Val Glu Glu  
 330 335 340

gcc gtc ggc cgt atc aat ggt cgt ttc ggt cgc atg ggg cgt ccc gtg  
 1171  
 Ala Val Gly Arg Ile Asn Gly Arg Phe Gly Arg Met Gly Arg Pro Val  
 345 350 355

gtg cat tat cta cac agg tca ttg agc aaa aat gat ctc cag gtg ctg  
 1219  
 Val His Tyr Leu His Arg Ser Leu Ser Lys Asn Asp Leu Gln Val Leu  
 360 365 370

tat acc gca gcc gat gtc atg ctg gtt acg cct ttt aaa gac ggt atg  
 1267  
 Tyr Thr Ala Ala Asp Val Met Leu Val Thr Pro Phe Lys Asp Gly Met  
 375 380 385

aac ttg gtg gct aaa gaa ttc gtg gcc aac cac cgc gac ggc act ggt  
 1315  
 Asn Leu Val Ala Lys Glu Phe Val Ala Asn His Arg Asp Gly Thr Gly  
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&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1546)

&lt;223&gt; FRXA00351

&lt;400&gt; 19

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cgcaaagaag	accacaaaaga	agtcttaagc	cggatcttat	atg	gat	gāt	tcc	aat	115
				Met	Asp	Asp	Ser	Asn	
				1				5	

agc	ttt	gta	gtt	gtt	gct	aac	cgt	ctg	cca	gtg	gat	atg	act	gtc	cac	163
Ser	Phe	Val	Val	Val	Ala	Asn	Arg	Leu	Pro	Val	Asp	Met	Thr	Val	His	
			10					15						20		

cca	gat	ggt	agc	tat	agc	atc	tcc	ccc	agc	ccc	ggt	ggc	ctt	gtc	acg	211
Pro	Asp	Gly	Ser	Tyr	Ser	Ile	Ser	Pro	Ser	Pro	Gly	Gly	Leu	Val	Thr	
			25				30						35			

ggg	ctt	tcc	ccc	gtt	ctg	gaa	caa	cat	cgt	gga	tgt	tgg	gtc	gga	tgg	259
Gly	Leu	Ser	Pro	Val	Leu	Glu	Gln	His	Arg	Gly	Cys	Trp	Val	Gly	Trp	
		40				45						50				

cct	gga	act	gta	gat	gtt	gca	ccc	gaa	cca	ttt	cga	aca	gat	acg	ggg	307
Pro	Gly	Thr	Val	Asp	Val	Ala	Pro	Glu	Pro	Phe	Arg	Thr	Asp	Thr	Gly	
	55					60					65					

gtt	ttg	ctg	cac	cct	gtt	gtc	ctc	act	gca	agt	gac	tat	gaa	ggc	ttc	355
Val	Leu	Leu	His	Pro	Val	Val	Leu	Thr	Ala	Ser	Asp	Tyr	Glu	Gly	Phe	
70					75					80					85	

tac	gag	ggc	ttt	tca	aac	gca	acg	ctg	tgg	cct	ctt	ttc	cac	gat	ctg	403
Tyr	Glu	Gly	Phe	Ser	Asn	Ala	Thr	Leu	Trp	Pro	Leu	Phe	His	Asp	Leu	
				90					95					100		

att	gtt	act	ccg	gtg	tac	aac	acc	gat	tgg	tgg	cat	gcg	ttt	cgg	gag	451
Ile	Val	Thr	Pro	Val	Tyr	Asn	Thr	Asp	Trp	Trp	His	Ala	Phe	Arg	Glu	
			105					110					115			

gta	aac	ctc	aag	ttc	gct	gaa	gcc	gtg	agc	caa	gtg	gcg	gca	cac	ggg	499
Val	Asn	Leu	Lys	Phe	Ala	Glu	Ala	Val	Ser	Gln	Val	Ala	Ala	His	Gly	
		120					125				130					

gcc	act	gtg	tgg	gtg	cag	gac	tat	cag	ctg	ttg	ctg	gtt	cct	ggc	att	547
Ala	Thr	Val	Trp	Val	Gln	Asp	Tyr	Gln	Leu	Leu	Leu	Val	Pro	Gly	Ile	
	135				140						145					

ttg	cgc	cag	atg	cgc	cct	gat	ttg	aag	atc	ggg	ttc	ttc	ctc	cac	att	595
Leu	Arg	Gln	Met	Arg	Pro	Asp	Leu	Lys	Ile	Gly	Phe	Phe	Leu	His	Ile	
150					155					160					165	

ccc	ttc	cct	tcc	cct	gat	ctg	ttc	cgt	cag	ctg	ccg	tgg	cgt	gaa	gag	643
Pro	Phe	Pro	Ser	Pro	Asp	Leu	Phe	Arg	Gln	Leu	Pro	Trp	Arg	Glu	Glu	
				170				175						180		

att	gtt	cga	ggc	atg	ctg	ggc	gca	gat	ttg	gtg	gga	ttc	cat	ttg	gtt	691
Ile	Val	Arg	Gly	Met	Leu	Gly	Ala	Asp	Leu	Val	Gly	Phe	His	Leu	Val	
			185					190					195			

Gly Phe His Leu Val Gln Asn Ala Glu Asn Phe Leu Ala Leu Thr Gln  
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 Gln Val Ala Gly Thr Ala Gly Ser His Val Gly Gln Pro Asp Thr Leu  
 210 215 220  
 Gln Val Ser Gly Glu Ala Leu Val Arg Glu Ile Gly Ala His Val Glu  
 225 230 235 240  
 Thr Ala Asp Gly Arg Arg Val Ser Val Gly Ala Phe Pro Ile Ser Ile  
 245 250 255  
 Asp Val Glu Met Phe Gly Glu Ala Ser Lys Ser Ala Val Leu Asp Leu  
 260 265 270  
 Leu Lys Thr Leu Asp Glu Pro Glu Thr Val Phe Leu Gly Val Asp Arg  
 275 280 285  
 Leu Asp Tyr Thr Lys Gly Ile Leu Gln Arg Leu Leu Ala Phe Glu Glu  
 290 295 300  
 Leu Leu Glu Ser Gly Ala Leu Glu Ala Asp Lys Ala Val Leu Leu Gln  
 305 310 315 320  
 Val Ala Thr Pro Ser Arg Glu Arg Ile Asp His Tyr Arg Val Ser Arg  
 325 330 335  
 Ser Gln Val Glu Glu Ala Val Gly Arg Ile Asn Gly Arg Phe Gly Arg  
 340 345 350  
 Met Gly Arg Pro Val Val His Tyr Leu His Arg Ser Leu Ser Lys Asn  
 355 360 365  
 Asp Leu Gln Val Leu Tyr Thr Ala Ala Asp Val Met Leu Val Thr Pro  
 370 375 380  
 Phe Lys Asp Gly Met Asn Leu Val Ala Lys Glu Phe Val Ala Asn His  
 385 390 395 400  
 Arg Asp Gly Thr Gly Ala Leu Val Leu Ser Glu Phe Ala Gly Ala Ala  
 405 410 415  
 Thr Glu Leu Thr Gly Ala Tyr Leu Cys Asn Pro Phe Asp Val Glu Ser  
 420 425 430  
 Ile Lys Arg Gln Met Val Ala Ala Val His Asp Leu Lys His Asn Pro  
 435 440 445  
 Glu Ser Ala Ala Thr Arg Met Lys Thr Asn Ser Glu Gln Val Tyr Thr  
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 Ser Gly Glu Asn Ser  
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cga atg aaa acg aac agc gag cag gtc tat acc cac gac gtc aac gtg  
1507

Arg Met Lys Thr Asn Ser Glu Gln Val Tyr Thr His Asp Val Asn Val  
455 460 465

tggt gct aat agt ttc ctg gat tgt ttg gca cag tcg gga gaa aac tca  
1555

Trp Ala Asn Ser Phe Leu Asp Cys Leu Ala Gln Ser Gly Glu Asn Ser  
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tgaaccgcgc acgaatcgcg acc  
1578

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<211> 485

<212> PRT

<213> Corynebacterium glutamicum

<400> 18

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Gly Gly Leu Val Thr Gly Leu Ser Pro Val Leu Glu Gln His Arg Gly  
35 40 45

Cys Trp Val Gly Trp Pro Gly Thr Val Asp Val Ala Pro Glu Pro Phe  
50 55 60

Arg Thr Asp Thr Gly Val Leu Leu His Pro Val Val Leu Thr Ala Ser  
65 70 75 80

Asp Tyr Glu Gly Phe Tyr Glu Gly Phe Ser Asn Ala Thr Leu Trp Pro  
85 90 95

Leu Phe His Asp Leu Ile Val Thr Pro Val Tyr Asn Thr Asp Trp Trp  
100 105 110

His Ala Phe Arg Glu Val Asn Leu Lys Phe Ala Glu Ala Val Ser Gln  
115 120 125

Val Ala Ala His Gly Ala Thr Val Trp Val Gln Asp Tyr Gln Leu Leu  
130 135 140

Leu Val Pro Gly Ile Leu Arg Gln Met Arg Pro Asp Leu Lys Ile Gly  
145 150 155 160

Phe Phe Leu His Ile Pro Phe Pro Ser Pro Asp Leu Phe Arg Gln Leu  
165 170 175

Pro Trp Arg Glu Glu Ile Val Arg Gly Met Leu Gly Ala Asp Leu Val  
180 185 190

gca ttg gtg cgt gag att ggc gct cat gtt gaa acc gct gac gga agg 835  
 Ala Leu Val Arg Glu Ile Gly Ala His Val Glu Thr Ala Asp Gly Arg  
 230 235 240 245

cga gtt agc gtc ggg gcg ttc ccg atc tcg att gat gtt gaa atg ttt 883  
 Arg Val Ser Val Gly Ala Phe Pro Ile Ser Ile Asp Val Glu Met Phe  
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 265 270 275

gag ccg gaa acc gta ttc ctg ggc gtt gac cga ctg gac tac acc aag 979  
 Glu Pro Glu Thr Val Phe Leu Gly Val Asp Arg Leu Asp Tyr Thr Lys  
 280 285 290

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 1027  
 Gly Ile Leu Gln Arg Leu Leu Ala Phe Glu Glu Leu Leu Glu Ser Gly  
 295 300 305

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 1075  
 Ala Leu Glu Ala Asp Lys Ala Val Leu Leu Gln Val Ala Thr Pro Ser  
 310 315 320 325

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 1123  
 Arg Glu Arg Ile Asp His Tyr Arg Val Ser Arg Ser Gln Val Glu Glu  
 330 335 340

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 1171  
 Ala Val Gly Arg Ile Asn Gly Arg Phe Gly Arg Met Gly Arg Pro Val  
 345 350 355

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 1219  
 Val His Tyr Leu His Arg Ser Leu Ser Lys Asn Asp Leu Gln Val Leu  
 360 365 370

tat acc gca gcc gat gtc atg ctg gtt acg cct ttt aaa gac ggt atg  
 1267  
 Tyr Thr Ala Ala Asp Val Met Leu Val Thr Pro Phe Lys Asp Gly Met  
 375 380 385

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 1315  
 Asn Leu Val Ala Lys Glu Phe Val Ala Asn His Arg Asp Gly Thr Gly  
 390 395 400 405

gct ttg gtg ctg tcc gaa ttt gcc ggc gcg gcc act gag ctg acc ggt  
 1363  
 Ala Leu Val Leu Ser Glu Phe Ala Gly Ala Ala Thr Glu Leu Thr Gly  
 410 415 420

gcg tat tta tgc aac cca ttt gat gtg gaa tcc atc aaa cgg caa atg  
 1411  
 Ala Tyr Leu Cys Asn Pro Phe Asp Val Glu Ser Ile Lys Arg Gln Met  
 425 430 435

cgcaaagaag accacaaaga agtcttaagc cggatcttat	atg gat gat tcc aat	115
	Met Asp Asp Ser Asn	
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agc ttt gta gtt gtt gct aac cgt ctg cca gtg gat atg act gtc cac	163	
Ser Phe Val Val Val Ala Asn Arg Leu Pro Val Asp Met Thr Val His		
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cca gat ggt agc tat agc atc tcc ccc agc ccc ggt ggc ctt gtc acg	211	
Pro Asp Gly Ser Tyr Ser Ile Ser Pro Ser Pro Gly Gly Leu Val Thr		
	25 30 35	
ggg ctt tcc ccc gtt ctg gaa caa cat cgt gga tgt tgg gtc gga tgg	259	
Gly Leu Ser Pro Val Leu Glu Gln His Arg Gly Cys Trp Val Gly Trp		
	40 45 50	
cct gga act gta gat gtt gca ccc gaa cca ttt cga aca gat acg ggt	307	
Pro Gly Thr Val Asp Val Ala Pro Glu Pro Phe Arg Thr Asp Thr Gly		
	55 60 65	
gtt ttg ctg cac cct gtt gtc ctc act gca agt gac tat gaa ggc ttc	355	
Val Leu Leu His Pro Val Val Leu Thr Ala Ser Asp Tyr Glu Gly Phe		
	70 75 80 85	
tac gag ggc ttt tca aac gca acg ctg tgg cct ctt ttc cac gat ctg	403	
Tyr Glu Gly Phe Ser Asn Ala Thr Leu Trp Pro Leu Phe His Asp Leu		
	90 95 100	
att gtt act ccg gtg tac aac acc gat tgg tgg cat gcg ttt cgg gag	451	
Ile Val Thr Pro Val Tyr Asn Thr Asp Trp Trp His Ala Phe Arg Glu		
	105 110 115	
gta aac ctc aag ttc gct gaa gcc gtg agc caa gtg gcg gca cac ggt	499	
Val Asn Leu Lys Phe Ala Glu Ala Val Ser Gln Val Ala Ala His Gly		
	120 125 130	
gcc act gtg tgg gtg cag gac tat cag ctg ttg ctg gtt cct ggc att	547	
Ala Thr Val Trp Val Gln Asp Tyr Gln Leu Leu Leu Val Pro Gly Ile		
	135 140 145	
ttg cgc cag atg cgc cct gat ttg aag atc ggt ttc ttc ctc cac att	595	
Leu Arg Gln Met Arg Pro Asp Leu Lys Ile Gly Phe Phe Leu His Ile		
	150 155 160 165	
ccc ttc cct tcc cct gat ctg ttc cgt cag ctg ccg tgg cgt gaa gag	643	
Pro Phe Pro Ser Pro Asp Leu Phe Arg Gln Leu Pro Trp Arg Glu Glu		
	170 175 180	
att gtt cga ggc atg ctg ggc gca gat ttg gtg gga ttc cat ttg gtt	691	
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caa aac gca gaa aac ttc ctt gcg tta acc cag cag gtt gcc ggc act	739	
Gln Asn Ala Glu Asn Phe Leu Ala Leu Thr Gln Gln Val Ala Gly Thr		
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gcc ggg tct cat gtg ggt cag ccg gac acc ttg cag gtc agt ggt gaa	787	
Ala Gly Ser His Val Gly Gln Pro Asp Thr Leu Gln Val Ser Gly Glu		
	215 220 225	

Glu Tyr Pro Gly Phe Asn Arg Met Gln Phe Lys Trp Ser Glu Gly Gly  
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 Ala Glu Asp Phe Pro Lys Leu Ser Val Lys Val Arg Asp Glu Ile Val  
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 Ala Phe Gly Ala Pro Asp Glu Leu Lys Val Asp Glu Asn Gly Val Val  
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 130 135 140  
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 145 150 155 160  
 Thr His Asp Phe Ile Ala Glu Ile Glu Ser Gly Lys Tyr Asp Asp Leu  
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 Lys Asp Lys Pro Val Val Thr Tyr Cys Thr Gly Gly Ile Arg Cys Glu  
 180 185 190  
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 195 200 205  
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 210 215 220  
 Leu Trp Glu Gly Ser Leu Tyr Val Phe Asp Lys Arg Met His Met Glu  
 225 230 235 240  
 Phe Gly Glu Asp Tyr Lys Glu Val Gly His Cys Ile His Cys Asp Thr  
 245 250 255  
 Pro Thr Asn Lys Phe Glu His Cys Leu Asn Glu Asp Asp Cys Arg Glu  
 260 265 270  
 Leu Val Leu Met Cys Pro Asp Cys Phe Ala Asn Val Glu Thr Arg His  
 275 280 285  
 Cys Lys Arg Glu Arg Cys Ala Ala Ile Ala Ala Asp Phe Ala Glu Gln  
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 Gly Ile Asp Pro Leu Val Thr Ser  
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&lt;210&gt; 17

&lt;211&gt; 1578

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101) .. (1555)

&lt;223&gt; RXN00351

&lt;400&gt; 17

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 Ala Glu Ile Glu Ser Gly Lys Tyr Asp Asp Leu Lys Asp Lys Pro Val  
 170 175 180

gtc acc tac tgc acc ggc gga att cgt tgt gag atc ctg agt tca ctc 691  
 Val Thr Tyr Cys Thr Gly Gly Ile Arg Cys Glu Ile Leu Ser Ser Leu  
 185 190 195

atg atc aac cgt ggt ttc aaa gag gtc tac caa atc gat ggc ggc atc 739  
 Met Ile Asn Arg Gly Phe Lys Glu Val Tyr Gln Ile Asp Gly Gly Ile  
 200 205 210

gtt cgc tac ggc gag cag ttt ggc aac aag ggc ctg tgg gaa ggc tcc 787  
 Val Arg Tyr Gly Glu Gln Phe Gly Asn Lys Gly Leu Trp Glu Gly Ser  
 215 220 225

ctc tac gtt ttc gat aag cgc atg cat atg gaa ttc ggc gag gat tac 835  
 Leu Tyr Val Phe Asp Lys Arg Met His Met Glu Phe Gly Glu Asp Tyr  
 230 235 240 245

aaa gag gtc gga cac tgc atc cat tgc gat act ccc acc aac aaa ttt 883  
 Lys Glu Val Gly His Cys Ile His Cys Asp Thr Pro Thr Asn Lys Phe  
 250 255 260

gag cac tgc ctc aac gaa gat gat tgc cgc gag ctc gtg ttg atg tgc 931  
 Glu His Cys Leu Asn Glu Asp Asp Cys Arg Glu Leu Val Leu Met Cys  
 265 270 275

cct gat tgc ttc gcc aat gtt gag acc cgt cat tgc aag cgc gaa cgc 979  
 Pro Asp Cys Phe Ala Asn Val Glu Thr Arg His Cys Lys Arg Glu Arg  
 280 285 290

tgt gca gca att gct gcg gat ttc gct gag caa gga att gat ccg ctc  
 1027  
 Cys Ala Ala Ile Ala Ala Asp Phe Ala Glu Gln Gly Ile Asp Pro Leu  
 295 300 305

gtt act tct taaaaagggt atgggtggctg ggt  
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 Val Thr Ser  
 310

&lt;210&gt; 16

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 16

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Asn Leu Arg Gly Arg Ile Leu Ile Ser Thr His Gly Ile Asn Gly Thr  
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 Val Ala Thr Ser Lys  
 1 5  
 att ctt ctt tat tac gca ttc acc ccg ctc tct gac cct aaa gcg gtt 163  
 Ile Leu Leu Tyr Tyr Ala Phe Thr Pro Leu Ser Asp Pro Lys Ala Val  
 10 15 20  
 cag ctg tgg cag cgt gag ctc tgc gag tca ctg aat ctt cgt ggc cgc 211  
 Gln Leu Trp Gln Arg Glu Leu Cys Glu Ser Leu Asn Leu Arg Gly Arg  
 25 30 35  
 atc ctg atc tcc act cac ggc atc aat gga acc gtg ggc gga gat att 259  
 Ile Leu Ile Ser Thr His Gly Ile Asn Gly Thr Val Gly Gly Asp Ile  
 40 45 50  
 gat gat tgc aag gcg tac att aaa aag acc ccg gag tac cca ggt ttc 307  
 Asp Asp Cys Lys Ala Tyr Ile Lys Lys Thr Arg Glu Tyr Pro Gly Phe  
 55 60 65  
 aac cgc atg cag ttt aag tgg tcc gag ggt ggc gct gag gat ttc cca 355  
 Asn Arg Met Gln Phe Lys Trp Ser Glu Gly Gly Ala Glu Asp Phe Pro  
 70 75 80 85  
 aag ctc agt gtc aaa gtc cgc gat gag atc gtt gcc ttc ggc gct cca 403  
 Lys Leu Ser Val Lys Val Arg Asp Glu Ile Val Ala Phe Gly Ala Pro  
 90 95 100  
 gat gag ctc aaa gtg gat gaa aac ggc gtc gtc ggt ggc ggc gtt cac 451  
 Asp Glu Leu Lys Val Asp Glu Asn Gly Val Val Gly Gly Gly Val His  
 105 110 115  
 ctg aaa cca cag cag gtc aat gag ctt gtg gaa gcc cgt ggc gat gaa 499  
 Leu Lys Pro Gln Gln Val Asn Glu Leu Val Glu Ala Arg Gly Asp Glu  
 120 125 130  
 gtt gtg ttc ttt gac ggc cgc aac gca atg gaa gcc cag atc ggc aag 547  
 Val Val Phe Phe Asp Gly Arg Asn Ala Met Glu Ala Gln Ile Gly Lys  
 135 140 145  
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 Phe Lys Asp Ala Val Val Pro Asp Val Glu Thr Thr His Asp Phe Ile  
 150 155 160 165

<210> 14  
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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 14

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      35              40              45

Ala Glu Gly Met Val Pro Pro Gln Glu Leu Phe Asp Asp Leu Gln Ala
 50              55              60

Glu Ala Leu Glu Lys Ile Asn Glu Ala Arg Asp Ile Ala His Glu Val
 65              70              75              80

Ala Pro Glu Ile Lys Ile Gly His Thr Ile Ala Glu Gly Ser Pro Ile
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Asp Met Leu Leu Glu Met Ser Pro Asp Ala Thr Met Ile Val Met Gly
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Ser Arg Gly Leu Gly Gly Leu Ser Gly Met Val Met Gly Ser Val Ser
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Gly Ala Val Val Ser His Ala Lys Cys Pro Val Val Val Val Arg Glu
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Asp Ser Ala Val Asn Glu Asp Ser Lys Tyr Gly Pro Val Val Val Gly
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Val Asp Gly Ser Glu Val Ser Gln Gln Ala Thr Glu Tyr Ala Phe Ala
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Glu Ala Glu Ala Arg Gly Ala Glu Leu Val Ala Val His Thr Trp Met
      180              185              190

Asp Met Gln Val Gln Ala Ser Leu Ala Gly Leu Ala Ala Ala Gln Gln
      195              200              205

Gln Trp Asp Glu Val Glu Arg Gln Gln Thr Asp Met Leu Ile Glu Arg
      210              215              220

Leu Ala Pro Leu Val Glu Lys Tyr Pro Ser Val Thr Val Lys Lys Ile
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Ile Thr Arg Asp Arg Pro Val Arg Ala Leu Ala Glu Ala Ser Glu Asn
      245              250              255

Ala Gln Leu Leu Val Val Gly Ser His Gly Arg Gly Gly Phe Lys Gly
      260              265              270

Met Leu Leu Gly Ser Thr Ser Arg Ala Leu Leu Gln Ser Ala Pro Cys
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Ile Gly His Thr Ile Ala Glu Gly Ser Pro Ile Asp Met Leu Leu Glu
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atg tct ccc gat gcc aca atg atc gtc atg ggt tcc cgc gga ctc ggc 451
Met Ser Pro Asp Ala Thr Met Ile Val Met Gly Ser Arg Gly Leu Gly
105 110 115

gga ctc tcc gga atg gtc atg ggc tcc gtc tcc ggt gca gtg gtc agc 499
Gly Leu Ser Gly Met Val Met Gly Ser Val Ser Gly Ala Val Val Ser
120 125 130

cac gca aag tgt cca gtc gtt gtt gtc cgt gaa gac agc gca gtc aac 547
His Ala Lys Cys Pro Val Val Val Val Arg Glu Asp Ser Ala Val Asn
135 140 145

gaa gac agc aag tac ggc cca gtc gtc gtc ggt gtg gat ggc tcc gaa 595
Glu Asp Ser Lys Tyr Gly Pro Val Val Val Gly Val Asp Gly Ser Glu
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gtc tcc caa cag gca acc gaa tac gca ttt gcg gaa gct gaa gct cgt 643
Val Ser Gln Gln Ala Thr Glu Tyr Ala Phe Ala Glu Ala Glu Ala Arg
170 175 180

ggc gcc gaa ctc gtt gca gtt cac acc tgg atg gac atg cag gta cag 691
Gly Ala Glu Leu Val Ala Val His Thr Trp Met Asp Met Gln Val Gln
185 190 195

gca tca ctt gca ggt ctt gca gct gct caa cag cag tgg gat gaa gtg 739
Ala Ser Leu Ala Gly Leu Ala Ala Ala Gln Gln Gln Trp Asp Glu Val
200 205 210

gaa cgt cag caa acc gac atg ctg atc gaa cgc ctc gca cca ctg gtg 787
Glu Arg Gln Gln Thr Asp Met Leu Ile Glu Arg Leu Ala Pro Leu Val
215 220 225

gaa aag tac cca agt gta acc gtc aag aag atc atc acc cgt gac cgc 835
Glu Lys Tyr Pro Ser Val Thr Val Lys Lys Ile Ile Thr Arg Asp Arg
230 235 240 245

cca gtt cgc gca ctt gca gaa gca tct gaa aac gcg cag ctc cta gtc 883
Pro Val Arg Ala Leu Ala Glu Ala Ser Glu Asn Ala Gln Leu Leu Val
250 255 260

gtt ggt tcc cat ggt cgt ggc gga ttt aag ggc atg ctc ctt ggc tcc 931
Val Gly Ser His Gly Arg Gly Gly Phe Lys Gly Met Leu Leu Gly Ser
265 270 275

acc tcc cgc gca ctg ctg caa tcc gca ccg tgc cca atg atg gtg gtt 979
Thr Ser Arg Ala Leu Leu Gln Ser Ala Pro Cys Pro Met Met Val Val
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295 300

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				1				5									
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Ile	Val	Val	Val	Ala	Val	Asp	Gly	Ser	Asp	Ala	Ser	Lys	Gln	Ala	Val		
				10				15						20			
cgg	tgg	gct	gca	aat	acc	gcc	aac	aaa	cgt	ggc	att	cca	ctt	cgc	ttg		211
Arg	Trp	Ala	Ala	Asn	Thr	Ala	Asn	Lys	Arg	Gly	Ile	Pro	Leu	Arg	Leu		
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gct	tcc	agc	tac	acc	atg	cct	cag	ttc	ctc	tac	gca	gag	gga	atg	gtt		259
Ala	Ser	Ser	Tyr	Thr	Met	Pro	Gln	Phe	Leu	Tyr	Ala	Glu	Gly	Met	Val		
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cca	cca	caa	gag	ctt	ttc	gat	gac	ctc	cag	gcc	gaa	gcc	ctg	gaa	aag		307
Pro	Pro	Gln	Glu	Leu	Phe	Asp	Asp	Leu	Gln	Ala	Glu	Ala	Leu	Glu	Lys		
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 Val Pro Gln Ala Pro Ser Leu Pro Trp Asn Leu Gly Asp Thr Arg Gly  
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 Thr Val Met Leu Arg Met Pro Leu His Pro Val Ala Ile Glu Leu Leu  
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 Arg Gln Thr Gly Pro Met Ala Val Ser Ser Ala Asn Ile Ser Gly His  
 135 140 145  
 act cct cca acc acc gtg ctg gag gct cgt cag cag ctc aac caa aat 595  
 Thr Pro Pro Thr Thr Val Leu Glu Ala Arg Gln Gln Leu Asn Gln Asn  
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 gtc gct gtc tac ctc gat ggt ggc gaa tgc gcg ctg gcc acc cct tca 643  
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 Thr Ile Val Asp Ile Ser Gly Pro Ala Pro Lys Ile Leu Arg Glu Gly  
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&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 12

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 Leu Lys Ala Ala Val Asp Ala Val Lys Ala Gly Gln Leu Val Val Leu  
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 Pro Thr Asp Thr Leu Tyr Gly Leu Gly Cys Asp Ala Phe Asn Asn Glu  
 35 40 45  
 Ala Val Ala Asn Leu Leu Ala Thr Lys His Arg Gly Pro Asp Met Pro  
 50 55 60  
 Val Pro Val Leu Val Gly Ser Trp Asp Thr Ile Gln Gly Leu Val His  
 65 70 75 80

130	135	140
Gly Thr Leu Gly Leu Ser Asn Tyr Asn Asp Pro Gly Ala Asp Ser Asn		
145	150	155 160
Ala Val Lys Ile Glu Leu Gln Ala Asp Cys Tyr Ala Gly Ile Trp Ala		
	165	170 175
Asn His Ser Ser Glu Gly Pro Asp Pro Leu Leu Gln Pro Ile Thr Glu		
	180	185 190
Ser Glu Leu Asp Ser Ala Leu Leu Ala Ala Ser Ala Val Gly Asp Asp		
	195	200 205
Asn Ile Gln Gln Arg Ser Gly Gly Asp Val Asn Pro Glu Ser Trp Thr		
	210	215 220
His Gly Ser Ser Gln Gln Arg Lys Asp Ala Phe Leu Ala Gly Tyr Asn		
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Thr Gly Gln Met Ser Ala Cys Asp Phe Leu Gly Arg Gly Val Tyr Asn		
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 Val Ser Arg Ile Tyr  
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 Asp Cys Ala Asp Gln Asp Ser Arg Ala Ala Gly Leu Lys Ala Ala Val  
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gat gca gtc aaa gcc ggt cag ctc gtt gtc ctt ccc acg gat acc ctt 211  
 Asp Ala Val Lys Ala Gly Gln Leu Val Val Leu Pro Thr Asp Thr Leu  
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tat gga ctc ggc tgc gac gct ttc aac aac gag gca gta gcc aac ctt 259  
 Tyr Gly Leu Gly Cys Asp Ala Phe Asn Asn Glu Ala Val Ala Asn Leu  
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ctg gcc acc aaa cac cgt ggc ccc gat atg ccc gtt cca gtg ctc gtc 307  
 Leu Ala Thr Lys His Arg Gly Pro Asp Met Pro Val Pro Val Leu Val  
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Ser Asn Tyr Asn Asp Pro Gly Ala Asp Ser Asn Ala Val Lys Ile Glu  
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 Leu Gln Ala Asp Cys Tyr Ala Gly Ile Trp Ala Asn His Ser Ser Glu  
 170 175 180  
 ggc ccg gat ccg cta ctc caa ccc atc acc gaa tct gag cta gat tcc 691  
 Gly Pro Asp Pro Leu Leu Gln Pro Ile Thr Glu Ser Glu Leu Asp Ser  
 185 190 195  
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 Ser Gly Gly Asp Val Asn Pro Glu Ser Trp Thr His Gly Ser Ser Gln  
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 Gln Arg Lys Asp Ala Phe Leu Ala Gly Tyr Asn Thr Gly Gln Met Ser  
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 Asp His Cys Gln Thr Gly Ala Asp Ala Asn Ala Ser Asp Asp Cys Arg  
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 50 55 60  
 Pro Ala Gln Ala Gly Ile Glu Tyr Thr Glu Pro Thr Leu Thr Leu Phe  
 65 70 75 80  
 Lys Asn Ser Thr Gln Thr Gly Cys Gly Phe Ala Ser Ala Ser Thr Gly  
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 Pro Phe Tyr Cys Pro Ser Asp Gln Asp Ala Tyr Phe Asp Leu Thr Phe  
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 Phe Asp Gln Met Arg Gln Phe Gly Ala Glu Asn Ala Pro Leu Ala Gln  
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 Met Tyr Ile Val Ala His Glu Tyr Gly His His Val Gln Asn Leu Glu



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Val Gly Val Thr Leu Leu Tyr Glu Gly Leu Thr Gly Leu Leu Gly  
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 Leu Leu Leu Gly Gly  
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aac cct gcc gag atc gac cag gtt tta ggt ggc gat caa acc cag atc 163  
 Asn Pro Ala Glu Ile Asp Gln Val Leu Gly Gly Asp Gln Thr Gln Ile  
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ggc gca gat gcc aac gcc agt gat gat tgt cgc ctt tac tac acc tca 259  
 Gly Ala Asp Ala Asn Ala Ser Asp Asp Cys Arg Leu Tyr Tyr Thr Ser  
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 Ile Glu Tyr Thr Glu Pro Thr Leu Thr Leu Phe Lys Asn Ser Thr Gln  
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acc ggc tgc ggt ttc gct tct gcg tcc act ggg ccg ttt tac tgt ccg 403  
 Thr Gly Cys Gly Phe Ala Ser Ala Ser Thr Gly Pro Phe Tyr Cys Pro  
 90 95 100

tca gac caa gat gct tat ttt gac ttg act ttc ttc gat cag atg cgt 451  
 Ser Asp Gln Asp Ala Tyr Phe Asp Leu Thr Phe Phe Asp Gln Met Arg  
 105 110 115

cag ttc ggt gca gaa aac gcc ccg ctt gcc cag atg tac atc gtg gcg 499  
 Gln Phe Gly Ala Glu Asn Ala Pro Leu Ala Gln Met Tyr Ile Val Ala  
 120 125 130

cac gag tac ggc cac cac gtc caa aac ctc gag ggc aca ctc gga ctg 547  
 His Glu Tyr Gly His His Val Gln Asn Leu Glu Gly Thr Leu Gly Leu  
 135 140 145

tcc aat tac aac gat ccg ggc gct gat tcc aac gcc gtc aag atc gag 595

gcg att tta gtg cag acc ttt gtt acc ttc tct gct gtg tgc ctc att 643  
 Ala Ile Leu Val Gln Thr Phe Val Thr Phe Ser Ala Val Cys Leu Ile  
                   170                  175                  180

gtc tct acg gag cgt gtg cgc aaa gca atg ctg cgt gca ggt ccc tgg 691  
 Val Ser Thr Glu Arg Val Arg Lys Ala Met Leu Arg Ala Gly Pro Trp  
                   185                  190                  195

ttt gac ctg ctt gct ggc gtt gtc ttc ctc gtt gtg ggt gtg act ctg 739  
 Phe Asp Leu Leu Ala Gly Val Val Phe Leu Val Val Gly Val Thr Leu  
                   200                  205                  210

ctg tat gaa ggc ctg acc ggt tta ctc ggg taaaggcata aaaaatggct 789  
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tcc 792

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Arg Ser Arg Ala His Ala Ile Ala Gly Val Ala Gly Ile Val Thr Gly  
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Leu Thr Val Trp Val Thr Leu Thr Val Val Gly Ala Ala Ala Leu Leu  
                   50                  55                  60

Thr Thr Tyr Pro Ser Ile Leu Gly Ile Ile Gln Leu Val Gly Gly Thr  
                   65                  70                  75                  80

Tyr Leu Ser Phe Ile Gly Tyr Lys Leu Leu Arg Ser Ala Ser Arg Glu  
                   85                  90                  95

Leu Ile Asp Ala Arg Gln Phe Arg Phe Asn Ala Asp Ala Arg Pro Ile  
                   100                  105                  110

Pro Asp Ala Val Glu Ala Leu Gly Thr Arg Thr Gln Val Tyr Arg Gln  
                   115                  120                  125

Gly Leu Ala Thr Asn Leu Ser Asn Pro Lys Val Val Met Tyr Phe Ala  
                   130                  135                  140

Ala Ile Leu Ala Pro Leu Met Pro Ala His Pro Ser Pro Val Leu Ala  
                   145                  150                  155                  160

Phe Ser Ile Ile Val Ala Ile Leu Val Gln Thr Phe Val Thr Phe Ser  
                   165                  170                  175

Ala Val Cys Leu Ile Val Ser Thr Glu Arg Val Arg Lys Ala Met Leu  
                   180                  185                  190

tcg agg gtc atg ctt gct ggt cat atc gat aca gtg ccg atc gcg gac	355
Ser Arg Val Met Leu Ala Gly His Ile Asp Thr Val Pro Ile Ala Asp	
70 75 80 85	
aat ctg cca agc cgt gtg gaa gac ggc atc atg tat ggc tgt ggc acc	403
Asn Leu Pro Ser Arg Val Glu Asp Gly Ile Met Tyr Gly Cys Gly Thr	
90 95 100	
gtc gat atg aaa tct ggg ttg gcg gtg tat ttg cat act ttt gcc acc	451
Val Asp Met Lys Ser Gly Leu Ala Val Tyr Leu His Thr Phe Ala Thr	
105 110 115	
ttg gcc acg tcg act gag ctt aaa cat gat ctg acg ctg att gcg tat	499
Leu Ala Thr Ser Thr Glu Leu Lys His Asp Leu Thr Leu Ile Ala Tyr	
120 125 130	
gag tgc gag gaa gtt gct gat cac ctc aat ggt ttg ggc cac att cgc	547
Glu Cys Glu Glu Val Ala Asp His Leu Asn Gly Leu Gly His Ile Arg	
135 140 145	
gat gag cat ccg gag tgg ttg gcg gct gat ttg gcg ttg ttg ggt gag	595
Asp Glu His Pro Glu Trp Leu Ala Ala Asp Leu Ala Leu Leu Gly Glu	
150 155 160 165	
cct act ggc ggc tgg att gag gcg ggc tgc cag ggc aat ctg cgc atc	643
Pro Thr Gly Gly Trp Ile Glu Ala Gly Cys Gln Gly Asn Leu Arg Ile	
170 175 180	
aag gtg acg gcg cat ggt gtg cgt gcc cat tcg gcg aga agc tgg ttg	691
Lys Val Thr Ala His Gly Val Arg Ala His Ser Ala Arg Ser Trp Leu	
185 190 195	
ggt gat aat gcg atg cat aag ttg tcg ccg atc att tcg aag gtt gct	739
Gly Asp Asn Ala Met His Lys Leu Ser Pro Ile Ile Ser Lys Val Ala	
200 205 210	
gcg tat aag gcc gca gaa gtc aac att gat ggc ttg acc tac cgt gaa	787
Ala Tyr Lys Ala Ala Glu Val Asn Ile Asp Gly Leu Thr Tyr Arg Glu	
215 220 225	
ggc ctc aac atc gtt ttc tgc gaa tcg ggc gtg gca aac aac gtc att	835
Gly Leu Asn Ile Val Phe Cys Glu Ser Gly Val Ala Asn Asn Val Ile	
230 235 240 245	
cca gac ctc gcg tgg atg aac ctc aac ttc cgt ttc gcg ccg aat cgc	883
Pro Asp Leu Ala Trp Met Asn Leu Asn Phe Arg Phe Ala Pro Asn Arg	
250 255 260	
gat ctc aac gag gcg atc gag cat gtc gtc gaa acg ctt gag ctt gac	931
Asp Leu Asn Glu Ala Ile Glu His Val Val Glu Thr Leu Glu Leu Asp	
265 270 275	
ggt caa gac ggc atc gaa tgg gcc gta gaa gac ggg gca ggc ggt gcc	979
Gly Gln Asp Gly Ile Glu Trp Ala Val Glu Asp Gly Ala Gly Gly Ala	
280 285 290	
ctt cca ggc ttg ggg cag cag gtg aca agc ggg ctt atc gac gcc gtc	1027
Leu Pro Gly Leu Gly Gln Gln Val Thr Ser Gly Leu Ile Asp Ala Val	
295 300 305	

Lys Ile Val Thr Thr Thr Ile Asp Thr Asp Ala Ala Pro Thr Asp Thr  
 50 55 60  
 Tyr Asp Ala Trp Leu Arg Leu His Leu Leu Ser His Arg Val Phe Arg  
 65 70 75 80  
 Pro His Thr Ile Asn Leu Asp Gly Ile Phe Gly Leu Leu Asn Asn Val  
 85 90 95  
 Val Trp Thr Asn Phe Gly Pro Cys Ala Val Asp Gly Phe Ala Leu Thr  
 100 105 110  
 Arg Ala Arg Leu Ser Arg Arg Gly Gln Val Thr Val Tyr Ser Val Asp  
 115 120 125  
 Lys Phe Pro Arg Met Val Asp Tyr Val Val Pro Ser Gly Val Arg Ile  
 130 135 140  
 Gly Asp Ala Asp Arg Val Arg Leu Gly Ala Tyr Leu Ala Asp Gly Thr  
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 Ala Ser Met Val  
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 Val Asn Ser Glu Leu  
 1 5  
 aaa cca gga tta gat ctc ctc ggc gac cca att gtc ctt act caa cgt 163  
 Lys Pro Gly Leu Asp Leu Leu Gly Asp Pro Ile Val Leu Thr Gln Arg  
 10 15 20  
 ttg gta gat ata ccg agt ccg tcc ggt cag gaa aag cag att gct gat 211  
 Leu Val Asp Ile Pro Ser Pro Ser Gly Gln Glu Lys Gln Ile Ala Asp  
 25 30 35  
 gaa att gaa gat gcc ctt cgg aac ctt aat cta cct ggt gta gag gtc 259  
 Glu Ile Glu Asp Ala Leu Arg Asn Leu Asn Leu Pro Gly Val Glu Val  
 40 45 50  
 ttc cgc ttc aac aac aac gtt ctt gct cgc acg aac agg gga ttg gcc 307  
 Phe Arg Phe Asn Asn Asn Val Leu Ala Arg Thr Asn Arg Gly Leu Ala  
 55 60 65

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acc ggc gac gtc ctg gac gtg tgg tat cca gaa atc ggg tcc acc gac			158
Thr Gly Asp Val Leu Asp Val Trp Tyr Pro Glu Ile Gly Ser Thr Asp			
15	20	25	30
cag tcc gcg ctc aca cct cta gaa ggc gtc gat gaa gat cga aac gtc			206
Gln Ser Ala Leu Thr Pro Leu Glu Gly Val Asp Glu Asp Arg Asn Val			
35	40		45
acc cgc aaa atc gtg acg aca act atc gac acc gac gca gcc ccc acc			254
Thr Arg Lys Ile Val Thr Thr Thr Ile Asp Thr Asp Ala Ala Pro Thr			
50	55		60
gac acc tac gat gca tgg ctg cgc ctt cac ctc ctc tcc cac cgc gtt			302
Asp Thr Tyr Asp Ala Trp Leu Arg Leu His Leu Leu Ser His Arg Val			
65	70		75
ttc cgc cct cac acc atc aac cta gac ggc att ttc ggc ctc ctc aac			350
Phe Arg Pro His Thr Ile Asn Leu Asp Gly Ile Phe Gly Leu Leu Asn			
80	85		90
aat gtc gtg tgg acc aac ttc gga ccg tgc gca gtt gac ggt ttc gca			398
Asn Val Val Trp Thr Asn Phe Gly Pro Cys Ala Val Asp Gly Phe Ala			
95	100	105	110
ctc acc cgc gcg cgc ctg tca cgc cga ggc caa gtt acg gtt tat agc			446
Leu Thr Arg Ala Arg Leu Ser Arg Arg Gly Gln Val Thr Val Tyr Ser			
115	120		125
gtc gac aag ttc cca cgc atg gtc gac tat gtg gtt ccc tcg ggc gtg			494
Val Asp Lys Phe Pro Arg Met Val Asp Tyr Val Val Pro Ser Gly Val			
130	135		140
cgc atc ggt gac gcc gac cgc gtc cga ctt ggc gcg tac ctg gca gat			542
Arg Ile Gly Asp Ala Asp Arg Val Arg Leu Gly Ala Tyr Leu Ala Asp			
145	150		155
ggc acc acc gtg atg cat gag ggc ttc gtg aac ttc aac gct ggc acg			590
Gly Thr Thr Val Met His Glu Gly Phe Val Asn Phe Asn Ala Gly Thr			
160	165	170	
ctc ggc gct tcc atg gtt			608
Leu Gly Ala Ser Met Val			
175	180		

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&lt;211&gt; 180

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 30

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Asp Val Leu Asp Val Trp Tyr Pro Glu Ile Gly Ser Thr Asp Gln Ser			
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Ala Leu Thr Pro Leu Glu Gly Val Asp Glu Asp Arg Asn Val Thr Arg			
35	40		45

Val Asn Pro Ser Asp Lys Asp Ser Leu Val Lys Gly Ile Ile Ala Asn  
 115 120 125  
 Pro Asn Cys Thr Thr Met Ala Ala Met Pro Val Leu Lys Pro Leu His  
 130 135 140  
 Asp Ala Ala Gly Leu Val Lys Leu His Val Ser Ser Tyr Gln Ala Val  
 145 150 155 160  
 Ser Gly Ser Gly Leu Ala Gly Val Glu Thr Leu Ala Lys Gln Val Ala  
 165 170 175  
 Ala Val Gly Asp His Asn Val Glu Phe Val His Asp Gly Gln Ala Ala  
 180 185 190  
 Asp Ala Gly Asp Val Gly Pro Tyr Val Ser Pro Ile Ala Tyr Asn Val  
 195 200 205  
 Leu Pro Phe Ala Gly Asn Leu Val Asp Asp Gly Thr Phe Glu Thr Asp  
 210 215 220  
 Glu Glu Gln Lys Leu Arg Asn Glu Ser Arg Lys Ile Leu Gly Leu Pro  
 225 230 235 240  
 Asp Leu Lys Val Ser Gly Thr Cys Val Arg Val Pro Val Phe Thr Gly  
 245 250 255  
 His Thr Leu Thr Ile His Ala Glu Phe Asp Lys Ala Ile Thr Val Asp  
 260 265 270  
 Gln Ala Gln Glu Ile Leu Gly Ala Ala Ser Gly Val Lys Leu Val Asp  
 275 280 285  
 Val Pro Thr Pro Leu Ala Ala Ala Gly Ile Asp Glu Ser Leu Val Gly  
 290 295 300  
 Arg Ile Arg Gln Asp Ser Thr Val Asp Asp Asn Arg Gly Leu Val Leu  
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 Gln Ile Ala Glu Leu Leu Val Lys  
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 Met Thr Thr Ala Ser Ala Thr Gly Ile Ala Thr Leu Thr Ser

ggc acc tgc gtc cgc gtg ccg gtt ttc acc ggc cac acg ctg acc att 883  
 Gly Thr Cys Val Arg Val Pro Val Phe Thr Gly His Thr Leu Thr Ile  
 250 255 260  
  
 cac gcc gaa ttc gac aag gca atc acc gtg gac cag gcg cag gag atc 931  
 His Ala Glu Phe Asp Lys Ala Ile Thr Val Asp Gln Ala Gln Glu Ile  
 265 270 275  
  
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 Leu Gly Ala Ala Ser Gly Val Lys Leu Val Asp Val Pro Thr Pro Leu  
 280 285 290  
  
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 Ala Ala Ala Gly Ile Asp Glu Ser Leu Val Gly Arg Ile Arg Gln Asp  
 295 300 305  
  
 tcc act gtc gac gat aac cgc ggt ctg gtt ctc gtc gta tct ggc gac  
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 Ser Thr Val Asp Asp Asn Arg Gly Leu Val Leu Val Val Ser Gly Asp  
 310 315 320 325  
  
 aac ctc cgc aag ggt gct gcg cta aac acc atc cag atc gct gag ctg  
 1123  
 Asn Leu Arg Lys Gly Ala Ala Leu Asn Thr Ile Gln Ile Ala Glu Leu  
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 Leu Val Lys

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 Phe Phe Ala Ser Pro Arg Ser Ala Gly Arg Lys Ile Glu Phe Arg Gly  
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 Thr Glu Ile Glu Val Glu Asp Ile Thr Gln Ala Thr Glu Glu Ser Leu  
 50 55 60  
  
 Lys Asp Ile Asp Val Ala Leu Phe Ser Ala Gly Gly Thr Ala Ser Lys  
 65 70 75 80  
  
 Gln Tyr Ala Pro Leu Phe Ala Ala Ala Gly Ala Thr Val Val Asp Asn  
 85 90 95  
  
 Ser Ser Ala Trp Arg Lys Asp Asp Glu Val Pro Leu Ile Val Ser Glu  
 100 105 110

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Val	Val	Gly	Ala	Thr	Gly	Gln	Val	Gly	Gln	Val	Met	Arg	Thr	Leu	Leu					
				10					15					20						
gaa	gag	cgc	aat	ttc	cca	gct	gac	act	ggt	cgt	ttc	ttt	gct	tcc	cca	211				
Glu	Glu	Arg	Asn	Phe	Pro	Ala	Asp	Thr	Val	Arg	Phe	Phe	Ala	Ser	Pro					
				25					30					35						
cgt	tcc	gca	ggc	cgt	aag	att	gaa	ttc	cgt	ggc	acg	gaa	atc	gag	gta	259				
Arg	Ser	Ala	Gly	Arg	Lys	Ile	Glu	Phe	Arg	Gly	Thr	Glu	Ile	Glu	Val					
				40					45					50						
gaa	gac	att	act	cag	gca	acc	gag	gag	tcc	ctc	aag	gac	atc	gac	ggt	307				
Glu	Asp	Ile	Thr	Gln	Ala	Thr	Glu	Glu	Ser	Leu	Lys	Asp	Ile	Asp	Val					
				55					60					65						
gcg	ttg	ttc	tcc	gct	gga	ggc	acc	gct	tcc	aag	cag	tac	gct	cca	ctg	355				
Ala	Leu	Phe	Ser	Ala	Gly	Gly	Thr	Ala	Ser	Lys	Gln	Tyr	Ala	Pro	Leu					
				70					75					80						
ttc	gct	gct	gca	ggc	gcg	act	ggt	gtg	gat	aac	tct	tct	gct	tgg	cgc	403				
Phe	Ala	Ala	Ala	Gly	Ala	Thr	Val	Val	Asp	Asn	Ser	Ser	Ala	Trp	Arg					
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aag	gac	gac	gag	ggt	cca	cta	atc	gtc	tct	gag	gtg	aac	cct	tcc	gac	451				
Lys	Asp	Asp	Glu	Val	Pro	Leu	Ile	Val	Ser	Glu	Val	Asn	Pro	Ser	Asp					
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aag	gat	tcc	ctg	gtc	aag	ggc	att	att	gcg	aac	cct	aac	tgc	acc	acc	499				
Lys	Asp	Ser	Leu	Val	Lys	Gly	Ile	Ile	Ala	Asn	Pro	Asn	Cys	Thr	Thr					
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atg	gct	gcg	atg	cca	gtg	ctg	aag	cca	ctt	cac	gat	gcc	gct	ggt	ctt	547				
Met	Ala	Ala	Met	Pro	Val	Leu	Lys	Pro	Leu	His	Asp	Ala	Ala	Gly	Leu					
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gta	aag	ctt	cac	ggt	tcc	tct	tac	cag	gct	ggt	tcc	ggt	tct	ggt	ctt	595				
Val	Lys	Leu	His	Val	Ser	Ser	Tyr	Gln	Ala	Val	Ser	Gly	Ser	Gly	Leu					
				150					155					160						
gca	ggt	gtg	gaa	acc	ttg	gca	aag	cag	ggt	gct	gca	ggt	gga	gac	cac	643				
Ala	Gly	Val	Glu	Thr	Leu	Ala	Lys	Gln	Val	Ala	Ala	Val	Gly	Asp	His					
				170					175					180						
aac	ggt	gag	ttc	gtc	cat	gat	gga	cag	gct	gct	gac	gca	ggc	gat	gtc	691				
Asn	Val	Glu	Phe	Val	His	Asp	Gly	Gln	Ala	Ala	Asp	Ala	Gly	Asp	Val					
				185					190					195						
gga	cct	tat	ggt	tca	cca	atc	gct	tac	aac	gtg	ctg	cca	ttc	gcc	gga	739				
Gly	Pro	Tyr	Val	Ser	Pro	Ile	Ala	Tyr	Asn	Val	Leu	Pro	Phe	Ala	Gly					
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aac	ctc	gtc	gat	gac	ggc	acc	ttc	gaa	acc	gat	gaa	gag	cag	aag	ctg	787				
Asn	Leu	Val	Asp	Asp	Gly	Thr	Phe	Glu	Thr	Asp	Glu	Glu	Gln	Lys	Leu					
				215					220					225						
cgc	aac	gaa	tcc	cgc	aag	att	ctc	ggt	ctc	cca	gac	ctc	aag	gtc	tca	835				
Arg	Asn	Glu	Ser	Arg	Lys	Ile	Leu	Gly	Leu	Pro	Asp	Leu	Lys	Val	Ser					
				230					235					240						



Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly  
 195 200 205  
 Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn  
 210 215 220  
 Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu  
 225 230 235 240  
 Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr  
 245 250 255  
 Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile  
 260 265 270  
 Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp  
 275 280 285  
 Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu  
 290 295 300  
 Asp Gly Thr Thr Asp Ile Thr Phe Thr Cys Pro Arg Ser Asp Gly Arg  
 305 310 315 320  
 Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr  
 325 330 335  
 Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala  
 340 345 350  
 Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu  
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 370 375 380  
 Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala  
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 Met Thr Thr Ile Ala

aac atc gaa ttg att tcc acc tct gag att cgt att tcc gtg ctg atc  
1267

Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg Ile Ser Val Leu Ile  
375 380 385

cgt gaa gat gat ctg gat gct gct gca cgt gca ttg cat gag cag ttc  
1315

Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala Leu His Glu Gln Phe  
390 395 400 405

cag ctg ggc ggc gaa gac gaa gcc gtc gtt tat gca ggc acc gga cgc  
1363

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1386

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35 40 45

Glu Leu Leu Glu Leu Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg  
50 55 60

Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu  
65 70 75 80

Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr  
85 90 95

Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg  
100 105 110

Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly  
115 120 125

Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg  
130 135 140

Asp Val Thr Thr Leu Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala  
145 150 155 160

Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val  
165 170 175

Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys  
180 185 190

Gly	Arg	Gly	Gly	Ser	Asp	Thr	Thr	Ala	Val	Ala	Leu	Ala	Ala	Ala	Leu	
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Asn	Ala	Asp	Val	Cys	Glu	Ile	Tyr	Ser	Asp	Val	Asp	Gly	Val	Tyr	Thr	
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gct	gac	ccg	cgc	atc	gtt	cct	aat	gca	cag	aag	ctg	gaa	aag	ctc	agc	691
Ala	Asp	Pro	Arg	Ile	Val	Pro	Asn	Ala	Gln	Lys	Leu	Glu	Lys	Leu	Ser	
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ttc	gaa	gaa	atg	ctg	gaa	ctt	gct	gct	gtt	ggc	tcc	aag	att	ttg	gtg	739
Phe	Glu	Glu	Met	Leu	Glu	Leu	Ala	Ala	Val	Gly	Ser	Lys	Ile	Leu	Val	
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ctg	cgc	agt	gtt	gaa	tac	gct	cgt	gca	ttc	aat	gtg	cca	ctt	cgc	gta	787
Leu	Arg	Ser	Val	Glu	Tyr	Ala	Arg	Ala	Phe	Asn	Val	Pro	Leu	Arg	Val	
	215					220					225					
cgc	tcg	tct	tat	agt	aat	gat	ccc	ggc	act	ttg	att	gcc	ggc	tct	atg	835
Arg	Ser	Ser	Tyr	Ser	Asn	Asp	Pro	Gly	Thr	Leu	Ile	Ala	Gly	Ser	Met	
230					235					240					245	
gag	gat	att	cct	gtg	gaa	gaa	gca	gtc	ctt	acc	ggg	gtc	gca	acc	gac	883
Glu	Asp	Ile	Pro	Val	Glu	Glu	Ala	Val	Leu	Thr	Gly	Val	Ala	Thr	Asp	
				250				255						260		
aag	tcc	gaa	gcc	aaa	gta	acc	gtt	ctg	ggg	att	tcc	gat	aag	cca	ggc	931
Lys	Ser	Glu	Ala	Lys	Val	Thr	Val	Leu	Gly	Ile	Ser	Asp	Lys	Pro	Gly	
			265					270					275			
gag	gct	gcg	aag	gtt	ttc	cgt	gcg	ttg	gct	gat	gca	gaa	atc	aac	att	979
Glu	Ala	Ala	Lys	Val	Phe	Arg	Ala	Leu	Ala	Asp	Ala	Glu	Ile	Asn	Ile	
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gac	atg	gtt	ctg	cag	aac	gtc	tct	tct	gta	gaa	gac	ggc	acc	acc	gac	
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atc	acc	ttc	acc	tgc	cct	cgt	tcc	gac	ggc	cgc	cgc	gcg	atg	gag	atc	
1075																
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1123																
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gac	cag	gtc	ggc	aaa	gtc	tcc	ctc	gtg	ggg	gct	ggc	atg	aag	tct	cac	
1171																
Asp	Gln	Val	Gly	Lys	Val	Ser	Leu	Val	Gly	Ala	Gly	Met	Lys	Ser	His	
			345					350					355			
cca	ggg	gtt	acc	gca	gag	ttc	atg	gaa	gct	ctg	cgc	gat	gtc	aac	gtg	
1219																
Pro	Gly	Val	Thr	Ala	Glu	Phe	Met	Glu	Ala	Leu	Arg	Asp	Val	Asn	Val	
		360					365					370				

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 Val Ala Leu Val Val  
 1 5  
 cag aaa tat ggc ggt tcc tcg ctt gag agt gcg gaa cgc att aga aac 163  
 Gln Lys Tyr Gly Gly Ser Ser Leu Glu Ser Ala Glu Arg Ile Arg Asn  
 10 15 20  
 gtc gct gaa cgg atc gtt gcc acc aag aag gct gga aat gat gtc gtg 211  
 Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala Gly Asn Asp Val Val  
 25 30 35  
 gtt gtc tgc tcc gca atg gga gac acc acg gat gaa ctt cta gaa ctt 259  
 Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp Glu Leu Leu Glu Leu  
 40 45 50  
 gca gcg gca gtg aat ccc gtt ccg cca gct cgt gaa atg gat atg ctc 307  
 Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg Glu Met Asp Met Leu  
 55 60 65  
 ctg act gct ggt gag cgt att tct aac gct ctc gtc gcc atg gct att 355  
 Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu Val Ala Met Ala Ile  
 70 75 80 85  
 gag tcc ctt ggc gca gaa gcc caa tct ttc acg ggc tct cag gct ggt 403  
 Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr Gly Ser Gln Ala Gly  
 90 95 100  
 gtg ctc acc acc gag cgc cac gga aac gca cgc att gtt gat gtc act 451  
 Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg Ile Val Asp Val Thr  
 105 110 115  
 cca ggt cgt gtg cgt gaa gca ctc gat gag ggc aag atc tgc att gtt 499  
 Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly Lys Ile Cys Ile Val  
 120 125 130  
 gct ggt ttc cag ggt gtt aat aaa gaa acc cgc gat gtc acc acg ttg 547  
 Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg Asp Val Thr Thr Leu  
 135 140 145  
 ggt cgt ggt ggt tct gac acc act gca gtt gcg ttg gca gct gct ttg 595

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 24

Val Leu Gln Thr Ser Trp His Phe Ser Ile Leu Ala Gly Met Thr Asp  
 1 5 10 15  
 Thr Ser Pro Leu Asn Ser Gln Pro Ser Ala Asp His His Pro Asp His  
 20 25 30  
 Ala Ala Arg Pro Val Leu Asp Ala His Gly Leu Ile Val Glu His Glu  
 35 40 45  
 Ser Glu Glu Phe Pro Val Pro Ala Pro Ala Pro Gly Glu Gln Pro Trp  
 50 55 60  
 Glu Lys Lys Asn Arg Glu Trp Tyr Lys Asp Ala Val Phe Tyr Glu Val  
 65 70 75 80  
 Leu Val Arg Ala Phe Tyr Asp Pro Glu Gly Asn Gly Val Gly Ser Leu  
 85 90 95  
 Lys Gly Leu Thr Glu Lys Leu Asp Tyr Ile Gln Trp Leu Gly Val Asp  
 100 105 110  
 Cys Ile Trp Ile Pro Pro Phe Tyr Asp Ser Pro Leu Arg Asp Gly Gly  
 115 120 125  
 Tyr Asp Ile Arg Asn Phe Arg Glu Ile Leu Pro Glu Phe Gly Thr Val  
 130 135 140  
 Asp Asp Phe Val Glu Leu Val Asp His Ala His Arg Arg Gly Leu Arg  
 145 150 155 160  
 Val Ile Thr Asp Leu Val Met Asn His Thr Ser Asp Gln His Ala Trp  
 165 170 175  
 Phe Gln Glu Ser Arg Arg Asp Pro Thr Gly Pro Tyr Gly Asp Phe Tyr  
 180 185 190  
 Val Trp Ser Asp Asp Pro Thr Leu Tyr Asn Glu Ala Arg Ile Ile Phe  
 195 200 205  
 Val Asp Thr Glu Glu Ser Asn Trp Thr Tyr Asp Pro Val Arg Gly Gln  
 210 215 220  
 Tyr Phe Trp His Arg Phe Phe Ser His Gln Pro Asp Leu Asn Tyr Asp  
 225 230 235 240  
 Asn Pro Ala Val Gln Glu Ala Met Leu Asp Val Leu Arg Phe Trp Leu  
 245 250 255  
 Asp Leu Gly Leu Asp Gly Phe Arg Leu Asp Ala Val Pro Tyr Leu Phe  
 260 265 270  
 Glu Arg Glu Gly Thr Asn Gly Glu Asn Leu Lys Glu Thr His Asp Phe  
 275 280 285  
 Leu Lys Leu Cys Arg Ser Val Ile Glu Lys Glu Tyr Pro Gly Arg Ile  
 290 295 300

Pro Phe Tyr Asp Ser Pro Leu Arg Asp Gly Gly Tyr Asp Ile Arg Asn  
 120 125 130  
 ttc cgt gaa atc ctg ccc gaa ttc ggc acc gtc gat gac ttc gtg gaa 547  
 Phe Arg Glu Ile Leu Pro Glu Phe Gly Thr Val Asp Asp Phe Val Glu  
 135 140 145  
 ctc gtt gac cac gcc cac cgc cgt ggc ctg cgt gtt atc acc gac ttg 595  
 Leu Val Asp His Ala His Arg Arg Gly Leu Arg Val Ile Thr Asp Leu  
 150 155 160 165  
 gtc atg aat cac acc tcc gac cag cac gca tgg ttc caa gaa tcc cgg 643  
 Val Met Asn His Thr Ser Asp Gln His Ala Trp Phe Gln Glu Ser Arg  
 170 175 180  
 cgc gac cca acc ggc ccc tac gga gat ttc tat gtg tgg agc gat gat 691  
 Arg Asp Pro Thr Gly Pro Tyr Gly Asp Phe Tyr Val Trp Ser Asp Asp  
 185 190 195  
 ccc acc ctg tac aac gaa gcc cgc atc atc ttt gta gat aca gaa gaa 739  
 Pro Thr Leu Tyr Asn Glu Ala Arg Ile Ile Phe Val Asp Thr Glu Glu  
 200 205 210  
 tcc aac tgg acc tat gat ccg gtg cgt ggc cag tac ttc tgg cac cgc 787  
 Ser Asn Trp Thr Tyr Asp Pro Val Arg Gly Gln Tyr Phe Trp His Arg  
 215 220 225  
 ttc ttc tcc cac caa cca gac ctc aac tac gac aac ccc gca gtc caa 835  
 Phe Phe Ser His Gln Pro Asp Leu Asn Tyr Asp Asn Pro Ala Val Gln  
 230 235 240 245  
 gag gcc atg cta gat gtc ttg cgt ttc tgg ctg gac ctg gga ctt gat 883  
 Glu Ala Met Leu Asp Val Leu Arg Phe Trp Leu Asp Leu Gly Leu Asp  
 250 255 260  
 ggt ttc cga cta gat gcc gtt cct tat ctt ttt gaa cgc gaa ggc acc 931  
 Gly Phe Arg Leu Asp Ala Val Pro Tyr Leu Phe Glu Arg Glu Gly Thr  
 265 270 275  
 aac ggc gaa aac ctc aaa gaa acc cac gat ttc ctc aaa ctg tgt cgc 979  
 Asn Gly Glu Asn Leu Lys Glu Thr His Asp Phe Leu Lys Leu Cys Arg  
 280 285 290  
 tct gtc att gag aag gaa tac ccc ggc cga atc ctg ctc gca gaa gcc  
 1027  
 Ser Val Ile Glu Lys Glu Tyr Pro Gly Arg Ile Leu Leu Ala Glu Ala  
 295 300 305  
 aac caa tgg ccc caa gat gtg gtc gaa tac ttc ggt gaa aaa gac aaa  
 1075  
 Asn Gln Trp Pro Gln Asp Val Val Glu Tyr Phe Gly Glu Lys Asp Lys  
 310 315 320 325  
 ggc gat gaa tgc cac atg gcc ttc cac  
 1102  
 Gly Asp Glu Cys His Met Ala Phe His  
 330

&lt;210&gt; 24

&lt;211&gt; 334

ggt aat gac aca ttg tcg cga tca tta cat gac ata atc ccg aag tgg 739  
 Gly Asn Asp Thr Leu Ser Arg Ser Leu His Asp Ile Ile Pro Lys Trp  
 200 205 210

gct cgt cga gtt atc cgc gac gcg agc acg tat ccc gat agg gta cat 787  
 Ala Arg Arg Val Ile Arg Asp Ala Ser Thr Tyr Pro Asp Arg Val His  
 215 220 225

ggt act cca ccg ctt ccg gca cgg ttg gaa ccc tgg gcg gaa aag ctc 835  
 Gly Thr Pro Pro Leu Pro Ala Arg Leu Glu Pro Trp Ala Glu Lys Leu  
 230 235 240 245

act tca gat ccg gcc aca tgc cgc cac ctg att gaa gaa ttc ggg agt 883  
 Thr Ser Asp Pro Ala Thr Cys Arg His Leu Ile Glu Glu Phe Gly Ser  
 250 255 260

cct gtg aat gta ctc cat tca ggt tct atg cct cgt aat ata aat gag 931  
 Pro Val Asn Val Leu His Ser Gly Ser Met Pro Arg Asn Ile Asn Glu  
 265 270 275

ttg gtt gac gcc ggc att cag atg ggg gtg gat act cga ata ttt ttt 979  
 Leu Val Asp Ala Gly Ile Gln Met Gly Val Asp Thr Arg Ile Phe Phe  
 280 285 290

gcc cgc aaa gcg aat aag ggt ctt acc ttc gtt gat gcc gtt aaa gac  
 1027  
 Ala Arg Lys Ala Asn Lys Gly Leu Thr Phe Val Asp Ala Val Lys Asp  
 295 300 305

acc ggt cat ggt gta gat gta gcc agt gaa cga gag tta tct cag gtg  
 1075  
 Thr Gly His Gly Val Asp Val Ala Ser Glu Arg Glu Leu Ser Gln Val  
 310 315 320 325

ctt aat cgt gga gtc cca gga gag cgg atc att cta tcc gca gct atc  
 1123  
 Leu Asn Arg Gly Val Pro Gly Glu Arg Ile Ile Leu Ser Ala Ala Ile  
 330 335 340

aaa ccg gac aga cta ttg gca tta gcg atc gaa aat ggc gtg atc atc  
 1171  
 Lys Pro Asp Arg Leu Leu Ala Leu Ala Ile Glu Asn Gly Val Ile Ile  
 345 350 355

tct gtg gat tcg cgt gat gaa tta gat cgc att tcg gct ttg gtt ggt  
 1219  
 Ser Val Asp Ser Arg Asp Glu Leu Asp Arg Ile Ser Ala Leu Val Gly  
 360 365 370

gac cgc gtt gca cga gtt gcg cct aga gta gct cca gat cct gca gtc  
 1267  
 Asp Arg Val Ala Arg Val Ala Pro Arg Val Ala Pro Asp Pro Ala Val  
 375 380 385

tta cct cca act aga ttt ggt gag cgt gct gca gac tgg ggt aat cgg  
 1315  
 Leu Pro Pro Thr Arg Phe Gly Glu Arg Ala Ala Asp Trp Gly Asn Arg  
 390 395 400 405

ctt acc gag gtg ata ccc ggc gtg gat att gtg ggt ctt cac gtt cac  
 1363

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(2098)

&lt;223&gt; RXA02653

&lt;400&gt; 47

agacagagtg ttagtgctg gggcagctct cactttcacc gacatcactc gagtatgctc 60

accggccgta ttcattccaa taaccgcac agggaaacta atg ata ccg aag ccc 115  
 Met Ile Pro Lys Pro  
 1 5

gac gtg acc gac tta tat tta gag gac ctc tta aat gag ggt tcg gaa 163  
 Asp Val Thr Asp Leu Tyr Leu Glu Asp Leu Leu Asn Glu Gly Ser Glu  
 10 15 20

aag att cgg tcc gcc aag gat ctt tcc gaa ctt agg aca gtt cta aaa 211  
 Lys Ile Arg Ser Ala Lys Asp Leu Ser Glu Leu Arg Thr Val Leu Lys  
 25 30 35

gag gtt tcc tcc caa att cag gaa cga gct ggg aaa aaa gat gaa gaa 259  
 Glu Val Ser Ser Gln Ile Gln Glu Arg Ala Gly Lys Lys Asp Glu Glu  
 40 45 50

tgg gga atg ggg gcc act tgg cgg gag ctg tac ccc agc atc gtg gaa 307  
 Trp Gly Met Gly Ala Thr Trp Arg Glu Leu Tyr Pro Ser Ile Val Glu  
 55 60 65

cgc gct tcc tac gaa ggg cgt gac agc cta atc gga ttt gat cac tta 355  
 Arg Ala Ser Tyr Glu Gly Arg Asp Ser Leu Ile Gly Phe Asp His Leu  
 70 75 80 85

gcc cgg gaa atg gaa aga tta gcc ttc ggc cca cca tcc gaa agt ttt 403  
 Ala Arg Glu Met Glu Arg Leu Ala Phe Gly Pro Pro Ser Glu Ser Phe  
 90 95 100

gaa tac ctc caa gaa ctc gta aaa tcc gga gtg gta gac atc act cac 451  
 Glu Tyr Leu Gln Glu Leu Val Lys Ser Gly Val Val Asp Ile Thr His  
 105 110 115

ctg cat cgt ggc cgg gaa cca ctg aca gat tta gtt cgt gaa ctt gaa 499  
 Leu His Arg Gly Arg Glu Pro Leu Thr Asp Leu Val Arg Glu Leu Glu  
 120 125 130

ata act gtg gtg ata gac gct gtt ctt ccc ccg ccg gga gta gtg cca 547  
 Ile Thr Val Val Ile Asp Ala Val Leu Pro Pro Pro Gly Val Val Pro  
 135 140 145

ggc aca ttg gtg cac aat ttg gta aaa gag gga tat gcc aga atg cgt 595  
 Gly Thr Leu Val His Asn Leu Val Lys Glu Gly Tyr Ala Arg Met Arg  
 150 155 160 165

cct ggg act cgg ggg tta gat gta gcg gct gac ggc acc gtt caa ggg 643  
 Pro Gly Thr Arg Gly Leu Asp Val Ala Ala Asp Gly Thr Val Gln Gly  
 170 175 180

caa cga cat ttg gct gca gtc gga cgg atg acg gaa gat gtg gtt ttg 691  
 Gln Arg His Leu Ala Ala Val Gly Arg Met Thr Glu Asp Val Val Leu  
 185 190 195



				165					170					175			
Ile	Arg	Val	Lys 180	Pro	Gly	Ile	Glu	Ala 185	His	Thr	His	Glu	Phe 190	Ile	Ala		
Thr	Ser	His 195	Glu	Asp	Gln	Lys	Phe 200	Gly	Phe	Ser	Leu	Ala 205	Ser	Gly	Ser		
Ala	Phe 210	Glu	Ala	Ala	Lys 215	Ala	Ala	Asn	Asn	Ala	Glu 220	Asn	Leu	Asn	Leu		
Val 225	Gly	Leu	His	Cys 230	His	Val	Gly	Ser	Gln	Val 235	Phe	Asp	Ala	Glu	Gly 240		
Phe	Lys	Leu	Ala	Ala 245	Glu	Arg	Val	Leu	Gly 250	Leu	Tyr	Ser	Gln	Ile 255	His		
Ser	Glu	Leu	Gly 260	Val	Ala	Leu	Pro	Glu 265	Leu	Asp	Leu	Gly	Gly 270	Gly	Tyr		
Gly	Ile 275	Ala	Tyr	Thr	Ala	Ala	Glu 280	Glu	Pro	Leu	Asn	Val 285	Ala	Glu	Val		
Ala	Ser 290	Asp	Leu	Leu	Thr	Ala 295	Val	Gly	Lys	Met	Ala 300	Ala	Glu	Leu	Gly		
Ile 305	Asp	Ala	Pro	Thr	Val 310	Leu	Val	Glu	Pro	Gly 315	Arg	Ala	Ile	Ala	Gly 320		
Pro	Ser	Thr	Val	Thr 325	Ile	Tyr	Glu	Val	Gly 330	Thr	Thr	Lys	Asp	Val 335	His		
Val	Asp	Asp 340	Asp	Lys	Thr	Arg	Arg	Tyr 345	Ile	Ala	Val	Asp	Gly 350	Gly	Met		
Ser	Asp	Asn 355	Ile	Arg	Pro	Ala	Leu	Tyr 360	Gly	Ser	Glu	Tyr 365	Asp	Ala	Arg		
Val 370	Val	Ser	Arg	Phe	Ala	Glu 375	Gly	Asp	Pro	Val	Ser 380	Thr	Arg	Ile	Val		
Gly 385	Ser	His	Cys	Glu 390	Ser	Gly	Asp	Ile	Leu	Ile 395	Asn	Asp	Glu	Ile 400	Tyr		
Pro	Ser	Asp	Ile	Thr 405	Ser	Gly	Asp	Phe	Leu 410	Ala	Leu	Ala	Ala	Thr 415	Gly		
Ala	Tyr	Cys	Tyr 420	Ala	Met	Ser	Ser	Arg 425	Tyr	Asn	Ala	Phe	Thr 430	Arg	Pro		
Ala	Val 435	Val	Ser	Val	Arg	Ala	Gly 440	Ser	Ser	Arg	Leu	Met 445	Leu	Arg	Arg		
Glu 450	Thr	Leu	Asp	Asp	Ile 455	Leu	Ser	Leu	Glu	Ala							

<210> 47  
<211> 2121  
<212> DNA  
<213> *Corynebacterium glutamicum*

cca tct gac atc acc agc ggc gac ttc ctt gca ctc gca gcc acc ggc  
1248

Pro Ser Asp Ile Thr Ser Gly Asp Phe Leu Ala Leu Ala Ala Thr Gly  
405 410 415

gca tac tgc tac gcc atg agc tcc cgc tac aac gcc ttc aca cgg ccc  
1296

Ala Tyr Cys Tyr Ala Met Ser Ser Arg Tyr Asn Ala Phe Thr Arg Pro  
420 425 430

gcc gtc gtg tcc gtc cgc gct ggc agc tcc cgc ctc atg ctg cgc cgc  
1344

Ala Val Val Ser Val Arg Ala Gly Ser Ser Arg Leu Met Leu Arg Arg  
435 440 445

gaa acg ctc gac gac atc ctc tca cta gag gca taacgctttt cgacgcctga  
1397

Glu Thr Leu Asp Asp Ile Leu Ser Leu Glu Ala  
450 455

ccc  
1400

<210> 46

<211> 459

<212> PRT

<213> Corynebacterium glutamicum

<400> 46

Pro Ala Pro Gly Trp Arg Phe Arg Thr Gly Glu Asp Val Thr Met Ala  
1 5 10 15

Thr Val Glu Asn Phe Asn Glu Leu Pro Ala His Val Trp Pro Arg Asn  
20 25 30

Ala Val Arg Gln Glu Asp Gly Val Val Thr Val Ala Gly Val Pro Leu  
35 40 45

Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val Asp Glu  
50 55 60

Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe Gly Gly  
65 70 75 80

Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys Thr Ile  
85 90 95

Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala Ser Ile  
100 105 110

Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser Arg Ile  
115 120 125

Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala Leu Val  
130 135 140

Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu Leu Glu  
145 150 155 160

Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp Val Leu

atc cgc gta aag cca ggc atc gaa gca cac acc cac gag ttc atc gcc	576
Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Phe Ile Ala	
180 185 190	
act agc cac gaa gac cag aag ttc gga ttc tcc ctg gca tcc ggt tcc	624
Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser Gly Ser	
195 200 205	
gca ttc gaa gca gca aaa gcc gcc aac aac gca gaa aac ctg aac ctg	672
Ala Phe Glu Ala Ala Lys Ala Ala Asn Asn Ala Glu Asn Leu Asn Leu	
210 215 220	
gtt ggc ctg cac tgc cac gtt ggt tcc cag gtg ttc gac gcc gaa ggc	720
Val Gly Leu His Cys His Val Gly Ser Gln Val Phe Asp Ala Glu Gly	
225 230 235 240	
ttc aag ctg gca gca gaa cgc gtg ttg ggc ctg tac tca cag atc cac	768
Phe Lys Leu Ala Ala Glu Arg Val Leu Gly Leu Tyr Ser Gln Ile His	
245 250 255	
agc gaa ctg ggc gtt gcc ctt cct gaa ctg gat ctc ggt ggc gga tac	816
Ser Glu Leu Gly Val Ala Leu Pro Glu Leu Asp Leu Gly Gly Gly Tyr	
260 265 270	
ggc att gcc tat acc gca gct gaa gaa cca ctc aac gtc gca gaa gtt	864
Gly Ile Ala Tyr Thr Ala Ala Glu Glu Pro Leu Asn Val Ala Glu Val	
275 280 285	
gcc tcc gac ctg ctc acc gca gtc gga aaa atg gca gcg gaa cta ggc	912
Ala Ser Asp Leu Leu Thr Ala Val Gly Lys Met Ala Ala Glu Leu Gly	
290 295 300	
atc gac gca cca acc gtg ctt gtt gag ccc ggc cgc gct atc gca ggc	960
Ile Asp Ala Pro Thr Val Leu Val Glu Pro Gly Arg Ala Ile Ala Gly	
305 310 315 320	
ccc tcc acc gtg acc atc tac gaa gtc ggc acc acc aaa gac gtc cac	
1008	
Pro Ser Thr Val Thr Ile Tyr Glu Val Gly Thr Thr Lys Asp Val His	
325 330 335	
gta gac gac gac aaa acc cgc cgt tac atc gcc gtg gac gga ggc atg	
1056	
Val Asp Asp Asp Lys Thr Arg Arg Tyr Ile Ala Val Asp Gly Gly Met	
340 345 350	
tcc gac aac atc cgc cca gca ctc tac ggg tcc gaa tac gac gcc cgc	
1104	
Ser Asp Asn Ile Arg Pro Ala Leu Tyr Gly Ser Glu Tyr Asp Ala Arg	
355 360 365	
gta gta tcc cgc ttc gcc gaa gga gac cca gta agc acc cgc atc gtg	
1152	
Val Val Ser Arg Phe Ala Glu Gly Asp Pro Val Ser Thr Arg Ile Val	
370 375 380	
ggc tcc cac tgc gaa tcc ggc gat atc ctg atc aac gat gaa atc tac	
1200	
Gly Ser His Cys Glu Ser Gly Asp Ile Leu Ile Asn Asp Glu Ile Tyr	
385 390 395 400	

260	265	270	
Asp Thr Gly Gly Phe Asn His Thr Val Glu Tyr Ile Leu Lys			
275	280	285	
<210> 45			
<211> 1400			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
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<222> (1)..(1377)			
<223> RXA00972			
<400> 45			
cct gca cct ggt tgg cgt ttc cgc acc gga gaa gat gta aca atg gct			48
Pro Ala Pro Gly Trp Arg Phe Arg Thr Gly Glu Asp Val Thr Met Ala			
1	5	10	15
aca gtt gaa aat ttc aat gaa ctt ccc gca cac gta tgg cca cgc aat			96
Thr Val Glu Asn Phe Asn Glu Leu Pro Ala His Val Trp Pro Arg Asn			
20	25	30	
gcc gtg cgc caa gaa gac ggc gtt gtc acc gtc gct ggt gtg cct ctg			144
Ala Val Arg Gln Glu Asp Gly Val Val Thr Val Ala Gly Val Pro Leu			
35	40	45	
cct gac ctc gct gaa gaa tac gga acc cca ctg ttc gta gtc gac gag			192
Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val Asp Glu			
50	55	60	
gac gat ttc cgt tcc cgc tgt cgc gac atg gct acc gca ttc ggt gga			240
Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe Gly Gly			
65	70	75	80
cca ggc aat gtg cac tac gca tct aaa gcg ttc ctg acc aag acc att			288
Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys Thr Ile			
85	90	95	
gca cgt tgg gtt gat gaa gag ggg ctg gca ctg gac att gca tcc atc			336
Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala Ser Ile			
100	105	110	
aac gaa ctg ggc att gcc ctg gcc gct ggt ttc ccc gcc agc cgt atc			384
Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser Arg Ile			
115	120	125	
acc gcg cac ggc aac aac aaa ggc gta gag ttc ctg cgc gcg ttg gtt			432
Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala Leu Val			
130	135	140	
caa aac ggt gtg gga cac gtg gtg ctg gac tcc gca cag gaa cta gaa			480
Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu Leu Glu			
145	150	155	160
ctg ttg gat tac gtt gcc gct ggt gaa ggc aag att cag gac gtg ttg			528
Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp Val Leu			
165	170	175	

aac cac acc gtg gaa tac atc ctc aag  
 Asn His Thr Val Glu Tyr Ile Leu Lys  
           280                    285

958

<210> 44  
 <211> 286  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 44  
 Met His Leu Gly Lys Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu  
       1                    5                    10                    15  
 Asp Tyr Lys Asn Met Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly  
                     20                    25                    30  
 Asn Leu Gly Arg Ser Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met  
                     35                    40                    45  
 Asp Leu Val Gly Ile Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr  
       50                    55                    60  
 Pro Val Phe Asp Val Ala Asp Val Asp Lys His Ala Asp Asp Val Asp  
       65                    70                    75                    80  
 Val Leu Phe Leu Cys Met Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala  
                     85                    90                    95  
 Pro Lys Phe Ala Gln Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His  
                     100                    105                    110  
 Arg Asp Ile Pro Arg His Arg Gln Val Met Asn Glu Ala Ala Thr Ala  
       115                    120                    125  
 Ala Gly Asn Val Ala Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe  
       130                    135                    140  
 Ser Ile Asn Arg Val Tyr Ala Ala Ala Val Leu Ala Glu His Gln Gln  
       145                    150                    155                    160  
 His Thr Phe Trp Gly Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu  
                     165                    170                    175  
 Arg Arg Ile Pro Gly Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser  
                     180                    185                    190  
 Glu Asp Ala Leu Glu Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr  
       195                    200                    205  
 Gly Lys Gln Thr His Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala  
       210                    215                    220  
 Asp His Glu Arg Ile Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe  
       225                    230                    235                    240  
 Val Gly Tyr Glu Val Glu Val Asn Phe Ile Asp Glu Ala Thr Phe Asp  
                     245                    250                    255  
 Ser Glu His Thr Gly Met Pro His Gly Gly His Val Ile Thr Thr Gly

25										30					35					
gtc	gaa	aag	ctt	att	gcc	aag	cag	ccc	gac	atg	gac	ctt	gta	gga	atc	259				
Val	Glu	Lys	Leu	Ile	Ala	Lys	Gln	Pro	Asp	Met	Asp	Leu	Val	Gly	Ile					
40					45					50										
ttc	tcg	cgc	cgg	gcc	acc	ctc	gac	aca	aag	acg	cca	gtc	ttt	gat	gtc	307				
Phe	Ser	Arg	Arg	Ala	Thr	Leu	Asp	Thr	Lys	Thr	Pro	Val	Phe	Asp	Val					
55					60					65										
gcc	gac	gtg	gac	aag	cac	gcc	gac	gac	gtg	gac	gtg	ctg	ttc	ctg	tgc	355				
Ala	Asp	Val	Asp	Lys	His	Ala	Asp	Asp	Val	Asp	Val	Leu	Phe	Leu	Cys					
70					75					80					85					
atg	ggc	tcc	gcc	acc	gac	atc	cct	gag	cag	gca	cca	aag	ttc	gcg	cag	403				
Met	Gly	Ser	Ala	Thr	Asp	Ile	Pro	Glu	Gln	Ala	Pro	Lys	Phe	Ala	Gln					
90					95					100										
ttc	gcc	tgc	acc	gta	gac	acc	tac	gac	aac	cac	cgc	gac	atc	cca	cgc	451				
Phe	Ala	Cys	Thr	Val	Asp	Thr	Tyr	Asp	Asn	His	Arg	Asp	Ile	Pro	Arg					
105					110					115										
cac	cgc	cag	gtc	atg	aac	gaa	gcc	gcc	acc	gca	gcc	ggc	aac	gtt	gca	499				
His	Arg	Gln	Val	Met	Asn	Glu	Ala	Ala	Thr	Ala	Ala	Gly	Asn	Val	Ala					
120					125					130										
ctg	gtc	tct	acc	ggc	tgg	gat	cca	gga	atg	ttc	tcc	atc	aac	cgc	gtc	547				
Leu	Val	Ser	Thr	Gly	Trp	Asp	Pro	Gly	Met	Phe	Ser	Ile	Asn	Arg	Val					
135					140					145										
tac	gca	gcg	gca	gtc	tta	gcc	gag	cac	cag	cag	cac	acc	ttc	tgg	ggc	595				
Tyr	Ala	Ala	Ala	Val	Leu	Ala	Glu	His	Gln	Gln	His	Thr	Phe	Trp	Gly					
150					155					160					165					
cca	ggt	ttg	tca	cag	ggc	cac	tcc	gat	gct	ttg	cga	cgc	atc	cct	ggc	643				
Pro	Gly	Leu	Ser	Gln	Gly	His	Ser	Asp	Ala	Leu	Arg	Arg	Ile	Pro	Gly					
170					175					180										
gtt	caa	aag	gca	gtc	cag	tac	acc	ctc	cca	tcc	gaa	gac	gcc	ctg	gaa	691				
Val	Gln	Lys	Ala	Val	Gln	Tyr	Thr	Leu	Pro	Ser	Glu	Asp	Ala	Leu	Glu					
185					190					195										
aag	gcc	cgc	cgc	ggc	gaa	gcc	ggc	gac	ctt	acc	gga	aag	caa	acc	cac	739				
Lys	Ala	Arg	Arg	Gly	Glu	Ala	Gly	Asp	Leu	Thr	Gly	Lys	Gln	Thr	His					
200					205					210										
aag	cgc	caa	tgc	ttc	gtg	gtt	gcc	gac	gcg	gcc	gat	cac	gag	cgc	atc	787				
Lys	Arg	Gln	Cys	Phe	Val	Val	Ala	Asp	Ala	Ala	Asp	His	Glu	Arg	Ile					
215					220					225										
gaa	aac	gac	atc	cgc	acc	atg	cct	gat	tac	ttc	gtt	ggc	tac	gaa	gtc	835				
Glu	Asn	Asp	Ile	Arg	Thr	Met	Pro	Asp	Tyr	Phe	Val	Gly	Tyr	Glu	Val					
230					235					240					245					
gaa	gtc	aac	ttc	atc	gac	gaa	gca	acc	ttc	gac	tcc	gag	cac	acc	ggc	883				
Glu	Val	Asn	Phe	Ile	Asp	Glu	Ala	Thr	Phe	Asp	Ser	Glu	His	Thr	Gly					
250					255					260										
atg	cca	cac	ggt	ggc	cac	gtg	att	acc	acc	ggc	gac	acc	ggt	ggc	ttc	931				
Met	Pro	His	Gly	Gly	His	Val	Ile	Thr	Thr	Gly	Asp	Thr	Gly	Gly	Phe					
265					270					275										

His Thr Phe Trp Gly Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu  
 165 170 175  
 Arg Arg Ile Pro Gly Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser  
 180 185 190  
 Glu Asp Ala Leu Glu Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr  
 195 200 205  
 Gly Lys Gln Thr His Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala  
 210 215 220  
 Asp His Glu Arg Ile Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe  
 225 230 235 240  
 Val Gly Tyr Glu Val Glu Val Asn Phe Ile Asp Glu Ala Thr Phe Asp  
 245 250 255  
 Ser Glu His Thr Gly Met Pro His Gly Gly His Val Ile Thr Thr Gly  
 260 265 270  
 Asp Thr Gly Gly Phe Asn His Thr Val Glu Tyr Ile Leu Lys Leu Asp  
 275 280 285  
 Arg Asn Pro Asp Phe Thr Ala Ser Ser Gln Ile Ala Phe Gly Arg Ala  
 290 295 300  
 Ala His Arg Met Lys Gln Gln Gly Gln Ser Gly Ala Phe Thr Val Leu  
 305 310 315 320  
 Glu Val Ala Pro Tyr Leu Leu Ser Pro Glu Asn Leu Asp Asp Leu Ile  
 325 330 335  
 Ala Arg Asp Val  
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<220>  
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 <223> FRXA00352

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 Met His Leu Gly Lys  
 1 5  
 ctc gac cag gac agt gcc acc aca att ttg gag gat tac aag aac atg 163  
 Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu Asp Tyr Lys Asn Met  
 10 15 20  
 acc aac atc cgc gta gct atc gtg ggc tac gga aac ctg gga cgc agc 211  
 Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly Asn Leu Gly Arg Ser

Met Pro His Gly Gly His Val Ile Thr Thr Gly Asp Thr Gly Gly Phe  
 265 270 275  
 aac cac acc gtg gaa tac atc ctc aag ctg gac cga aac cca gat ttc 979  
 Asn His Thr Val Glu Tyr Ile Leu Lys Leu Asp Arg Asn Pro Asp Phe  
 280 285 290  
 acc gct tcc tca cag atc gct ttc ggt cgc gca gct cac cgc atg aag  
 1027  
 Thr Ala Ser Ser Gln Ile Ala Phe Gly Arg Ala Ala His Arg Met Lys  
 295 300 305  
 cag cag ggc caa agc gga gct ttc acc gtc ctc gaa gtt gct cca tac  
 1075  
 Gln Gln Gly Gln Ser Gly Ala Phe Thr Val Leu Glu Val Ala Pro Tyr  
 310 315 320 325  
 ctg ctc tcc cca gag aac ttg gac gat ctg atc gca cgc gac gtc  
 1120  
 Leu Leu Ser Pro Glu Asn Leu Asp Asp Leu Ile Ala Arg Asp Val  
 330 335 340  
 taatttagct cgaggggcaa gga  
 1143

<210> 42  
 <211> 340  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 42  
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 Asp Tyr Lys Asn Met Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly  
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 Asn Leu Gly Arg Ser Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met  
 35 40 45  
 Asp Leu Val Gly Ile Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr  
 50 55 60  
 Pro Val Phe Asp Val Ala Asp Val Asp Lys His Ala Asp Asp Val Asp  
 65 70 75 80  
 Val Leu Phe Leu Cys Met Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala  
 85 90 95  
 Pro Lys Phe Ala Gln Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His  
 100 105 110  
 Arg Asp Ile Pro Arg His Arg Gln Val Met Asn Glu Ala Ala Thr Ala  
 115 120 125  
 Ala Gly Asn Val Ala Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe  
 130 135 140  
 Ser Ile Asn Arg Val Tyr Ala Ala Ala Val Leu Ala Glu His Gln Gln  
 145 150 155 160



acc aac atc cgc gta gct atc gtg ggc tac gga aac ctg gga cgc agc	211
Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly Asn Leu Gly Arg Ser	
25 30 35	
gtc gaa aag ctt att gcc aag cag ccc gac atg gac ctt gta gga atc	259
Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met Asp Leu Val Gly Ile	
40 45 50	
ttc tcg cgc cgg gcc acc ctc gac aca aag acg cca gtc ttt gat gtc	307
Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr Pro Val Phe Asp Val	
55 60 65	
gcc gac gtg gac aag cac gcc gac gac gtg gac gtg ctg ttc ctg tgc	355
Ala Asp Val Asp Lys His Ala Asp Asp Val Asp Val Leu Phe Leu Cys	
70 75 80 85	
atg ggc tcc gcc acc gac atc cct gag cag gca cca aag ttc gcg cag	403
Met Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala Pro Lys Phe Ala Gln	
90 95 100	
ttc gcc tgc acc gta gac acc tac gac aac cac cgc gac atc cca cgc	451
Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His Arg Asp Ile Pro Arg	
105 110 115	
cac cgc cag gtc atg aac gaa gcc gcc acc gca gcc ggc aac gtt gca	499
His Arg Gln Val Met Asn Glu Ala Ala Thr Ala Ala Gly Asn Val Ala	
120 125 130	
ctg gtc tct acc ggc tgg gat cca gga atg ttc tcc atc aac cgc gtc	547
Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe Ser Ile Asn Arg Val	
135 140 145	
tac gca gcg gca gtc tta gcc gag cac cag cag cac acc ttc tgg ggc	595
Tyr Ala Ala Ala Val Leu Ala Glu His Gln Gln His Thr Phe Trp Gly	
150 155 160 165	
cca ggt ttg tca cag ggc cac tcc gat gct ttg cga cgc atc cct ggc	643
Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu Arg Arg Ile Pro Gly	
170 175 180	
gtt caa aag gca gtc cag tac acc ctc cca tcc gaa gac gcc ctg gaa	691
Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser Glu Asp Ala Leu Glu	
185 190 195	
aag gcc cgc cgc ggc gaa gcc ggc gac ctt acc gga aag caa acc cac	739
Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr Gly Lys Gln Thr His	
200 205 210	
aag cgc caa tgc ttc gtg gtt gcc gac gcg gcc gat cac gag cgc atc	787
Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala Asp His Glu Arg Ile	
215 220 225	
gaa aac gac atc cgc acc atg cct gat tac ttc gtt ggc tac gaa gtc	835
Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe Val Gly Tyr Glu Val	
230 235 240 245	
gaa gtc aac ttc atc gac gaa gca acc ttc gac tcc gag cac acc ggc	883
Glu Val Asn Phe Ile Asp Glu Ala Thr Phe Asp Ser Glu His Thr Gly	
250 255 260	
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<213> Corynebacterium glutamicum

<400> 40

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20 25 30

Ala Leu Thr Pro Leu Glu Gly Val Asp Glu Asp Arg Asn Val Thr Arg  
35 40 45

Lys Ile Val Thr Thr Thr Ile Asp Thr Asp Ala Ala Pro Thr Asp Thr  
50 55 60

Tyr Asp Ala Trp Leu Arg Leu His Leu Leu Ser His Arg Val Phe Arg  
65 70 75 80

Pro His Thr Ile Asn Leu Asp Gly Ile Phe Gly Leu Leu Asn Asn Val  
85 90 95

Val Trp Thr Asn Phe Gly Pro Cys Ala Val Asp Gly Phe Ala Leu Thr  
100 105 110

Arg Ala Arg Leu Ser Arg Arg Gly Gln Val Thr Val Tyr Ser Val Asp  
115 120 125

Lys Phe Pro Arg Met Val Asp Tyr Val Val Pro Ser Gly Val Arg Ile  
130 135 140

Gly Asp Ala Asp Arg Val Arg Leu Gly Ala Tyr Leu Ala Asp Gly Thr  
145 150 155 160

Thr Val Met His Glu Gly Phe Val Asn Phe Asn Ala Gly Thr Leu Gly  
165 170 175

Ala Ser Met Val  
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<210> 41

<211> 1143

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1120)

<223> RXN00355

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ggcctgatg aaagagatgt ccctgaatca tcatctaagt atg cat ctc ggt aag 115  
Met His Leu Gly Lys  
1 5

ctc gac cag gac agt gcc acc aca att ttg gag gat tac aag aac atg 163  
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10 15 20



<210> 38  
 <211> 250  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 38  
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 Phe Thr Pro Pro Ala Asp Val Glu Trp Ser Thr Asp Val Glu Gly Ala  
                     20                    25                    30  
 Glu Ala Leu Val Glu Phe Ala Gly Arg Ala Cys Tyr Glu Thr Phe Asp  
                     35                    40                    45  
 Lys Pro Asn Pro Arg Thr Ala Ser Asn Ala Ala Tyr Leu Arg His Ile  
     50                    55                    60  
 Met Glu Val Gly His Thr Ala Leu Leu Glu His Ala Asn Ala Thr Met  
     65                    70                    75                    80  
 Tyr Ile Arg Gly Ile Ser Arg Ser Ala Thr His Glu Leu Val Arg His  
                     85                    90                    95  
 Arg His Phe Ser Phe Ser Gln Leu Ser Gln Arg Phe Val His Ser Gly  
                     100                    105                    110  
 Glu Ser Glu Val Val Val Pro Thr Leu Ile Asp Glu Asp Pro Gln Leu  
                     115                    120                    125  
 Arg Glu Leu Phe Met His Ala Met Asp Glu Ser Arg Phe Ala Phe Asn  
     130                    135                    140  
 Glu Leu Leu Asn Ala Leu Glu Glu Lys Leu Gly Asp Glu Pro Asn Ala  
     145                    150                    155                    160  
 Leu Leu Arg Lys Lys Gln Ala Arg Gln Ala Ala Arg Ala Val Leu Pro  
                     165                    170                    175  
 Asn Ala Thr Glu Ser Arg Ile Val Val Ser Gly Asn Phe Arg Thr Trp  
                     180                    185                    190  
 Arg His Phe Ile Gly Met Arg Ala Ser Glu His Ala Asp Val Glu Ile  
                     195                    200                    205  
 Arg Glu Val Ala Val Glu Cys Leu Arg Lys Leu Gln Val Ala Ala Pro  
     210                    215                    220  
 Thr Val Phe Gly Asp Phe Glu Ile Glu Thr Leu Ala Asp Gly Ser Gln  
     225                    230                    235                    240  
 Met Ala Thr Ser Pro Tyr Val Met Asp Phe  
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<210> 39  
 <211> 608  
 <212> DNA  
 <213> Corynebacterium glutamicum

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Asp Val Glu Trp Ser Thr Asp Val Glu Gly Ala Glu Ala Leu Val Glu																				
25 30 35																				
ttt gcg ggt cgt gcc tgc tac gaa act ttt gat aag ccg aac cct cga	259																			
Phe Ala Gly Arg Ala Cys Tyr Glu Thr Phe Asp Lys Pro Asn Pro Arg																				
40 45 50																				
act gct tcc aat gct gcg tat ctg cgc cac atc atg gaa gtg ggg cac	307																			
Thr Ala Ser Asn Ala Ala Tyr Leu Arg His Ile Met Glu Val Gly His																				
55 60 65																				
act gct ttg ctt gag cat gcc aat gcc acg atg tat atc cga ggc att	355																			
Thr Ala Leu Leu Glu His Ala Asn Ala Thr Met Tyr Ile Arg Gly Ile																				
70 75 80 85																				
tct cgg tcc gcg acc cat gaa ttg gtc cga cac cgc cat ttt tcc ttc	403																			
Ser Arg Ser Ala Thr His Glu Leu Val Arg His Arg His Phe Ser Phe																				
90 95 100																				
tct caa ctg tct cag cgt ttc gtg cac agc gga gaa tcg gaa gta gtg	451																			
Ser Gln Leu Ser Gln Arg Phe Val His Ser Gly Glu Ser Glu Val Val																				
105 110 115																				
gtg ccc act ctc atc gat gaa gat ccg cag ttg cgt gaa ctt ttc atg	499																			
Val Pro Thr Leu Ile Asp Glu Asp Pro Gln Leu Arg Glu Leu Phe Met																				
120 125 130																				
cac gcc atg gat gag tct cgg ttc gct ttc aat gag ctg ctt aat gcg	547																			
His Ala Met Asp Glu Ser Arg Phe Ala Phe Asn Glu Leu Leu Asn Ala																				
135 140 145																				
ctg gaa gaa aaa ctt ggc gat gaa ccg aat gca ctt tta agg aaa aag	595																			
Leu Glu Glu Lys Leu Gly Asp Glu Pro Asn Ala Leu Leu Arg Lys Lys																				
150 155 160 165																				
cag gct cgt caa gca gct cgc gct gtg ctg ccc aac gct aca gag tcc	643																			
Gln Ala Arg Gln Ala Ala Arg Ala Val Leu Pro Asn Ala Thr Glu Ser																				
170 175 180																				
aga atc gtg gtg tct gga aac ttc cgc acc tgg agg cat ttc att ggc	691																			
Arg Ile Val Val Ser Gly Asn Phe Arg Thr Trp Arg His Phe Ile Gly																				
185 190 195																				
atg cga gcc agt gaa cat gca gac gtc gaa atc cgc gaa gta gcg gta	739																			
Met Arg Ala Ser Glu His Ala Asp Val Glu Ile Arg Glu Val Ala Val																				
200 205 210																				
gaa tgt tta aga aag ctg cag gta gca gcg cca act gtt ttc ggt gat	787																			
Glu Cys Leu Arg Lys Leu Gln Val Ala Ala Pro Thr Val Phe Gly Asp																				
215 220 225																				
ttt gag att gaa act ttg gca gac gga tcg caa atg gca aca agc ccg	835																			
Phe Glu Ile Glu Thr Leu Ala Asp Gly Ser Gln Met Ala Thr Ser Pro																				
230 235 240 245																				
tat gtc atg gac ttt taacgcaaag ctcacacca cga	873																			
Tyr Val Met Asp Phe																				
250																				

35	40	45
Glu Val Val Val Asp Phe Thr Thr Pro Asn Ala Val Met Gly Asn Leu 50 55 60		
Glu Phe Cys Ile Asn Asn Gly Ile Ser Ala Val Val Gly Thr Thr Gly 65 70 75 80		
Phe Asp Asp Ala Arg Leu Glu Gln Val Arg Asp Trp Leu Glu Gly Lys 85 90 95		
Asp Asn Val Gly Val Leu Ile Ala Pro Asn Phe Ala Ile Ser Ala Val 100 105 110		
Leu Thr Met Val Phe Ser Lys Gln Ala Ala Arg Phe Phe Glu Ser Ala 115 120 125		
Glu Val Ile Glu Leu His His Pro Asn Lys Leu Asp Ala Pro Ser Gly 130 135 140		
Thr Ala Ile His Thr Ala Gln Gly Ile Ala Ala Ala Arg Lys Glu Ala 145 150 155 160		
Gly Met Asp Ala Gln Pro Asp Ala Thr Glu Gln Ala Leu Glu Gly Ser 165 170 175		
Arg Gly Ala Ser Val Asp Gly Ile Pro Val His Ala Val Arg Met Ser 180 185 190		
Gly Met Val Ala His Glu Gln Val Ile Phe Gly Thr Gln Gly Gln Thr 195 200 205		
Leu Thr Ile Lys Gln Asp Ser Tyr Asp Arg Asn Ser Phe Ala Pro Gly 210 215 220		
Val Leu Val Gly Val Arg Asn Ile Ala Gln His Pro Gly Leu Val Val 225 230 235 240		
Gly Leu Glu His Tyr Leu Gly Leu 245		

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 <211> 873  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(850)  
 <223> RXA00864

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 agcagcgggt ggaattttttt aaaaggagcg tttaaaggct gtg gcc gaa caa gtt 115  
 Val Ala Glu Gln Val  
 1 5  
 aaa ttg agc gtg gag ttg ata gcg tgc agt tct ttt act cca ccc gct 163  
 Lys Leu Ser Val Glu Leu Ile Ala Cys Ser Ser Phe Thr Pro Pro Ala

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Asn Gly Ile Ser Ala Val Val Gly Thr Thr Gly Phe Asp Asp Ala Arg
 70                      75                      80                      85

ttg gag cag gtt cgc gac tgg ctt gaa gga aaa gac aat gtc ggt gtt    403
Leu Glu Gln Val Arg Asp Trp Leu Glu Gly Lys Asp Asn Val Gly Val
                      90                      95                      100

ctg atc gca cct aac ttt gct atc tct gcg gtg ttg acc atg gtc ttt    451
Leu Ile Ala Pro Asn Phe Ala Ile Ser Ala Val Leu Thr Met Val Phe
                      105                      110                      115

tcc aag cag gct gcc cgc ttc ttc gaa tca gct gaa gtt att gag ctg    499
Ser Lys Gln Ala Ala Arg Phe Phe Glu Ser Ala Glu Val Ile Glu Leu
                      120                      125                      130

cac cac ccc aac aag ctg gat gca cct tca ggc acc gcg atc cac act    547
His His Pro Asn Lys Leu Asp Ala Pro Ser Gly Thr Ala Ile His Thr
                      135                      140                      145

gct cag ggc att gct gcg gca cgc aaa gaa gca ggc atg gac gca cag    595
Ala Gln Gly Ile Ala Ala Ala Arg Lys Glu Ala Gly Met Asp Ala Gln
150                      155                      160                      165

cca gat gcg acc gag cag gca ctt gag ggt tcc cgt ggc gca agc gta    643
Pro Asp Ala Thr Glu Gln Ala Leu Glu Gly Ser Arg Gly Ala Ser Val
                      170                      175                      180

gat gga atc ccg gtt cat gca gtc cgc atg tcc ggc atg gtt gct cac    691
Asp Gly Ile Pro Val His Ala Val Arg Met Ser Gly Met Val Ala His
                      185                      190                      195

gag caa gtt atc ttt ggc acc cag ggt cag acc ttg acc atc aag cag    739
Glu Gln Val Ile Phe Gly Thr Gln Gly Gln Thr Leu Thr Ile Lys Gln
200                      205                      210

gac tcc tat gat cgc aac tca ttt gca cca ggt gtc ttg gtg ggt gtg    787
Asp Ser Tyr Asp Arg Asn Ser Phe Ala Pro Gly Val Leu Val Gly Val
215                      220                      225

cgc aac att gca cag cac cca ggc cta gtc gta gga ctt gag cat tac    835
Arg Asn Ile Ala Gln His Pro Gly Leu Val Val Gly Leu Glu His Tyr
230                      235                      240                      245

cta ggc ctg taaaggctca tttcagcagc ggg    867
Leu Gly Leu

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&lt;210&gt; 36

&lt;211&gt; 248

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 36

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Met Gly Ile Lys Val Gly Val Leu Gly Ala Lys Gly Arg Val Gly Gln
 1                      5                      10                      15

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Thr Ile Val Ala Ala Val Asn Glu Ser Asp Asp Leu Glu Leu Val Ala
      20                      25                      30

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Glu Ile Gly Val Asp Asp Asp Leu Ser Leu Leu Val Asp Asn Gly Ala

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180	185	190
Ile Leu Thr Gly Ser Glu Thr Thr Val Asp Phe Ala Tyr Leu Ala Gly 195 200 205		
Ala Asp Gly Val Val Pro Gly Leu Gly Asn Val Asp Pro Ala Ala Tyr 210 215 220		
Ala Ala Leu Ala Lys Leu Cys Leu Asp Gly Lys Trp Ala Glu Ala Ala 225 230 235 240		
Ala Leu Gln Lys Arg Ile Asn His Leu Phe His Ile Val Phe Val Gly 245 250 255		
Asp Thr Ser His Met Ser Gly Ser Ser Ala Gly Leu Gly Gly Phe Lys 260 265 270		
Thr Ala Leu Ala His Leu Gly Ile Ile Glu Ser Asn Ala Met Ala Val 275 280 285		
Pro His Gln Ser Leu Ser Asp Glu Glu Thr Ala Arg Ile His Ala Ile 290 295 300		
Val Asp Glu Phe Leu Tyr Thr Ala 305 310		

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 <212> DNA  
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<220>  
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Met Gly Ile Lys Val	
1 5	
ggc gtt ctc gga gcc aaa ggc cgt gtt ggt caa act att gtg gca gca 163	
Gly Val Leu Gly Ala Lys Gly Arg Val Gly Gln Thr Ile Val Ala Ala	
10 15 20	
gtc aat gag tcc gac gat ctg gag ctt gtt gca gag atc ggc gtc gac 211	
Val Asn Glu Ser Asp Asp Leu Glu Leu Val Ala Glu Ile Gly Val Asp	
25 30 35	
gat gat ttg agc ctt ctg gta gac aac ggc gct gaa gtt gtc gtt gac 259	
Asp Asp Leu Ser Leu Leu Val Asp Asn Gly Ala Glu Val Val Val Asp	
40 45 50	
ttc acc act cct aac gct gtg atg ggc aac ctg gag ttc tgc atc aac 307	
Phe Thr Thr Pro Asn Ala Val Met Gly Asn Leu Glu Phe Cys Ile Asn	
55 60 65	
aac ggc att tct gcg gtt gtt gga acc acg ggc ttc gat gat gct cgt 355	



250	255	260	
tcc gga tcc agc gct ggt ttg ggc ggt ttc aag aca gca ctc gca cac			931
Ser Gly Ser Ser Ala Gly Leu Gly Gly Phe Lys Thr Ala Leu Ala His			
265	270	275	
ctt ggc att att gaa tcc aat gcg atg gca gtt cct cac cag agc ctc			979
Leu Gly Ile Ile Glu Ser Asn Ala Met Ala Val Pro His Gln Ser Leu			
280	285	290	
agc gac gaa gaa act gct cgc att cac gcc att gtt gat gaa ttc ctg			
1027			
Ser Asp Glu Glu Thr Ala Arg Ile His Ala Ile Val Asp Glu Phe Leu			
295	300	305	
tac acc gct taaggccac acctcatgac tga			
1059			
Tyr Thr Ala			
310			
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<211> 312			
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<213> Corynebacterium glutamicum			
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Asp His Leu Ile Asn Gly Gly Val Asp Gly Leu Phe Ala Leu Gly Ser			
35	40	45	
Ser Gly Glu Ala Ala Phe Leu Thr Arg Ala Gln Arg Lys Leu Ala Leu			
50	55	60	
Thr Thr Ile Ile Glu His Thr Ala Gly Arg Val Pro Val Thr Ala Gly			
65	70	75	80
Val Ile Glu Thr Thr Thr Ala Arg Val Ile Glu Leu Val Glu Asp Ala			
85	90	95	
Leu Glu Ala Gly Ala Glu Gly Leu Val Ala Thr Ala Pro Phe Tyr Thr			
100	105	110	
Arg Thr His Asp Val Glu Ile Glu Glu His Phe Arg Lys Ile His Ala			
115	120	125	
Ala Ala Pro Glu Leu Pro Leu Phe Ala Tyr Asn Ile Pro Val Ser Val			
130	135	140	
His Ser Asn Leu Asn Pro Val Met Leu Leu Thr Leu Ala Lys Asp Gly			
145	150	155	160
Val Leu Ala Gly Thr Lys Asp Ser Ser Gly Asn Asp Gly Ala Ile Arg			
165	170	175	
Ser Leu Ile Glu Ala Arg Asp Asp Ala Gly Leu Thr Glu Gln Phe Lys			

Phe Thr Gly Val Ile Pro Pro Val Met Thr Pro Leu His Ala Asp Gly	
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agt gtg gat gta gaa agc ctc cgc aag ctc gtt gac cac ctc atc aat	211
Ser Val Asp Val Glu Ser Leu Arg Lys Leu Val Asp His Leu Ile Asn	
25 30 35	
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Gly Gly Val Asp Gly Leu Phe Ala Leu Gly Ser Ser Gly Glu Ala Ala	
40 45 50	
ttc ctc acc cgc gcc cag cgc aaa ctc gca ctg acc acc atc atc gag	307
Phe Leu Thr Arg Ala Gln Arg Lys Leu Ala Leu Thr Thr Thr Ile Ile Glu	
55 60 65	
cac acc gca ggc cgc gtt ccc gta act gct ggt gtc att gaa acc acc	355
His Thr Ala Gly Arg Val Pro Val Thr Ala Gly Val Ile Glu Thr Thr	
70 75 80 85	
act gct cgc gtg att gag ctc gtg gaa gat gcc ctg gag gct ggt gcc	403
Thr Ala Arg Val Ile Glu Leu Val Glu Asp Ala Leu Glu Ala Gly Ala	
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gaa ggc ctc gtt gcc act gca cct ttc tac acc cgc acc cac gat gtg	451
Glu Gly Leu Val Ala Thr Ala Pro Phe Tyr Thr Arg Thr His Asp Val	
105 110 115	
gaa att gaa gaa cac ttc cgc aag atc cac gcc gcc gct cca gag ctt	499
Glu Ile Glu Glu His Phe Arg Lys Ile His Ala Ala Ala Pro Glu Leu	
120 125 130	
cca ctg ttt gcc tac aac atc cca gtg tcg gtg cac tcc aac ctc aac	547
Pro Leu Phe Ala Tyr Asn Ile Pro Val Ser Val His Ser Asn Leu Asn	
135 140 145	
cca gtc atg ctt ttg acg ctg gcc aag gat ggc gtt ctt gca ggc acc	595
Pro Val Met Leu Leu Thr Leu Ala Lys Asp Gly Val Leu Ala Gly Thr	
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aag gat tcc agt ggc aat gat ggc gca atc cgc tca ctg atc gaa gct	643
Lys Asp Ser Ser Gly Asn Asp Gly Ala Ile Arg Ser Leu Ile Glu Ala	
170 175 180	
cgt gat gat gct gga ctc act gag cag ttc aag atc ctc acc ggc agc	691
Arg Asp Asp Ala Gly Leu Thr Glu Gln Phe Lys Ile Leu Thr Gly Ser	
185 190 195	
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Glu Thr Thr Val Asp Phe Ala Tyr Leu Ala Gly Ala Asp Gly Val Val	
200 205 210	
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Pro Gly Leu Gly Asn Val Asp Pro Ala Ala Tyr Ala Ala Leu Ala Lys	
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Leu Cys Leu Asp Gly Lys Trp Ala Glu Ala Ala Ala Leu Gln Lys Arg	
230 235 240 245	
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Ile Asn His Leu Phe His Ile Val Phe Val Gly Asp Thr Ser His Met	

Ala Leu Leu Gly Glu Pro Thr Gly Gly Trp Ile Glu Ala Gly Cys Gln  
 165 170 175

Gly Asn Leu Arg Ile Lys Val Thr Ala His Gly Val Arg Ala His Ser  
 180 185 190

Ala Arg Ser Trp Leu Gly Asp Asn Ala Met His Lys Leu Ser Pro Ile  
 195 200 205

Ile Ser Lys Val Ala Ala Tyr Lys Ala Ala Glu Val Asn Ile Asp Gly  
 210 215 220

Leu Thr Tyr Arg Glu Gly Leu Asn Ile Val Phe Cys Glu Ser Gly Val  
 225 230 235 240

Ala Asn Asn Val Ile Pro Asp Leu Ala Trp Met Asn Leu Asn Phe Arg  
 245 250 255

Phe Ala Pro Asn Arg Asp Leu Asn Glu Ala Ile Glu His Val Val Glu  
 260 265 270

Thr Leu Glu Leu Asp Gly Gln Asp Gly Ile Glu Trp Ala Val Glu Asp  
 275 280 285

Gly Ala Gly Gly Ala Leu Pro Gly Leu Gly Gln Gln Val Thr Ser Gly  
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Leu Ile Asp Ala Val Gly Arg Glu Lys Ile Arg Ala Lys Phe Gly Trp  
 305 310 315 320

Thr Asp Val Ser Arg Phe Ser Ala Met Gly Ile Pro Ala Leu Asn Phe  
 325 330 335

Gly Ala Gly Asp Pro Ser Phe Ala His Lys Arg Asp Glu Gln Cys Pro  
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Phe Ser Ala Met Gly Ile Pro Ala Leu Asn Phe Gly Ala Gly Asp Pro  
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1171

Ser Phe Ala His Lys Arg Asp Glu Gln Cys Pro Val Glu Gln Ile Thr  
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Lys Gln Ile Ala Asp Glu Ile Glu Asp Ala Leu Arg Asn Leu Asn Leu  
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Pro Gly Val Glu Val Phe Arg Phe Asn Asn Asn Val Leu Ala Arg Thr  
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Asn Arg Gly Leu Ala Ser Arg Val Met Leu Ala Gly His Ile Asp Thr  
65 70 75 80

Val Pro Ile Ala Asp Asn Leu Pro Ser Arg Val Glu Asp Gly Ile Met  
85 90 95

Tyr Gly Cys Gly Thr Val Asp Met Lys Ser Gly Leu Ala Val Tyr Leu  
100 105 110

His Thr Phe Ala Thr Leu Ala Thr Ser Thr Glu Leu Lys His Asp Leu  
115 120 125

Thr Leu Ile Ala Tyr Glu Cys Glu Glu Val Ala Asp His Leu Asn Gly  
130 135 140

Leu Gly His Ile Arg Asp Glu His Pro Glu Trp Leu Ala Ala Asp Leu  
145 150 155 160

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Ala Gly Thr Thr Gly Glu Ser Pro Thr Thr Thr Ala Ala Glu Lys Leu	
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Glu Leu Leu Lys Ala Val Arg Glu Glu Val Gly Asp Arg Ala Lys Leu	
70 75 80 85	
atc gcc ggt gtc gga acc aac aac acg cgg aca tct gtg gaa ctt gcg	403
Ile Ala Gly Val Gly Thr Asn Asn Thr Arg Thr Ser Val Glu Leu Ala	
90 95 100	
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Glu Ala Ala Ala Ser Ala Gly Ala Asp Gly Leu Leu Val Val Thr Pro	
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Tyr Tyr Ser Lys Pro Ser Gln Glu Gly Leu Leu Ala His Phe Gly Ala	
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Ile Ala Ala Ala Thr Glu Val Pro Ile Cys Leu Tyr Asp Ile Pro Gly	
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Arg Ser Gly Ile Pro Ile Glu Ser Asp Thr Met Arg Arg Leu Ser Glu	
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Leu Pro Thr Ile Leu Ala Val Lys Asp Ala Lys Gly Asp Leu Val Ala	
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Ala Thr Ser Leu Ile Lys Glu Thr Gly Leu Ala Trp Tyr Ser Gly Asp	
185 190 195	
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Asp Pro Leu Asn Leu Val Trp Leu Ala Leu Gly Gly Ser Gly Phe Ile	
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Ser Val Ile Gly His Ala Ala Pro Thr Ala Leu Arg Glu Leu Tyr Thr	
215 220 225	
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Ser Phe Glu Glu Gly Asp Leu Val Arg Ala Arg Glu Ile Asn Ala Lys	
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Leu Ser Pro Leu Val Ala Ala Gln Gly Arg Leu Gly Gly Val Ser Leu	
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Ala Lys Ala Ala Leu Arg Leu Gln Gly Ile Asn Val Gly Asp Pro Arg	
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Leu Pro Ile Met Ala Pro Asn Glu Gln Glu Leu Glu Ala Leu Arg Glu	
280 285 290	

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Trp	Phe	Ala	Val	Met	Ala	Ala	Lys	Asp	Ala	Met	Thr	Asn	Lys	Val	Glu
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Ala	Pro	Gln	Ile	Ile	Glu	Glu	Thr	Glu	Pro	Thr	Val	Pro	Asp	Asp	Thr
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Pro	Leu	Gly	Gly	Ser	Ala	Val	Ala	Thr	Asp	Thr	Arg	Asn	Arg	Val	Arg
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Val	Glu	Val	Ser	Val	Asp	Lys	Gln	Arg	Val	Trp	Val	Lys	Pro	Met	Leu
	130					135					140				
Met	Ala	Ile	Val	Leu	Thr	Trp	Leu	Asn	Pro	Asn	Ala	Tyr	Leu	Asp	Ala
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Phe	Val	Phe	Ile	Gly	Gly	Val	Gly	Ala	Gln	Tyr	Gly	Asp	Thr	Gly	Arg
				165					170					175	
Trp	Ile	Phe	Ala	Ala	Gly	Ala	Phe	Ala	Ala	Ser	Leu	Ile	Trp	Phe	Pro
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Leu	Val	Gly	Phe	Gly	Ala	Ala	Ala	Leu	Ser	Arg	Pro	Leu	Ser	Ser	Pro
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Lys	Val	Trp	Arg	Trp	Ile	Asn	Val	Val	Val	Ala	Val	Val	Met	Thr	Ala
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 Met Ser Thr Gly Leu  
 1 5  
 aca gct aag acc gga gta gag cac ttc ggc acc gtt gga gta gca atg 163  
 Thr Ala Lys Thr Gly Val Glu His Phe Gly Thr Val Gly Val Ala Met  
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 gtt act cca ttc acg gaa tcc gga gac atc gat atc gct gct ggc cgc 211  
 Val Thr Pro Phe Thr Glu Ser Gly Asp Ile Asp Ile Ala Ala Gly Arg  
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 gaa gtc gcg gct tat ttg gtt gat aag ggc ttg gat tct ttg gtt ctc 259  
 Glu Val Ala Ala Tyr Leu Val Asp Lys Gly Leu Asp Ser Leu Val Leu  
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 Ala Ala Lys Asp Ala Met Thr Asn Lys Val Glu Ala Pro Gln Ile Ile  
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 Glu Glu Thr Glu Pro Thr Val Pro Asp Asp Thr Pro Leu Gly Gly Ser  
                     105                    110                    115

gcg gtg gcc act gac acg cgc aac cgg gtg cgg gtg gag gtg agc gtc 499  
 Ala Val Ala Thr Asp Thr Arg Asn Arg Val Arg Val Glu Val Ser Val  
                     120                    125                    130

gat aag cag cgg gtt tgg gta aag ccc atg ttg atg gca atc gtg ctg 547  
 Asp Lys Gln Arg Val Trp Val Lys Pro Met Leu Met Ala Ile Val Leu  
                     135                    140                    145

acc tgg ttg aac ccg aat gcg tat ttg gac gcg ttt gtg ttt atc ggc 595  
 Thr Trp Leu Asn Pro Asn Ala Tyr Leu Asp Ala Phe Val Phe Ile Gly  
                     150                    155                    160                    165

ggc gtc ggc gcg caa tac ggc gac acc gga cgg tgg att ttc gcc gct 643  
 Gly Val Gly Ala Gln Tyr Gly Asp Thr Gly Arg Trp Ile Phe Ala Ala  
                     170                    175                    180

ggc gcg ttc gcg gca agc ctg atc tgg ttc ccg ctg gtg ggt ttc ggc 691  
 Gly Ala Phe Ala Ala Ser Leu Ile Trp Phe Pro Leu Val Gly Phe Gly  
                     185                    190                    195

gca gca gca ttg tca cgc ccg ctg tcc agc ccc aag gtg tgg cgc tgg 739  
 Ala Ala Ala Leu Ser Arg Pro Leu Ser Ser Pro Lys Val Trp Arg Trp  
                     200                    205                    210

atc aac gtc gtc gtg gca gtt gtg atg acc gca ttg gcc atc aaa ctg 787  
 Ile Asn Val Val Val Ala Val Met Thr Ala Leu Ala Ile Lys Leu  
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 Met Leu Met Gly  
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&lt;210&gt; 54

&lt;211&gt; 233

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 54

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Ser Ile Gly Pro Gln Asn Val Leu Val Ile Lys Gln Gly Ile Lys Arg  
                     20                    25                    30

Glu Gly Leu Ile Ala Val Leu Leu Val Cys Leu Ile Ser Asp Val Phe  
                     35                    40                    45

Leu Phe Ile Ala Gly Thr Leu Gly Val Asp Leu Leu Ser Asn Ala Ala  
                     50                    55                    60

Pro Ile Val Leu Asp Ile Met Arg Trp Gly Gly Ile Ala Tyr Leu Leu

Ser Ala Phe Tyr Leu Val Met Leu Ala Thr Arg Gly Lys Gly Ile Thr  
 385 390 395 400

His Pro His Ala Gly Thr Arg Phe Asp Asp Ser Gly Pro Glu Ile Ser  
 405 410 415

Arg Arg Glu Asn Arg Lys His Leu Ile Val Gly Leu Val Ala Thr Val  
 420 425 430

Tyr Ser Val Trp Leu Phe Tyr Ala Ala Glu Pro Gln Phe Val Leu Phe  
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Gly Ala Met Ala Met Leu Pro Gly Leu Ile Pro Tyr Val Trp Thr Arg  
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Ile Tyr Arg Gly Glu Gln Val Phe Asn Arg Phe Glu Ile Gly Val Val  
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 Met Glu Ile Phe Ile  
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aca ggt ctg ctt ttg ggg gcc agt ctt tta ctg tcc atc gga ccg cag 163  
 Thr Gly Leu Leu Leu Gly Ala Ser Leu Leu Leu Ser Ile Gly Pro Gln  
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aat gta ctg gtg att aaa caa gga att aag cgc gaa gga ctc att gcg 211  
 Asn Val Leu Val Ile Lys Gln Gly Ile Lys Arg Glu Gly Leu Ile Ala  
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 Val Leu Leu Val Cys Leu Ile Ser Asp Val Phe Leu Phe Ile Ala Gly  
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Met Leu Ser Val Ala Phe Val Phe His Val Leu Ala Arg Arg Lys Pro  
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 His Leu Asp Ser Gly Val Tyr Ala Tyr Ala Arg Val Gly Leu Gly Asp  
 85 90 95  
 Tyr Val Gly Phe Ser Ser Ala Trp Gly Tyr Trp Leu Gly Ser Val Ile  
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 Ala Gln Val Gly Tyr Ala Thr Leu Phe Phe Ser Thr Leu Gly His Tyr  
 115 120 125  
 Val Pro Leu Phe Ser Gln Asp His Pro Phe Val Ser Ala Leu Ala Val  
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 Ser Ala Leu Thr Trp Leu Val Phe Gly Val Val Ser Arg Gly Ile Ser  
 145 150 155 160  
 Gln Ala Ala Phe Leu Thr Thr Val Thr Thr Val Ala Lys Ile Leu Pro  
 165 170 175  
 Leu Leu Cys Phe Ile Ile Leu Val Ala Phe Leu Gly Phe Ser Trp Glu  
 180 185 190  
 Lys Phe Thr Val Asp Leu Trp Ala Arg Asp Gly Gly Val Gly Ser Ile  
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 Phe Asp Gln Val Arg Gly Ile Met Val Tyr Thr Val Trp Val Phe Ile  
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 Gly Ile Glu Gly Ala Ser Val Tyr Ser Arg Gln Ala Arg Ser Arg Ser  
 225 230 235 240  
 Asp Val Ser Arg Ala Thr Val Ile Gly Phe Val Ala Val Leu Leu Leu  
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 275 280 285  
 Val Gly Pro Trp Gly Ala Ala Leu Ile Ser Leu Gly Leu Cys Leu Ser  
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 Val Leu Gly Ala Tyr Val Ser Trp Gln Met Leu Cys Ala Glu Pro Leu  
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 340 345 350  
 Ile Gln Ile Phe Ile Ile Ile Phe Phe Leu Asn Glu Thr Thr Tyr Val  
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 Ser Met Val Gln Leu Ala Thr Asn Leu Tyr Leu Val Pro Tyr Leu Phe  
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gct acc aac cta tac ttg gtg cct tac ctg ttc tct gcc ttt tat ctg  
1267

Ala Thr Asn Leu Tyr Leu Val Pro Tyr Leu Phe Ser Ala Phe Tyr Leu  
375 380 385

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1315

Val Met Leu Ala Thr Arg Gly Lys Gly Ile Thr His Pro His Ala Gly  
390 395 400 405

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1363

Thr Arg Phe Asp Asp Ser Gly Pro Glu Ile Ser Arg Arg Glu Asn Arg  
410 415 420

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Lys His Leu Ile Val Gly Leu Val Ala Thr Val Tyr Ser Val Trp Leu  
425 430 435

ttt tac gct gca gaa ccg cag ttt gtc ctc ttc gga gcc atg gcg atg  
1459

Phe Tyr Ala Ala Glu Pro Gln Phe Val Leu Phe Gly Ala Met Ala Met  
440 445 450

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1507

Leu Pro Gly Leu Ile Pro Tyr Val Trp Thr Arg Ile Tyr Arg Gly Glu  
455 460 465

cag gtg ttt aac cgc ttt gaa atc ggc gtg gtt gtt gtc ctg gtc gtt  
1555

Gln Val Phe Asn Arg Phe Glu Ile Gly Val Val Val Val Leu Val Val  
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gct gcc agc gcg ggc gtt att ggt ttg gtc aac gga tca cta tcg ctt  
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Ala Gly Pro Gly Ala Met Leu Ile Gly Trp Leu Ile Ala Gly Val Gly  
50 55 60

Leu Val Phe Gly Val Val Ser Arg Gly Ile Ser Gln Ala Ala Phe Leu	
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Thr Thr Val Thr Thr Val Ala Lys Ile Leu Pro Leu Leu Cys Phe Ile	
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atc ctt gtt gca ttc ttg ggc ttt agc tgg gag aag ttc act gtt gat	691
Ile Leu Val Ala Phe Leu Gly Phe Ser Trp Glu Lys Phe Thr Val Asp	
185 190 195	
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Leu Trp Ala Arg Asp Gly Gly Val Gly Ser Ile Phe Asp Gln Val Arg	
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Gly Ile Met Val Tyr Thr Val Trp Val Phe Ile Gly Ile Glu Gly Ala	
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Ser Val Tyr Ser Arg Gln Ala Arg Ser Arg Ser Asp Val Ser Arg Ala	
230 235 240 245	
acc gtg att ggt ttt gtg gct gtt ctc ctt ttg ctg gtg tcg att tct	883
Thr Val Ile Gly Phe Val Ala Val Leu Leu Leu Leu Val Ser Ile Ser	
250 255 260	
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Ser Leu Ser Phe Gly Val Leu Thr Gln Gln Glu Leu Ala Ala Leu Pro	
265 270 275	
gat aat tcc atg gcg tcg gtg ctc gaa gct gtt gtt ggt cca tgg ggt	979
Asp Asn Ser Met Ala Ser Val Leu Glu Ala Val Val Gly Pro Trp Gly	
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295 300 305	
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1075	
Val Ser Trp Gln Met Leu Cys Ala Glu Pro Leu Ala Leu Met Ala Met	
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330 335 340	
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1171	
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Arg Pro  
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 Val Asn Thr Gln Ser  
 1 5  
 gat tct gcg ggg tct caa ggt gca gcg gcc aca agt cgt act gta tct 163  
 Asp Ser Ala Gly Ser Gln Gly Ala Ala Thr Ser Arg Thr Val Ser  
 10 15 20  
 att aga acc ctc atc gcg ctg atc atc gga tgc acc gtc ggc gcg gga 211  
 Ile Arg Thr Leu Ile Ala Leu Ile Ile Gly Ser Thr Val Gly Ala Gly  
 25 30 35  
 att ttc tcc atc cct caa aac atc ggc tca gtc gca ggt ccc ggc gcg 259  
 Ile Phe Ser Ile Pro Gln Asn Ile Gly Ser Val Ala Gly Pro Gly Ala  
 40 45 50  
 atg ctc atc ggc tgg ctg atc gcc ggt gtg ggc atg ttg tcc gta gcg 307  
 Met Leu Ile Gly Trp Leu Ile Ala Gly Val Gly Met Leu Ser Val Ala  
 55 60 65  
 ttc gtg ttc cat gtt ctt gcc cgc cgt aaa cct cac ctc gat tct ggc 355  
 Phe Val Phe His Val Leu Ala Arg Arg Lys Pro His Leu Asp Ser Gly  
 70 75 80 85  
 gtc tac gca tat gcg cgt gtt gga ttg ggc gat tat gta ggt ttc tcc 403  
 Val Tyr Ala Tyr Ala Arg Val Gly Leu Gly Asp Tyr Val Gly Phe Ser  
 90 95 100  
 tcc gct tgg ggt tat tgg ctg ggt tca gtc atc gcc caa gtt ggc tac 451  
 Ser Ala Trp Gly Tyr Trp Leu Gly Ser Val Ile Ala Gln Val Gly Tyr  
 105 110 115  
 gca acg tta ttt ttc tcc acg ttg ggc cac tac gta ccg ctg ttt tcc 499  
 Ala Thr Leu Phe Phe Ser Thr Leu Gly His Tyr Val Pro Leu Phe Ser  
 120 125 130  
 caa gat cat cca ttt gtg tca gcg ttg gca gtt agc gct ttg acc tgg 547  
 Gln Asp His Pro Phe Val Ser Ala Leu Ala Val Ser Ala Leu Thr Trp  
 135 140 145  
 ctg gtg ttt gga gtt gtt tcc cga gga att agc caa gct gct ttc ttg 595

tgaaaagggtt cag

993

&lt;210&gt; 50

&lt;211&gt; 290

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 50

Met	Asn	Pro	Ile	Gln	Leu	Asp	Thr	Leu	Leu	Ser	Ile	Ile	Asp	Glu	Gly
1				5					10					15	

Ser	Phe	Glu	Gly	Ala	Ser	Leu	Ala	Leu	Ser	Ile	Ser	Pro	Ser	Ala	Val
			20					25					30		

Ser	Gln	Arg	Val	Lys	Ala	Leu	Glu	His	His	Val	Gly	Arg	Val	Leu	Val
		35					40					45			

Ser	Arg	Thr	Gln	Pro	Ala	Lys	Ala	Thr	Glu	Ala	Gly	Glu	Val	Leu	Val
	50					55					60				

Gln	Ala	Ala	Arg	Lys	Met	Val	Leu	Leu	Gln	Ala	Glu	Thr	Lys	Ala	Gln
65					70					75					80

Leu	Ser	Gly	Arg	Leu	Ala	Glu	Ile	Pro	Leu	Thr	Ile	Ala	Ile	Asn	Ala
				85					90					95	

Asp	Ser	Leu	Ser	Thr	Trp	Phe	Pro	Pro	Val	Phe	Asn	Glu	Val	Ala	Ser
			100					105					110		

Trp	Gly	Gly	Ala	Thr	Leu	Thr	Leu	Arg	Leu	Glu	Asp	Glu	Ala	His	Thr
		115					120					125			

Leu	Ser	Leu	Leu	Arg	Arg	Gly	Asp	Val	Leu	Gly	Ala	Val	Thr	Arg	Glu
130						135					140				

Ala	Asn	Pro	Val	Ala	Gly	Cys	Glu	Val	Val	Glu	Leu	Gly	Thr	Met	Arg
145					150					155					160

His	Leu	Ala	Ile	Ala	Thr	Pro	Ser	Leu	Arg	Asp	Ala	Tyr	Met	Val	Asp
				165					170					175	

Gly	Lys	Leu	Asp	Trp	Ala	Ala	Met	Pro	Val	Leu	Arg	Phe	Gly	Pro	Lys
			180					185					190		

Asp	Val	Leu	Gln	Asp	Arg	Asp	Leu	Asp	Gly	Arg	Val	Asp	Gly	Pro	Val
		195					200					205			

Gly	Arg	Arg	Arg	Val	Ser	Ile	Val	Pro	Ser	Ala	Glu	Gly	Phe	Gly	Glu
	210					215					220				

Ala	Ile	Arg	Arg	Gly	Leu	Gly	Trp	Gly	Leu	Leu	Pro	Glu	Thr	Gln	Ala
225					230					235					240

Ala	Pro	Met	Leu	Lys	Ala	Gly	Glu	Val	Ile	Leu	Leu	Asp	Glu	Ile	Pro
				245					250					255	

Ile	Asp	Thr	Pro	Met	Tyr	Trp	Gln	Arg	Trp	Arg	Leu	Glu	Ser	Arg	Ser
			260					265					270		

40	45	50	
gcc aaa gca acc gaa gcg ggt gaa gtc ctt gtg caa gca gcg cgg aaa Ala Lys Ala Thr Glu Ala Gly Glu Val Leu Val Gln Ala Ala Arg Lys 55 60 65			307
atg gtg ttg ctg caa gca gaa act aaa gcg caa cta tct gga cgc ctt Met Val Leu Leu Gln Ala Glu Thr Lys Ala Gln Leu Ser Gly Arg Leu 70 75 80 85			355
gct gaa atc ccg tta acc atc gcc atc aac gca gat tcg cta tcc aca Ala Glu Ile Pro Leu Thr Ile Ala Ile Asn Ala Asp Ser Leu Ser Thr 90 95 100			403
tgg ttt cct ccc gtg ttc aac gag gta gct tct tgg ggt gga gca acg Trp Phe Pro Pro Val Phe Asn Glu Val Ala Ser Trp Gly Gly Ala Thr 105 110 115			451
ctc acg ctg cgc ttg gaa gat gaa gcg cac aca tta tcc ttg ctg cgg Leu Thr Leu Arg Leu Glu Asp Glu Ala His Thr Leu Ser Leu Leu Arg 120 125 130			499
cgt gga gat gtt tta gga gcg gta acc cgt gaa gct aat ccc gtg gcg Arg Gly Asp Val Leu Gly Ala Val Thr Arg Glu Ala Asn Pro Val Ala 135 140 145			547
gga tgt gaa gta gta gaa ctt gga acc atg cgc cac ttg gcc att gca Gly Cys Glu Val Val Glu Leu Gly Thr Met Arg His Leu Ala Ile Ala 150 155 160 165			595
acc ccc tca ttg cgg gat gcc tac atg gtt gat ggg aaa cta gat tgg Thr Pro Ser Leu Arg Asp Ala Tyr Met Val Asp Gly Lys Leu Asp Trp 170 175 180			643
gct gcg atg ccc gtc tta cgc ttc ggt ccc aaa gat gtg ctt caa gac Ala Ala Met Pro Val Leu Arg Phe Gly Pro Lys Asp Val Leu Gln Asp 185 190 195			691
cgt gac ctg gac ggg cgc gtc gat ggt cct gtg ggg cgc agg cgc gta Arg Asp Leu Asp Gly Arg Val Asp Gly Pro Val Gly Arg Arg Arg Val 200 205 210			739
tcc att gtc ccg tcg gcg gaa ggt ttt ggt gag gca att cgc cga ggc Ser Ile Val Pro Ser Ala Glu Gly Phe Gly Glu Ala Ile Arg Arg Gly 215 220 225			787
ctt ggt tgg gga ctt ctt ccc gaa acc caa gct gct ccc atg cta aaa Leu Gly Trp Gly Leu Leu Pro Glu Thr Gln Ala Ala Pro Met Leu Lys 230 235 240 245			835
gca gga gaa gtg atc ctc ctc gat gag ata ccc att gac aca ccg atg Ala Gly Glu Val Ile Leu Leu Asp Glu Ile Pro Ile Asp Thr Pro Met 250 255 260			883
tat tgg caa cga tgg cgc ctg gaa tct aga tct cta gct aga ctc aca Tyr Trp Gln Arg Trp Arg Leu Glu Ser Arg Ser Leu Ala Arg Leu Thr 265 270 275			931
gac gcc gtc gtt gat gca gca atc gag gga ttg cgg cct tagttacttc Asp Ala Val Val Asp Ala Ala Ile Glu Gly Leu Arg Pro 280 285 290			980

Ser Asn Thr Tyr Pro Phe Tyr Gln Thr Pro Val Arg Gly Asn Trp Leu  
500 505 510

Lys Asp Val Leu Ser Lys Gly Val Ala Gln Met Leu Ile Asp Arg Gly  
515 520 525

Leu Arg Leu His Ile Glu Pro Gly Arg Ser Leu Leu Asp Gly Cys Gly  
530 535 540

Val Thr Leu Ala Glu Val Ala Phe Val Lys Thr Arg Ser Asp Gly Leu  
545 550 555 560

Pro Leu Val Gly Leu Ala Met Asn Arg Thr Gln Cys Arg Thr Thr Ser  
565 570 575

Asp Asp Phe Leu Ile Asp Pro Leu His Ile Thr Asp Gly Asp Val Gly  
580 585 590

Glu Glu Ile Glu Ala Tyr Leu Val Gly Ala Tyr Cys Ile Glu Asp Glu  
595 600 605

Leu Ile Leu Arg Arg Arg Ile Arg Phe Pro Arg Gly Val Lys Pro Gly  
610 615 620

Asp Ile Ile Gly Ile Pro Asn Thr Ala Gly Tyr Phe Met His Ile Leu  
625 630 635 640

Glu Ser Ala Ser His Gln Ile Pro Leu Ala Lys Asn Val Val Trp Pro  
645 650 655

Glu Gly Gln Leu Asp Asp Ile Asp Ala Asp  
660 665

&lt;210&gt; 49

&lt;211&gt; 993

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(970)

&lt;223&gt; RXA01393

&lt;400&gt; 49

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agtaaaatga ttggttctta acatgggttta atatagcttc atg aac ccc att caa 115  
Met Asn Pro Ile Gln  
1 5

ctg gac act ttg ctc tca atc att gat gaa ggc agc ttc gaa ggc gcc 163  
Leu Asp Thr Leu Leu Ser Ile Ile Asp Glu Gly Ser Phe Glu Gly Ala  
10 15 20

tcc tta gcc ctt tcc att tcc ccc tcg gcg gtg agt cag cgc gtt aaa 211  
Ser Leu Ala Leu Ser Ile Ser Pro Ser Ala Val Ser Gln Arg Val Lys  
25 30 35

gct ctc gag cat cac gtg ggt cga gtg ttg gta tcg cgc acc caa ccg 259  
Ala Leu Glu His His Val Gly Arg Val Leu Val Ser Arg Thr Gln Pro

Gly Thr Val Gln Gly Gln Arg His Leu Ala Ala Val Gly Arg Met Thr  
 180 185 190  
 Glu Asp Val Val Leu Gly Asn Asp Thr Leu Ser Arg Ser Leu His Asp  
 195 200 205  
 Ile Ile Pro Lys Trp Ala Arg Arg Val Ile Arg Asp Ala Ser Thr Tyr  
 210 215 220  
 Pro Asp Arg Val His Gly Thr Pro Pro Leu Pro Ala Arg Leu Glu Pro  
 225 230 235 240  
 Trp Ala Glu Lys Leu Thr Ser Asp Pro Ala Thr Cys Arg His Leu Ile  
 245 250 255  
 Glu Glu Phe Gly Ser Pro Val Asn Val Leu His Ser Gly Ser Met Pro  
 260 265 270  
 Arg Asn Ile Asn Glu Leu Val Asp Ala Gly Ile Gln Met Gly Val Asp  
 275 280 285  
 Thr Arg Ile Phe Phe Ala Arg Lys Ala Asn Lys Gly Leu Thr Phe Val  
 290 295 300  
 Asp Ala Val Lys Asp Thr Gly His Gly Val Asp Val Ala Ser Glu Arg  
 305 310 315 320  
 Glu Leu Ser Gln Val Leu Asn Arg Gly Val Pro Gly Glu Arg Ile Ile  
 325 330 335  
 Leu Ser Ala Ala Ile Lys Pro Asp Arg Leu Leu Ala Leu Ala Ile Glu  
 340 345 350  
 Asn Gly Val Ile Ile Ser Val Asp Ser Arg Asp Glu Leu Asp Arg Ile  
 355 360 365  
 Ser Ala Leu Val Gly Asp Arg Val Ala Arg Val Ala Pro Arg Val Ala  
 370 375 380  
 Pro Asp Pro Ala Val Leu Pro Pro Thr Arg Phe Gly Glu Arg Ala Ala  
 385 390 395 400  
 Asp Trp Gly Asn Arg Leu Thr Glu Val Ile Pro Gly Val Asp Ile Val  
 405 410 415  
 Gly Leu His Val His Leu His Gly Tyr Ala Ala Lys Asp Arg Ala Leu  
 420 425 430  
 Ala Leu Gln Glu Cys Cys Gln Leu Val Asp Ser Leu Arg Glu Cys Gly  
 435 440 445  
 His Ser Pro Gln Phe Ile Asp Leu Gly Gly Gly Val Pro Met Ser Tyr  
 450 455 460  
 Ile Glu Ser Glu Glu Asp Trp Ile Arg Tyr Gln Ser Ala Lys Ser Ala  
 465 470 475 480  
 Thr Ser Ala Gly Tyr Ala Glu Ser Phe Thr Trp Lys Asp Asp Pro Leu  
 485 490 495



600	605	610
cga atc cgc ttc ccg aga gga gtc aaa cca gga gat atc atc gga att 1987		
Arg Ile Arg Phe Pro Arg Gly Val Lys Pro Gly Asp Ile Ile Gly Ile 615	620	625
cct aac acc gca gga tac ttc atg cat atc ttg gaa agt gca tcg cac 2035		
Pro Asn Thr Ala Gly Tyr Phe Met His Ile Leu Glu Ser Ala Ser His 630	635	640 645
caa atc ccg ttg gcg aaa aat gta gtg tgg ccg gag ggg cag tta gac 2083		
Gln Ile Pro Leu Ala Lys Asn Val Val Trp Pro Glu Gly Gln Leu Asp 650	655	660
gat atc gat gcg gat taagacataa ccattcgcta atc 2121		
Asp Ile Asp Ala Asp 665		
<210> 48		
<211> 666		
<212> PRT		
<213> Corynebacterium glutamicum		
<400> 48		
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Asn Glu Gly Ser Glu Lys Ile Arg Ser Ala Lys Asp Leu Ser Glu Leu 20	25	30
Arg Thr Val Leu Lys Glu Val Ser Ser Gln Ile Gln Glu Arg Ala Gly 35	40	45
Lys Lys Asp Glu Glu Trp Gly Met Gly Ala Thr Trp Arg Glu Leu Tyr 50	55	60
Pro Ser Ile Val Glu Arg Ala Ser Tyr Glu Gly Arg Asp Ser Leu Ile 65	70	75 80
Gly Phe Asp His Leu Ala Arg Glu Met Glu Arg Leu Ala Phe Gly Pro 85	90	95
Pro Ser Glu Ser Phe Glu Tyr Leu Gln Glu Leu Val Lys Ser Gly Val 100	105	110
Val Asp Ile Thr His Leu His Arg Gly Arg Glu Pro Leu Thr Asp Leu 115	120	125
Val Arg Glu Leu Glu Ile Thr Val Val Ile Asp Ala Val Leu Pro Pro 130	135	140
Pro Gly Val Val Pro Gly Thr Leu Val His Asn Leu Val Lys Glu Gly 145	150	155 160
Tyr Ala Arg Met Arg Pro Gly Thr Arg Gly Leu Asp Val Ala Ala Asp 165	170	175

Leu Thr Glu Val Ile Pro Gly Val Asp Ile Val Gly Leu His Val His  
 410 415 420  
 ctc cat ggc tat gct gca aaa gac cgt gct ctg gct ctg cag gaa tgt  
 1411  
 Leu His Gly Tyr Ala Ala Lys Asp Arg Ala Leu Ala Leu Gln Glu Cys  
 425 430 435  
 tgc caa ctc gtc gat tct ctc aga gaa tgc ggg cat tcc cca cag ttt  
 1459  
 Cys Gln Leu Val Asp Ser Leu Arg Glu Cys Gly His Ser Pro Gln Phe  
 440 445 450  
 att gac ctt gga gga ggg gtg cct atg agc tac att gaa tct gag gaa  
 1507  
 Ile Asp Leu Gly Gly Gly Val Pro Met Ser Tyr Ile Glu Ser Glu Glu  
 455 460 465  
 gat tgg atc cgt tat caa tcc gct aaa tct gcg act tca gcc ggg tat  
 1555  
 Asp Trp Ile Arg Tyr Gln Ser Ala Lys Ser Ala Thr Ser Ala Gly Tyr  
 470 475 480 485  
 gcc gaa tcc ttt acg tgg aaa gac gat ccg tta tct aat acg tac ccg  
 1603  
 Ala Glu Ser Phe Thr Trp Lys Asp Asp Pro Leu Ser Asn Thr Tyr Pro  
 490 495 500  
 ttc tat cag acc cca gtg cgc ggt aat tgg ttg aaa gac gtg ctt tct  
 1651  
 Phe Tyr Gln Thr Pro Val Arg Gly Asn Trp Leu Lys Asp Val Leu Ser  
 505 510 515  
 aag ggg gta gct cag atg ctc att gac cgg gga ttg cgg tta cac ata  
 1699  
 Lys Gly Val Ala Gln Met Leu Ile Asp Arg Gly Leu Arg Leu His Ile  
 520 525 530  
 gag cct ggt cga agt tta cta gat ggg tgt ggc gtc act ctt gcc gaa  
 1747  
 Glu Pro Gly Arg Ser Leu Leu Asp Gly Cys Gly Val Thr Leu Ala Glu  
 535 540 545  
 gtt gct ttt gtg aaa acc cga agt gac ggg ttg cct cta gtg gga ctg  
 1795  
 Val Ala Phe Val Lys Thr Arg Ser Asp Gly Leu Pro Leu Val Gly Leu  
 550 555 560 565  
 gct atg aac cga acg cag tgc cgg act aca tcc gat gat ttt ctc att  
 1843  
 Ala Met Asn Arg Thr Gln Cys Arg Thr Thr Ser Asp Asp Phe Leu Ile  
 570 575 580  
 gat ccc ctg cat atc act gac ggt gat gta ggc gag gaa atc gaa gca  
 1891  
 Asp Pro Leu His Ile Thr Asp Gly Asp Val Gly Glu Glu Ile Glu Ala  
 585 590 595  
 tat cta gtg ggt gcc tac tgc atc gaa gat gag ctg att tta cgc cgg  
 1939  
 Tyr Leu Val Gly Ala Tyr Cys Ile Glu Asp Glu Leu Ile Leu Arg Arg

Pro Pro Glu Ala Gly Gln Glu Asn His Leu Asp Thr Pro Val Phe Gln  
 20 25 30  
 Ala Pro Asp Ala Ser Ser Asn Gln Ser Ala Val Lys Ala Glu Thr Ala  
 35 40 45  
 Gly Asn Asp Asn Arg Asp Ala Ala Gln Gly Ala Gln Gly Ser Gln Asp  
 50 55 60  
 Ser Gln Gly Ser Gln Asn Ala Gln Gly Ser Gln Asn Arg Glu Ser Gly  
 65 70 75 80  
 Asn Asn Asn Arg Asn Arg Ser Asn Asn Asn Arg Arg Gly Gly Arg Gly  
 85 90 95  
 Arg Arg Gly Ser Gly Asn Ala Asn Glu Gly Ala Asn Asn Asn Ser Gly  
 100 105 110  
 Asn Gln Asn Arg Gln Gly Gly Asn Arg Gly Asn Arg Gly Gly Gly Arg  
 115 120 125  
 Arg Asn Val Val Lys Ser Met Gln Gly Ala Asp Leu Thr Gln Arg Leu  
 130 135 140  
 Pro Glu Pro Pro Lys Ala Pro Ala Asn Gly Leu Arg Ile Tyr Ala Leu  
 145 150 155 160  
 Gly Gly Ile Ser Glu Ile Gly Arg Asn Met Thr Val Phe Glu Tyr Asn  
 165 170 175  
 Asn Arg Leu Leu Ile Val Asp Cys Gly Val Leu Phe Pro Ser Ser Gly  
 180 185 190  
 Glu Pro Gly Val Asp Leu Ile Leu Pro Asp Phe Gly Pro Ile Glu Asp  
 195 200 205  
 His Leu His Arg Val Asp Ala Leu Val Val Thr His Gly His Glu Asp  
 210 215 220  
 His Ile Gly Ala Ile Pro Trp Leu Leu Lys Leu Arg Asn Asp Ile Pro  
 225 230 235 240  
 Ile Leu Ala Ser Arg Phe Thr Leu Ala Leu Ile Ala Ala Lys Cys Lys  
 245 250 255  
 Glu His Arg Gln Arg Pro Lys Leu Ile Glu Val Asn Glu Gln Ser Asn  
 260 265 270  
 Glu Asp Arg Gly Pro Phe Asn Ile Arg Phe Trp Ala Val Asn His Ser  
 275 280 285  
 Ile Pro Asp Cys Leu Gly Leu Ala Ile Lys Thr Pro Ala Gly Leu Val  
 290 295 300  
 Ile His Thr Gly Asp Ile Lys Leu Asp Gln Thr Pro Pro Asp Gly Arg  
 305 310 315 320  
 Pro Thr

120	125	130	
tcg atg cag ggt gcg gat ctg acc cag cgc ctg cca gag cca cca aag			547
Ser Met Gln Gly Ala Asp Leu Thr Gln Arg Leu Pro Glu Pro Pro Lys			
135	140	145	
gca ccg gca aac ggt ctg cgt att tac gca ctt ggt ggc att tcc gaa			595
Ala Pro Ala Asn Gly Leu Arg Ile Tyr Ala Leu Gly Gly Ile Ser Glu			
150	155	160	165
atc ggt cgc aac atg acc gtg ttt gag tac aac aac cgt ctg ctc atc			643
Ile Gly Arg Asn Met Thr Val Phe Glu Tyr Asn Asn Arg Leu Leu Ile			
170	175		180
gtg gac tgt ggt gtg ctc ttc cca tct tca ggt gag cca ggc gtt gac			691
Val Asp Cys Gly Val Leu Phe Pro Ser Ser Gly Glu Pro Gly Val Asp			
185	190		195
ctg att ctt cct gac ttc ggc cca att gag gat cac ctg cac cgc gtc			739
Leu Ile Leu Pro Asp Phe Gly Pro Ile Glu Asp His Leu His Arg Val			
200	205		210
gat gca ttg gtg gtt act cac gga cac gaa gac cac att ggt gct att			787
Asp Ala Leu Val Val Thr His Gly His Glu Asp His Ile Gly Ala Ile			
215	220		225
ccc tgg ctg ctg aag ctg cgc aac gat atc cca atc ttg gca tcc cgt			835
Pro Trp Leu Leu Lys Leu Arg Asn Asp Ile Pro Ile Leu Ala Ser Arg			
230	235	240	245
ttc acc ttg gct ctg att gca gct aag tgt aag gaa cac cgt cag cgt			883
Phe Thr Leu Ala Leu Ile Ala Ala Lys Cys Lys Glu His Arg Gln Arg			
250	255		260
ccg aag ctg atc gag gtc aac gag cag tcc aat gag gac cgc gga ccg			931
Pro Lys Leu Ile Glu Val Asn Glu Gln Ser Asn Glu Asp Arg Gly Pro			
265	270		275
ttc aac att cgc ttc tgg gct gtt aac cac tcc atc cca gac tgc ctt			979
Phe Asn Ile Arg Phe Trp Ala Val Asn His Ser Ile Pro Asp Cys Leu			
280	285		290
ggg ctt gct atc aag act cct gct ggt ttg gtc atc cac acc ggt gac			
1027			
Gly Leu Ala Ile Lys Thr Pro Ala Gly Leu Val Ile His Thr Gly Asp			
295	300		305
atc aag ctg gat cag act cct cct gat gga cgc cca act			
1066			
Ile Lys Leu Asp Gln Thr Pro Pro Asp Gly Arg Pro Thr			
310	315		320
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1	5	10	15

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Met Asn Asp Ser Arg																
1 5																
aat cgc ggc cgg aag gtt acc cgc aag gcg ggc cca cca gaa gct ggt																163
Asn Arg Gly Arg Lys Val Thr Arg Lys Ala Gly Pro Pro Glu Ala Gly																
10 15 20																
cag gaa aac cat ctg gat acc cct gtc ttt cag gca cca gat gct tcc																211
Gln Glu Asn His Leu Asp Thr Pro Val Phe Gln Ala Pro Asp Ala Ser																
25 30 35																
tct aac cag agc gct gta aaa gct gag acc gcc gga aac gac aat cgg																259
Ser Asn Gln Ser Ala Val Lys Ala Glu Thr Ala Gly Asn Asp Asn Arg																
40 45 50																
gat gct gcg caa ggt gct caa gga tcc caa gat tct cag ggt tcc cag																307
Asp Ala Ala Gln Gly Ala Gln Gly Ser Gln Asp Ser Gln Gly Ser Gln																
55 60 65																
aac gct caa ggt tcc cag aac cgc gag tcc gga aac aac aac cgc aac																355
Asn Ala Gln Gly Ser Gln Asn Arg Glu Ser Gly Asn Asn Asn Arg Asn																
70 75 80 85																
cgt tcc aac aac aac cgt cgc ggt ggt cgt gga cgt cgt gga tcc gga																403
Arg Ser Asn Asn Asn Arg Arg Gly Gly Arg Gly Arg Arg Gly Ser Gly																
90 95 100																
aac gcc aat gag ggc gcg aac aac aac agc ggt aac cag aac cgt cag																451
Asn Ala Asn Glu Gly Ala Asn Asn Asn Ser Gly Asn Gln Asn Arg Gln																
105 110 115																
ggc gga aac cgt ggc aac cgc ggt ggc gga cgc cga aac gtt gtt aag																499
Gly Gly Asn Arg Gly Asn Arg Gly Gly Gly Arg Arg Asn Val Val Lys																

&lt;222&gt; (1)..(426)

&lt;223&gt; RXC00861

&lt;400&gt; 63

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atg gct cct cac aag gtc atg ctg att acc act ggt act cag ggt gag   48
Met Ala Pro His Lys Val Met Leu Ile Thr Thr Gly Thr Gln Gly Glu
  1             5             10             15

cct atg gct gcg ctg tct cgc atg gcg cgt cgt gag cac cga cag atc   96
Pro Met Ala Ala Leu Ser Arg Met Ala Arg Arg Glu His Arg Gln Ile
             20             25             30

act gtc cgt gat gga gac ttg att atc ctt tct tcc tcc ctg gtt cca  144
Thr Val Arg Asp Gly Asp Leu Ile Ile Leu Ser Ser Ser Leu Val Pro
             35             40             45

ggg aac gaa gaa gca gtg ttc ggt gtc atc aac atg ctg gct cag atc  192
Gly Asn Glu Glu Ala Val Phe Gly Val Ile Asn Met Leu Ala Gln Ile
             50             55             60

ggg gca act gtt gtt acc ggt cgc gac gcc aag gtg cac acc tcg ggc  240
Gly Ala Thr Val Val Thr Gly Arg Asp Ala Lys Val His Thr Ser Gly
             65             70             75             80

cac ggc tac tcc gga gag ctg ttg ttc ttg tac aac gcc gct cgt ccg  288
His Gly Tyr Ser Gly Glu Leu Leu Phe Leu Tyr Asn Ala Ala Arg Pro
             85             90             95

aag aac gct atg cct gtc cac ggc gag tgg cgc cac ctg cgc gcc aac  336
Lys Asn Ala Met Pro Val His Gly Glu Trp Arg His Leu Arg Ala Asn
             100            105            110

aag gaa ctg gct atc tcc act ggt gtt aac cgc gac aac gtt gtg ctt  384
Lys Glu Leu Ala Ile Ser Thr Gly Val Asn Arg Asp Asn Val Val Leu
             115            120            125

gca caa aac ggt gtt gtg gtt gat atg gtc aac ggt cgc gca   426
Ala Gln Asn Gly Val Val Val Asp Met Val Asn Gly Arg Ala
             130            135            140

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&lt;210&gt; 64

&lt;211&gt; 142

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 64

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Met Ala Pro His Lys Val Met Leu Ile Thr Thr Gly Thr Gln Gly Glu
  1             5             10             15

Pro Met Ala Ala Leu Ser Arg Met Ala Arg Arg Glu His Arg Gln Ile
             20             25             30

Thr Val Arg Asp Gly Asp Leu Ile Ile Leu Ser Ser Ser Leu Val Pro
             35             40             45

Gly Asn Glu Glu Ala Val Phe Gly Val Ile Asn Met Leu Ala Gln Ile
             50             55             60

Gly Ala Thr Val Val Thr Gly Arg Asp Ala Lys Val His Thr Ser Gly
             65             70             75             80

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20					25					30						
Phe	Gly	Ile	Leu	Gly	His	Asp	Arg	Asn	Thr	Leu	Ile	Phe	Val	Ile	Phe	
35					40					45						
Leu	Ala	Val	Leu	Ser	Val	Gly	Leu	Thr	Val	Leu	Gly	Pro	Trp	Leu	Leu	
50					55					60						
Gly	Lys	Ala	Thr	Asn	Val	Val	Phe	Glu	Gly	Phe	Leu	Ser	Lys	Arg	Met	
65					70					75					80	
Pro	Ala	Gly	Ala	Ser	Lys	Glu	Asp	Ile	Ile	Ala	Gln	Leu	Gln	Ala	Ala	
85					90					95						
Gly	Lys	His	Asn	Gln	Ala	Ser	Met	Met	Glu	Asp	Met	Asn	Leu	Val	Pro	
100					105					110						
Gly	Ser	Gly	Ile	Asp	Phe	Glu	Lys	Leu	Ala	Met	Ile	Leu	Gly	Leu	Val	
115					120					125						
Ile	Gly	Ala	Tyr	Leu	Ile	Gly	Ser	Leu	Leu	Ser	Leu	Phe	Gln	Ala	Arg	
130					135					140						
Met	Leu	Asn	Arg	Ile	Val	Gln	Ser	Ala	Met	His	Arg	Leu	Arg	Met	Glu	
145					150					155					160	
Val	Glu	Glu	Lys	Ile	His	Arg	Leu	Pro	Leu	Ser	Tyr	Phe	Asp	Ser	Ile	
165					170					175						
Lys	Arg	Gly	Asp	Leu	Leu	Ser	Arg	Val	Thr	Asn	Asp	Val	Asp	Asn	Ile	
180					185					190						
Gly	Gln	Ser	Leu	Gln	Gln	Thr	Leu	Ser	Gln	Ala	Ile	Thr	Ser	Leu	Leu	
195					200					205						
Thr	Val	Ile	Gly	Val	Leu	Val	Met	Met	Phe	Ile	Ile	Ser	Pro	Leu	Leu	
210					215					220						
Ala	Leu	Val	Ala	Leu	Val	Ser	Ile	Pro	Val	Thr	Ile	Val	Val	Thr	Val	
225					230					235					240	
Val	Val	Ala	Ser	Arg	Ser	Gln	Lys	Leu	Phe	Ala	Glu	Gln	Trp	Lys	Gln	
245					250					255						
Thr	Gly	Ile	Leu	Asn	Ala	Arg	Leu	Glu	Glu	Thr	Tyr	Ser	Gly	His	Ala	
260					265					270						
Val	Val	Lys	Val	Phe	Gly	His	Gln	Lys	Asp	Val	Gln	Glu	Ala	Phe	Glu	
275					280					285						
Glu	Glu	Asn	Gln	Ala	Cys	Val										
290					295											

&lt;210&gt; 63

&lt;211&gt; 426

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

ttt gaa aaa tta gcc atg atc ctc gga ctg gtg atc ggt gct tat ctc 499  
 Phe Glu Lys Leu Ala Met Ile Leu Gly Leu Val Ile Gly Ala Tyr Leu  
           120                          125                          130

atc ggt agc ctg ttg tcg ttg ttc cag gcg cgg atg ctc aac cgc atc 547  
 Ile Gly Ser Leu Leu Ser Leu Phe Gln Ala Arg Met Leu Asn Arg Ile  
           135                          140                          145

gtg caa agt gcc atg cac cgg ctg cgc atg gag gtg gag gaa aaa atc 595  
 Val Gln Ser Ala Met His Arg Leu Arg Met Glu Val Glu Glu Lys Ile  
           150                          155                          160                          165

cac cgc cta ccg ctg agc tat ttc gat tcc atc aaa cgt ggt gat ctg 643  
 His Arg Leu Pro Leu Ser Tyr Phe Asp Ser Ile Lys Arg Gly Asp Leu  
                           170                          175                          180

ctt agc cgt gtg acc aac gat gtg gat aat atc ggt caa tcc ctg caa 691  
 Leu Ser Arg Val Thr Asn Asp Val Asp Asn Ile Gly Gln Ser Leu Gln  
                           185                          190                          195

caa acc ttg tca cag gcg atc act tcc cta ctg acc gtc atc ggt gtg 739  
 Gln Thr Leu Ser Gln Ala Ile Thr Ser Leu Leu Thr Val Ile Gly Val  
           200                          205                          210

ttg gtg atg atg ttt atc atc tcc cca ctg ctc gca ctc gtg gcg ctg 787  
 Leu Val Met Met Phe Ile Ile Ser Pro Leu Leu Ala Leu Val Ala Leu  
           215                          220                          225

gta tcc att ccg gtc acc atc gtg gtc act gtg gtg gtt gcg agc cgt 835  
 Val Ser Ile Pro Val Thr Ile Val Val Thr Val Val Val Ala Ser Arg  
           230                          235                          240                          245

tcc cag aaa ctc ttt gcg gaa cag tgg aag cag acc ggt att ttg aat 883  
 Ser Gln Lys Leu Phe Ala Glu Gln Trp Lys Gln Thr Gly Ile Leu Asn  
                           250                          255                          260

gcg cgc ctg gag gaa acc tac tct ggc cac gcc gtg gtt aag gtt ttc 931  
 Ala Arg Leu Glu Glu Thr Tyr Ser Gly His Ala Val Val Lys Val Phe  
           265                          270                          275

gga cac caa aag gat gtt caa gaa gca ttc gag gaa gaa aat caa gct 979  
 Gly His Gln Lys Asp Val Gln Glu Ala Phe Glu Glu Glu Asn Gln Ala  
           280                          285                          290

tgt gta taaggccagc tttggtgccc agt  
 1008  
 Cys Val  
       295

<210> 62  
 <211> 295  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 62  
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       1                          5                          10                          15  
 Ala Pro Asn Gln Lys Ala Gln Asn Phe Gly Pro Ser Ala Lys Arg Leu



Ala Ile Ala Glu Thr Ile Ala  
385 390

gct tcc atg atg gaa gac atg aac ctt gtt cca ggc tca ggc att gat 451  
Ala Ser Met Met Glu Asp Met Asn Leu Val Pro Gly Ser Gly Ile Asp  
105 110 115

<400> 60  
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 1 5 10 15  
 Thr Pro Pro Val Glu Leu Val Ser Gly Lys Gly Ala Thr Val Thr Asp  
 20 25 30  
 Asp Gln Gly Asn Val Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn  
 35 40 45  
 Ala Leu Gly His Ala His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln  
 50 55 60  
 Ile Gly Gln Leu Gly His Val Ser Asn Leu Phe Ala Ser Arg Pro Val  
 65 70 75 80  
 Val Glu Val Ala Glu Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala  
 85 90 95  
 Thr Leu Ala Ala Gln Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu  
 100 105 110  
 Ala Asn Glu Ala Ala Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg  
 115 120 125  
 Ile Leu Ala Ala Val His Gly Phe His Gly Arg Thr Met Gly Ser Leu  
 130 135 140  
 Ala Leu Thr Gly Gln Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro  
 145 150 155 160  
 Ser Gly Val Glu Phe Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys  
 165 170 175  
 Met Val Glu Thr Asn Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro  
 180 185 190  
 Ile Gln Gly Glu Thr Gly Val Val Pro Ala Pro Glu Gly Phe Leu Lys  
 195 200 205  
 Ala Val Arg Glu Leu Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp  
 210 215 220  
 Glu Val Gln Thr Gly Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln  
 225 230 235 240  
 His Asp Gly Val Val Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly  
 245 250 255  
 Gly Gly Leu Pro Ile Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu  
 260 265 270  
 Leu Met Thr Pro Gly Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val  
 275 280 285  
 Ala Cys Ala Ala Ala Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe  
 290 295 300  
 Cys Ala Glu Val Ala Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala  
 305 310 315 320

tgc gat gag tac ggc atc ttg atg atc acc gat gaa gtc cag act ggc 787  
 Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp Glu Val Gln Thr Gly  
 215 220 225

gtt ggc cgt acc ggc gat ttc ttt gca cat cag cac gat ggc gtt gtt 835  
 Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln His Asp Gly Val Val  
 230 235 240 245

ccc gat gtg gtg acc atg gcc aag gga ctt ggc ggc ggt ctt ccc atc 883  
 Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly Gly Gly Leu Pro Ile  
 250 255 260

ggt gct tgt ttg gcc act ggc cgt gca gct gaa ttg atg acc cca ggc 931  
 Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu Leu Met Thr Pro Gly  
 265 270 275

aag cac ggc acc act ttc ggt ggc aac cca gtt gct tgt gca gct gcc 979  
 Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val Ala Cys Ala Ala Ala  
 280 285 290

aag gca gtg ctg tct gtt gtc gat gac gct ttc tgc gca gaa gtt gcc  
 1027  
 Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe Cys Ala Glu Val Ala  
 295 300 305

cgc aag ggc gag ctg ttc aag gaa ctt ctt gcc aag gtt gac ggc gtt  
 1075  
 Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala Lys Val Asp Gly Val  
 310 315 320 325

gta gac gtc cgt ggc agg ggc ttg atg ttg ggc gtg gtg ctg gag cgc  
 1123  
 Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly Val Val Leu Glu Arg  
 330 335 340

gac gtc gca aag caa gct gtt ctt gat ggt ttt aag cac ggc gtt att  
 1171  
 Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe Lys His Gly Val Ile  
 345 350 355

ttg aat gca ccg gcg gac aac att atc cgt ttg acc ccg ccg ctg gtg  
 1219  
 Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu Thr Pro Pro Leu Val  
 360 365 370

atc acc gac gaa gaa atc gca gac gca gtc aag gct att gcc gag aca  
 1267  
 Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys Ala Ile Ala Glu Thr  
 375 380 385

atc gca taaaggactc aaacttatga ctt  
 1296  
 Ile Ala  
 390

&lt;210&gt; 60

&lt;211&gt; 391

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;222&gt; (101)..(1273)

&lt;223&gt; RXS02157

&lt;400&gt; 59

gggtggaatt ggcacgatgg tgctgccgga tgtttttgat cgggagaatt atcctgaagg 60

caccgttttt agaaaagacg acaaggatgg ggaactgtaa atg agc acg ctg gaa 115  
 Met Ser Thr Leu Glu  
 1 5

act tgg cca cag gtc att att aat acg tac ggc acc cca cca gtt gag 163  
 Thr Trp Pro Gln Val Ile Ile Asn Thr Tyr Gly Thr Pro Pro Val Glu  
 10 15 20

ctg gtg tcc ggc aag ggc gca acc gtc act gat gac cag ggc aat gtc 211  
 Leu Val Ser Gly Lys Gly Ala Thr Val Thr Asp Asp Gln Gly Asn Val  
 25 30 35

tac atc gac ttg ctc gcg ggc atc gca gtc aac gcg ttg ggc cac gcc 259  
 Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn Ala Leu Gly His Ala  
 40 45 50

cac ccg gcg atc atc gag gcg gtc acc aac cag atc ggc caa ctt ggt 307  
 His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln Ile Gly Gln Leu Gly  
 55 60 65

cac gtc tca aac ttg ttc gca tcc agg ccc gtc gtc gag gtc gcc gag 355  
 His Val Ser Asn Leu Phe Ala Ser Arg Pro Val Val Glu Val Ala Glu  
 70 75 80 85

gag ctc atc aag cgt ttt tcg ctt gac gac gcc acc ctc gcc gcg caa 403  
 Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala Thr Leu Ala Ala Gln  
 90 95 100

acc cgg gtt ttc ttc tgc aac tcg ggc gcc gaa gca aac gag gct gct 451  
 Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu Ala Asn Glu Ala Ala  
 105 110 115

ttc aag att gca cgc ttg act ggt cgt tcc cgg att ctg gct gca gtt 499  
 Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg Ile Leu Ala Ala Val  
 120 125 130

cat ggt ttc cac ggc cgc acc atg ggt tcc ctc gcg ctg act ggc cag 547  
 His Gly Phe His Gly Arg Thr Met Gly Ser Leu Ala Leu Thr Gly Gln  
 135 140 145

cca gac aag cgt gaa gcg ttc ctg cca atg cca agc ggt gtg gag ttc 595  
 Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro Ser Gly Val Glu Phe  
 150 155 160 165

tac cct tac ggc gac acc gat tac ttg cgc aaa atg gta gaa acc aac 643  
 Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys Met Val Glu Thr Asn  
 170 175 180

cca acg gat gtg gct gct atc ttc ctc gag cca atc cag ggt gaa acg 691  
 Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro Ile Gln Gly Glu Thr  
 185 190 195

ggc gtt gtt cca gca cct gaa gga ttc ctc aag gca gtg cgc gag ctg 739  
 Gly Val Val Pro Ala Pro Glu Gly Phe Leu Lys Ala Val Arg Glu Leu  
 200 205 210

35					40					45					
Thr	Arg	Leu	Gly	Ala	Asn	Glu	Leu	Thr	Pro	Arg	Met	Leu	Gln	Leu	Val
	50					55					60				
Lys	Leu	Asp	Gln	Asp	Arg	Leu	Val	Glu	Gln	Val	Ala	Val	Arg	Thr	Val
	65					70					75				80
Ile	Pro	Asp	Leu	Ser	Gln	Pro	Pro	Val	Asp	Ala	His	Asp	Val	Tyr	Leu
				85					90					95	
Arg	Leu	His	Leu	Leu	Ser	His	Arg	Leu	Val	Arg	Pro	His	Glu	Met	His
			100					105					110		
Met	Gln	Asn	Thr	Leu	Glu	Leu	Leu	Ser	Asp	Val	Val	Trp	Thr	Asn	Lys
			115				120					125			
Gly	Pro	Cys	Leu	Pro	Glu	Asn	Phe	Glu	Trp	Val	Arg	Gly	Ala	Leu	Arg
	130					135					140				
Ser	Arg	Gly	Leu	Ile	His	Val	Tyr	Cys	Val	Asp	Arg	Leu	Pro	Arg	Met
	145					150					155				160
Val	Asp	Tyr	Val	Val	Pro	Pro	Gly	Val	Arg	Ile	Ser	Glu	Ala	Glu	Arg
				165					170					175	
Val	Arg	Leu	Gly	Ala	Tyr	Leu	Ala	Pro	Gly	Thr	Ser	Val	Leu	Arg	Glu
			180					185					190		
Gly	Phe	Val	Ser	Phe	Asn	Ser	Gly	Thr	Leu	Gly	Ala	Ala	Lys	Val	Glu
	195						200					205			
Gly	Arg	Leu	Ser	Ser	Gly	Val	Val	Ile	Gly	Glu	Gly	Ser	Glu	Ile	Gly
	210					215					220				
Leu	Ser	Ser	Thr	Ile	Gln	Ser	Pro	Arg	Asp	Glu	Gln	Arg	Arg	Arg	Leu
	225					230					235				240
Pro	Leu	Ser	Ile	Gly	Gln	Asn	Cys	Asn	Phe	Gly	Val	Ser	Ser	Gly	Ile
				245					250					255	
Ile	Gly	Val	Ser	Leu	Gly	Asp	Asn	Cys	Asp	Ile	Gly	Asn	Asn	Ile	Val
			260					265					270		
Leu	Asp	Gly	Asp	Thr	Pro	Ile	Trp	Phe	Ala	Ala	Asp	Glu	Glu	Leu	Arg
			275				280					285			
Thr	Ile	Asp	Ser	Ile	Glu	Gly	Gln	Ala	Asn	Trp	Ser	Ile	Lys	Arg	Glu
	290					295					300				
Ser	Gly	Phe	His	Glu	Pro	Val	Ala	Arg	Leu	Lys	Ala				
	305					310					315				

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<210> 59
<211> 1296
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS

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His Val Tyr Cys Val Asp Arg Leu Pro Arg Met Val Asp Tyr Val Val
150          155          160          165

ccc cct gga gtc cgc atc tcc gaa gca gaa cgc gtg cgc cta ggt gca 643
Pro Pro Gly Val Arg Ile Ser Glu Ala Glu Arg Val Arg Leu Gly Ala
          170          175          180

tac ctt gct ccg ggt acc tct gtg ctg cgt gaa ggt ttc gtg tct ttc 691
Tyr Leu Ala Pro Gly Thr Ser Val Leu Arg Glu Gly Phe Val Ser Phe
          185          190          195

aac tcc ggc acc ttg ggt gcc gca aag gtg gaa ggc cgc ctg agt tcc 739
Asn Ser Gly Thr Leu Gly Ala Ala Lys Val Glu Gly Arg Leu Ser Ser
          200          205          210

ggt gtg gtc atc ggt gaa ggt tcc gag att gga ctg tct tct act att 787
Gly Val Val Ile Gly Glu Gly Ser Glu Ile Gly Leu Ser Ser Thr Ile
          215          220          225

cag tcc ccg aga gat gaa cag cgc cgc cgt ttg ccg ttg agc atc ggc 835
Gln Ser Pro Arg Asp Glu Gln Arg Arg Arg Leu Pro Leu Ser Ile Gly
230          235          240          245

caa aac tgc aac ttt ggt gtc agc tcc gga atc atc gga gtc agt ctg 883
Gln Asn Cys Asn Phe Gly Val Ser Ser Gly Ile Ile Gly Val Ser Leu
          250          255          260

gga gac aat tgc gac atc gga aat aac att gtc ttg gat gga gat acc 931
Gly Asp Asn Cys Asp Ile Gly Asn Asn Ile Val Leu Asp Gly Asp Thr
          265          270          275

ccc att tgg ttc gca gcc gat gag gag tta cgc act atc gac tcc atc 979
Pro Ile Trp Phe Ala Ala Asp Glu Glu Leu Arg Thr Ile Asp Ser Ile
          280          285          290

gaa ggc caa gca aat tgg tca atc aag cgt gaa tcc ggc ttc cat gag
1027
Glu Gly Gln Ala Asn Trp Ser Ile Lys Arg Glu Ser Gly Phe His Glu
          295          300          305

cca gtt gcc cgc ctc aaa gct tgacccattt tcataaccag tgc
1071
Pro Val Ala Arg Leu Lys Ala
310          315

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&lt;210&gt; 58

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 58

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Met Ser Glu Asn Ile Arg Gly Ala Gln Ala Val Gly Ile Ala Asn Ile
  1           5           10           15

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Ala Met Asp Gly Thr Ile Leu Asp Thr Trp Tyr Pro Glu Pro Gln Ile
      20           25           30

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Phe Asn Pro Asp Gln Trp Ala Glu Arg Tyr Pro Leu Glu Val Gly Thr

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260	265	270	
Val Gly Asp Pro Arg Leu Pro Ile Met Ala Pro Asn Glu Gln Glu Leu			
275	280	285	
Glu Ala Leu Arg Glu Asp Met Lys Lys Ala Gly Val Leu			
290	295	300	
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<211> 1071			
<212> DNA			
<213> Corynebacterium glutamicum			
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<223> RXS02021			
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aaaccttagt taaaacatga tggaagcggg cgattaaaaa atg agt gaa aac att 115			
		Met Ser Glu Asn Ile	5
		1	
cgc gga gcc caa gca gtt gga atc gca aat atc gcc atg gac ggg acc 163			
Arg Gly Ala Gln Ala Val Gly Ile Ala Asn Ile Ala Met Asp Gly Thr			
	10	15	20
atc ctg gac acg tgg tac cca gaa ccc caa att ttc aac ccg gat cag 211			
Ile Leu Asp Thr Trp Tyr Pro Glu Pro Gln Ile Phe Asn Pro Asp Gln			
	25	30	35
tgg gct gaa cgc tac cca ttg gaa gtg ggc acc aca cgc ctc gga gca 259			
Trp Ala Glu Arg Tyr Pro Leu Glu Val Gly Thr Thr Arg Leu Gly Ala			
	40	45	50
aac gaa ctc acc cca cgg atg ctg cag ttg gta aaa ctg gac caa gat 307			
Asn Glu Leu Thr Pro Arg Met Leu Gln Leu Val Lys Leu Asp Gln Asp			
	55	60	65
cgc ctc gtc gaa cag gta gca gtc cgc acc gtt atc ccc gat ctg tct 355			
Arg Leu Val Glu Gln Val Ala Val Arg Thr Val Ile Pro Asp Leu Ser			
	70	75	80
caa cct cca gta gac gcg cac gat gtt tac ctg cgc ctc cac ctg ctt 403			
Gln Pro Pro Val Asp Ala His Asp Val Tyr Leu Arg Leu His Leu Leu			
	90	95	100
tcc cac cgg ctg gtc cgc ccc cac gaa atg cac atg caa aac acc ttg 451			
Ser His Arg Leu Val Arg Pro His Glu Met His Met Gln Asn Thr Leu			
	105	110	115
gag ctg ctg tcc gac gtg gtg tgg aca aac aag ggc cct tgc ctt cct 499			
Glu Leu Leu Ser Asp Val Val Trp Thr Asn Lys Gly Pro Cys Leu Pro			
	120	125	130
gaa aac ttt gag tgg gtg cgt ggt gct ctg cgg tcc cgc gga ctc atc 547			
Glu Asn Phe Glu Trp Val Arg Gly Ala Leu Arg Ser Arg Gly Leu Ile			
	135	140	145

gac atg aaa aaa gct gga gtt cta taaatatgaa tgattcccga aat  
 1026  
 Asp Met Lys Lys Ala Gly Val Leu  
           295                          300

<210> 56  
 <211> 301  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 56  
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 Val Gly Val Ala Met Val Thr Pro Phe Thr Glu Ser Gly Asp Ile Asp  
                   20                  25                  30  
 Ile Ala Ala Gly Arg Glu Val Ala Ala Tyr Leu Val Asp Lys Gly Leu  
                   35                  40                  45  
 Asp Ser Leu Val Leu Ala Gly Thr Thr Gly Glu Ser Pro Thr Thr Thr  
   50                          55                  60  
 Ala Ala Glu Lys Leu Glu Leu Leu Lys Ala Val Arg Glu Glu Val Gly  
   65                  70                  75                  80  
 Asp Arg Ala Lys Leu Ile Ala Gly Val Gly Thr Asn Asn Thr Arg Thr  
                   85                  90                  95  
 Ser Val Glu Leu Ala Glu Ala Ala Ala Ser Ala Gly Ala Asp Gly Leu  
                   100                  105                  110  
 Leu Val Val Thr Pro Tyr Tyr Ser Lys Pro Ser Gln Glu Gly Leu Leu  
   115                  120                  125  
 Ala His Phe Gly Ala Ile Ala Ala Ala Thr Glu Val Pro Ile Cys Leu  
   130                  135                  140  
 Tyr Asp Ile Pro Gly Arg Ser Gly Ile Pro Ile Glu Ser Asp Thr Met  
   145                  150                  155                  160  
 Arg Arg Leu Ser Glu Leu Pro Thr Ile Leu Ala Val Lys Asp Ala Lys  
                   165                  170                  175  
 Gly Asp Leu Val Ala Ala Thr Ser Leu Ile Lys Glu Thr Gly Leu Ala  
                   180                  185                  190  
 Trp Tyr Ser Gly Asp Asp Pro Leu Asn Leu Val Trp Leu Ala Leu Gly  
   195                  200                  205  
 Gly Ser Gly Phe Ile Ser Val Ile Gly His Ala Ala Pro Thr Ala Leu  
   210                  215                  220  
 Arg Glu Leu Tyr Thr Ser Phe Glu Glu Gly Asp Leu Val Arg Ala Arg  
   225                  230                  235                  240  
 Glu Ile Asn Ala Lys Leu Ser Pro Leu Val Ala Ala Gln Gly Arg Leu  
                   245                  250                  255  
 Gly Gly Val Ser Leu Ala Lys Ala Ala Leu Arg Leu Gln Gly Ile Asn



Ala Ser Arg Asn Tyr Ile Lys Ala Ala Thr Thr Gly Val Leu Lys Val  
 705 710 715 720  
 Met Ser Lys Met Gly Ile Ala Thr Val Ser Ser Tyr Arg Gly Ala Gln  
 725 730 735  
 Leu Ala Asp Val Thr Gly Leu His Gln Asp Leu Leu Asp Asn Tyr Phe  
 740 745 750  
 Gly Gly Ile Ala Ser Pro Ile Ser Gly Ile Gly Leu Asp Glu Val Ala  
 755 760 765  
 Ala Asp Val Glu Ala Arg His Arg Ser Ala Phe Leu Pro Arg Pro Glu  
 770 775 780  
 Glu His Ala His Arg Glu Leu Asp Leu Gly Gly Glu Tyr Lys Trp Arg  
 785 790 795 800  
 Arg Glu Gly Glu Tyr His Leu Phe Asn Pro Glu Thr Ile Phe Lys Leu  
 805 810 815  
 Gln His Ala Thr Arg Ser Gly Ser Tyr Glu Ile Phe Lys Asp Tyr Thr  
 820 825 830  
 Arg Lys Val Asp Asp Gln Ser Thr Arg Leu Gly Thr Ile Arg Gly Leu  
 835 840 845  
 Phe Glu Phe Ser Thr Asp Arg Lys Pro Ile Ser Val Ser Glu Val Glu  
 850 855 860  
 Pro Val Ser Glu Ile Val Lys Arg Phe Ser Thr Gly Ala Met Ser Tyr  
 865 870 875 880  
 Gly Ser Ile Ser Ala Glu Ala His Glu Val Leu Ala Ile Ala Met Asn  
 885 890 895  
 Arg Leu Gly Gly Met Ser Asn Ser Gly Glu Gly Gly Glu Asp Ala Arg  
 900 905 910  
 Arg Phe Asp Val Glu Pro Asn Gly Asp Trp Lys Arg Ser Ala Ile Lys  
 915 920 925  
 Gln Val Ala Ser Gly Arg Phe Gly Val Thr Ser His Tyr Leu Asn Asn  
 930 935 940  
 Cys Thr Asp Ile Gln Ile Lys Met Ala Gln Gly Ala Lys Pro Gly Glu  
 945 950 955 960  
 Gly Gly Gln Leu Pro Pro Asn Lys Val Tyr Pro Trp Val Ala Glu Val  
 965 970 975  
 Arg Ile Thr Thr Pro Gly Val Gly Leu Ile Ser Pro Pro Pro His His  
 980 985 990  
 Asp Ile Tyr Ser Ile Glu Asp Leu Ala Gln Leu Ile His Asp Leu Lys  
 995 1000 1005  
 Asn Ala Asn Pro Arg Ala Arg Ile His Val Lys Leu Val Ala Glu Gln  
 1010 1015 1020

370		375		380
Leu Arg Glu Glu Ser Val Val Lys Arg Thr Arg Val Gln Pro Gly Arg				
385		390		400
Met Phe Leu Val Asp Thr Ala Glu Gly Arg Ile Val Glu Asp Glu Glu				
	405		410	415
Ile Lys Gln Lys Leu Ser Glu Ala Gln Pro Tyr Gly Glu Trp Ile Arg				
	420		425	430
Asp Asn Phe Val His Leu Asp Arg Leu Pro Gln Thr Arg Tyr Asn Tyr				
	435		440	445
Met Ala His Ser Arg Ala Val Leu Arg Gln Arg Val Phe Gly Ile Thr				
	450		455	460
Glu Glu Asp Val Asp Leu Leu Leu Leu Pro Met Ala Arg Gln Gly Ala				
465		470		480
Glu Ala Ile Gly Ser Met Gly Ser Asp Thr Pro Ile Ala Ala Leu Ser				
	485		490	495
Gln Arg Pro Arg Met Leu Tyr Asp Phe Phe Ala Gln Arg Phe Ala Gln				
	500		505	510
Val Thr Asn Pro Pro Leu Asp Ser Ile Arg Glu Lys Pro Val Thr Ser				
	515		520	525
Met Phe Thr Leu Leu Gly Ala Gln Ser Asp Val Leu Asn Pro Gly Pro				
	530		535	540
Asp Ala Ala Arg Arg Ile Arg Leu Glu Ser Pro Ile Ile Asp Asn His				
545		550		560
Glu Leu Ala Thr Leu Ile Asn Ala Asn Ala His Gly Glu Trp Asp Ser				
	565		570	575
Phe Gly Ala Ala Val Ile Ser Gly Leu Tyr Pro Val Ala His His Gly				
	580		585	590
Ala Gly Met Lys Ala Ala Ile Ala Arg Val Arg Arg Glu Val Ser Glu				
	595		600	605
Ala Ile Arg Asn Gly Lys Thr Leu Ile Val Leu Ser Asp Arg Glu Ser				
	610		615	620
Asp Glu Arg Met Ala Pro Ile Pro Ala Leu Leu Leu Thr Ser Ala Val				
625		630		640
His Gln Tyr Leu Val Gln Gln Arg Thr Arg Thr Gln Cys Ser Leu Val				
	645		650	655
Val Glu Ser Gly Asp Ala Arg Glu Val His His Leu Ala Met Leu Ile				
	660		665	670
Gly Phe Gly Ala Asp Ala Ile Asn Pro Tyr Met Ala Phe Glu Thr Ile				
	675		680	685
Asp Glu Leu Arg Met Lys Gly Gln Leu Gly Asp Leu Ser Leu Asp Glu				
	690		695	700

Ala Gly Ala Glu Lys Asn Thr Gly Asp Gly Ala Gly Ile Leu Met Gln  
 50 55 60  
 Ile Pro Asp Gly Phe Tyr Arg Glu Val Ser Gly Ile Glu Leu Pro Glu  
 65 70 75 80  
 Ala Gly Glu Tyr Ala Thr Gly Ile Ala Phe Leu Pro Arg Gly Arg Met  
 85 90 95  
 Ala Met Met Asp Ala Gln Lys Glu Ile Glu Arg Ile Ala Lys Gln Glu  
 100 105 110  
 Gly Ala Asp Val Leu Gly Trp Arg Met Val Pro Phe Asp Ser Arg Asp  
 115 120 125  
 Leu Gly Ser Met Ala Glu Glu Ala Met Pro Ser Phe Ala Gln Ile Phe  
 130 135 140  
 Leu Thr Val Pro Gly Lys Ser Gly Glu Asp Leu Asp Arg Val Met Phe  
 145 150 155 160  
 Phe Ile Arg Lys Arg Cys Glu Arg Glu Leu Gly Thr Thr Asn Gly Arg  
 165 170 175  
 Asp Thr Val Tyr Phe Pro Ser Leu Ser Ser Arg Thr Ile Ile Tyr Lys  
 180 185 190  
 Gly Met Leu Thr Thr Leu Gln Leu Glu Gly Phe Phe Glu Asp Leu Gly  
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 Asp Ala Arg Leu Glu Ser Ala Ile Ala Ile Val His Ser Arg Phe Ser  
 210 215 220  
 Thr Asn Thr Phe Pro Ser Trp Pro Leu Ala His Pro Tyr Arg Phe Val  
 225 230 235 240  
 Ala His Asn Gly Glu Ile Asn Thr Val Arg Gly Asn Glu Asn Trp Met  
 245 250 255  
 Arg Ala Arg Glu Ala Leu Ile Lys Asn Asp Lys Leu Gly Asn Leu Ser  
 260 265 270  
 Ser Val Leu Pro Ile Cys Thr Pro Glu Gly Ser Asp Thr Ala Arg Phe  
 275 280 285  
 Asp Glu Ala Leu Glu Leu Leu His Leu Gly Gly Tyr Ser Leu Pro His  
 290 295 300  
 Ala Val Ala Met Met Ile Pro Gln Ala Trp Glu His Asn Lys Thr Leu  
 305 310 315 320  
 Ser Pro Glu Leu Arg Asp Phe Tyr Glu Tyr His Ser Cys Leu Met Glu  
 325 330 335  
 Pro Trp Asp Gly Pro Ala Ala Leu Ala Phe Thr Asp Gly Arg Phe Val  
 340 345 350  
 Gly Ala Val Leu Asp Arg Asn Gly Leu Arg Pro Gly Arg Ile Thr Ile  
 355 360 365  
 Thr Asp Ser Gly Leu Val Val Met Ala Ser Glu Ser Gly Val Leu Asp

aac tct ggc gcc acc gca gtg gtt gaa ggt atc gga aac cac ggt tgt  
4291

Asn Ser Gly Ala Thr Ala Val Val Glu Gly Ile Gly Asn His Gly Cys  
1385 1390 1395

gag tac atg act ggc ggc cga gtc ctg gtt ttg ggc ccg gtt ggt gag  
4339

Glu Tyr Met Thr Gly Gly Arg Val Leu Val Leu Gly Pro Val Gly Glu  
1400 1405 1410

aac ttt ggt gcc ggc atg tct ggt ggc att gca tac ctg gct aat tcc  
4387

Asn Phe Gly Ala Gly Met Ser Gly Gly Ile Ala Tyr Leu Ala Asn Ser  
1415 1420 1425

ccg gac cta aac cag aag atc aat ggc gaa ttg gtg gat gtt gtt cca  
4435

Pro Asp Leu Asn Gln Lys Ile Asn Gly Glu Leu Val Asp Val Val Pro  
1430 1435 1440 1445

ctg agc gct gac gat ctg acg tgg gct gat gag ctc att gct cgc cac  
4483

Leu Ser Ala Asp Asp Leu Thr Trp Ala Asp Glu Leu Ile Ala Arg His  
1450 1455 1460

cgc gaa ctc acc gga tcc gag acc aag ctg cgt gca caa gat ttg gtg  
4531

Arg Glu Leu Thr Gly Ser Glu Thr Lys Leu Arg Ala Gln Asp Leu Val  
1465 1470 1475

aaa atc atg ccg cgc gat ttc caa aaa gta ctc aac atc atc gaa acg  
4579

Lys Ile Met Pro Arg Asp Phe Gln Lys Val Leu Asn Ile Ile Glu Thr  
1480 1485 1490

gcc cac gct gag ggc caa gac cca gca atc aag atc atg gag gca gtg  
4627

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1495 1500 1505

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4653

Ser  
1510

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20 25 30

Val Asp Arg Ala Leu Glu Ala Leu Arg Asn Ile Asp His Arg Gly Ala  
35 40 45

aag cgt tcc gga atc cca gct gat tcc cgc gca gca cac ctg gat ttg  
3715  
Lys Arg Ser Gly Ile Pro Ala Asp Ser Arg Ala Ala His Leu Asp Leu  
1190 1195 1200 1205

agc cca att ttc cat cgc cca gaa act cca cac ttc cca act cag gat  
3763  
Ser Pro Ile Phe His Arg Pro Glu Thr Pro His Phe Pro Thr Gln Asp  
1210 1215 1220

gtg cgt tgc acc aag acc cag gaa cac agc cta gaa aaa gcc ctg gac  
3811  
Val Arg Cys Thr Lys Thr Gln Glu His Ser Leu Glu Lys Ala Leu Asp  
1225 1230 1235

aac gca ttt att gat aag gct tcg gac acg atc acc cgt gcc gca gcg  
3859  
Asn Ala Phe Ile Asp Lys Ala Ser Asp Thr Ile Thr Arg Ala Ala Ala  
1240 1245 1250

ggc gtg gaa acc agc att gtt att gat agc tcc atc agc aac gtc aac  
3907  
Gly Val Glu Thr Ser Ile Val Ile Asp Ser Ser Ile Ser Asn Val Asn  
1255 1260 1265

cgt tca gtt ggc acg atg ctg ggt tct gca gtc agc cgc gtg gct ggt  
3955  
Arg Ser Val Gly Thr Met Leu Gly Ser Ala Val Ser Arg Val Ala Gly  
1270 1275 1280 1285

gcc caa ggt ttg cca gac ggc acc atc acc ttg aat ctt caa ggc tgc  
4003  
Ala Gln Gly Leu Pro Asp Gly Thr Ile Thr Leu Asn Leu Gln Gly Cys  
1290 1295 1300

gcc ggt aac tcc ttt ggc gcg ttc atc cca cga ggc atc acc atc aac  
4051  
Ala Gly Asn Ser Phe Gly Ala Phe Ile Pro Arg Gly Ile Thr Ile Asn  
1305 1310 1315

ctc acc ggc gat gcc aat gac ttt gtg ggc aag gga tta tct ggc gga  
4099  
Leu Thr Gly Asp Ala Asn Asp Phe Val Gly Lys Gly Leu Ser Gly Gly  
1320 1325 1330

aag att gtg atc aag cct tcc gct cag gct ccg aag cag ctg aag aac  
4147  
Lys Ile Val Ile Lys Pro Ser Ala Gln Ala Pro Lys Gln Leu Lys Asn  
1335 1340 1345

aat cca aat atc att gcc gga aac gtg ctt gga tac ggc gca acc agt  
4195  
Asn Pro Asn Ile Ile Ala Gly Asn Val Leu Gly Tyr Gly Ala Thr Ser  
1350 1355 1360 1365

ggc gaa ttg ttc att cgt ggc cag gtc ggc gaa cgt ttc tgc gtc cgt  
4243  
Gly Glu Leu Phe Ile Arg Gly Gln Val Gly Glu Arg Phe Cys Val Arg  
1370 1375 1380

gag gat ctg gct cag ctg atc cac gac ctg aag aac gct aac cca cgc  
3139

Glu Asp Leu Ala Gln Leu Ile His Asp Leu Lys Asn Ala Asn Pro Arg  
1000 1005 1010

gca cga atc cac gtg aag cta gtg gca gaa caa ggc gtg ggc acc gtt  
3187

Ala Arg Ile His Val Lys Leu Val Ala Glu Gln Gly Val Gly Thr Val  
1015 1020 1025

gcc gca ggt gtg tcc aaa gca cac gct gat gtg gtg ctt att tcc ggc  
3235

Ala Ala Gly Val Ser Lys Ala His Ala Asp Val Val Leu Ile Ser Gly  
1030 1035 1040 1045

cac gat ggc gga act ggc gca tct cct ttg acc tcc ctg aag cat gcc  
3283

His Asp Gly Gly Thr Gly Ala Ser Pro Leu Thr Ser Leu Lys His Ala  
1050 1055 1060

ggt ggt cca tgg gag ttg ggc ttg gct gaa acc cag caa acg ttg ctg  
3331

Gly Gly Pro Trp Glu Leu Gly Leu Ala Glu Thr Gln Gln Thr Leu Leu  
1065 1070 1075

ctc aac ggc ctg cgc gat cgt att cgc gtg cag tgc gat ggt cag ctg  
3379

Leu Asn Gly Leu Arg Asp Arg Ile Arg Val Gln Cys Asp Gly Gln Leu  
1080 1085 1090

aaa act ggc cga gac gtg gtt atc gca gct ctt ctc ggt gcc gaa gaa  
3427

Lys Thr Gly Arg Asp Val Val Ile Ala Ala Leu Leu Gly Ala Glu Glu  
1095 1100 1105

ttc ggt ttt gcc acc gca ccg ctg gtg gtt gaa ggc tgc atc atg atg  
3475

Phe Gly Phe Ala Thr Ala Pro Leu Val Val Glu Gly Cys Ile Met Met  
1110 1115 1120 1125

cgc gtc tgc cac ctg gac acc tgc ccg gtg ggt atc gct acc cag aac  
3523

Arg Val Cys His Leu Asp Thr Cys Pro Val Gly Ile Ala Thr Gln Asn  
1130 1135 1140

ccg gat ttg cgt tcc aag ttc acc ggc aag gct gaa cac gtg gtc aac  
3571

Pro Asp Leu Arg Ser Lys Phe Thr Gly Lys Ala Glu His Val Val Asn  
1145 1150 1155

ttc ttc acc ttc atc gcc cag gaa gtc cgt gag tac ttg gca cag ctt  
3619

Phe Phe Thr Phe Ile Ala Gln Glu Val Arg Glu Tyr Leu Ala Gln Leu  
1160 1165 1170

ggt ttc cgc tct att gat gaa gcc gtc gga caa gcc cag gtg ctg cgc  
3667

Gly Phe Arg Ser Ile Asp Glu Ala Val Gly Gln Ala Gln Val Leu Arg  
1175 1180 1185

cac ctg ttc aac cca gaa acc atc ttc aag ctg cag cat gca acg cgt  
2563

His Leu Phe Asn Pro Glu Thr Ile Phe Lys Leu Gln His Ala Thr Arg  
810 815 820

tct ggc agc tac gag att ttc aag gat tac acc cgc aag gtt gat gat  
2611

Ser Gly Ser Tyr Glu Ile Phe Lys Asp Tyr Thr Arg Lys Val Asp Asp  
825 830 835

caa tcc act cgc ttg ggt act att cgt gga ctg ttt gag ttc agc acg  
2659

Gln Ser Thr Arg Leu Gly Thr Ile Arg Gly Leu Phe Glu Phe Ser Thr  
840 845 850

gac cgc aag cca att tcg gtg tct gag gtg gag ccg gtc agt gag atc  
2707

Asp Arg Lys Pro Ile Ser Val Ser Glu Val Glu Pro Val Ser Glu Ile  
855 860 865

gtg aag cgt ttc tcc act ggt gcg atg tct tat ggc tcg att tct gct  
2755

Val Lys Arg Phe Ser Thr Gly Ala Met Ser Tyr Gly Ser Ile Ser Ala  
870 875 880 885

gaa gcc cat gag gtc ttg gcc atc gcc atg aac cga ctg ggc ggt atg  
2803

Glu Ala His Glu Val Leu Ala Ile Ala Met Asn Arg Leu Gly Gly Met  
890 895 900

tcc aac tcc ggc gaa ggt ggc gag gac gcc cgc cga ttt gat gtg gaa  
2851

Ser Asn Ser Gly Glu Gly Gly Glu Asp Ala Arg Arg Phe Asp Val Glu  
905 910 915

ccc aac ggt gac tgg aag cgc tct gcc att aag cag gtg gcc tcg gga  
2899

Pro Asn Gly Asp Trp Lys Arg Ser Ala Ile Lys Gln Val Ala Ser Gly  
920 925 930

cgt ttc ggc gtg acc agc cac tac ttg aac aac tgc acc gat att cag  
2947

Arg Phe Gly Val Thr Ser His Tyr Leu Asn Asn Cys Thr Asp Ile Gln  
935 940 945

atc aag atg gca cag ggc gca aag ccc ggt gaa ggt ggc cag ctg cca  
2995

Ile Lys Met Ala Gln Gly Ala Lys Pro Gly Glu Gly Gly Gln Leu Pro  
950 955 960 965

cca aac aag gtg tac cca tgg gtt gca gaa gtc cgc atc acc acc cca  
3043

Pro Asn Lys Val Tyr Pro Trp Val Ala Glu Val Arg Ile Thr Thr Pro  
970 975 980

ggc gtt ggt ctg att tcc cct cca cca cac cac gat att tac tcc att  
3091

Gly Val Gly Leu Ile Ser Pro Pro Pro His His Asp Ile Tyr Ser Ile  
985 990 995

aag acg ttg atc gtg ctg tcg gat cgt gaa tct gat gag cgc atg gca  
1987

Lys Thr Leu Ile Val Leu Ser Asp Arg Glu Ser Asp Glu Arg Met Ala  
615 620 625

cct atc cct gcg ctg ctg ctg act tcc gct gtg cat cag tac ttg gtg  
2035

Pro Ile Pro Ala Leu Leu Leu Thr Ser Ala Val His Gln Tyr Leu Val  
630 635 640 645

cag caa cgt acc cgt acc cag tgc tcc ctg gtg gtg gaa tcc ggc gat  
2083

Gln Gln Arg Thr Arg Thr Gln Cys Ser Leu Val Val Glu Ser Gly Asp  
650 655 660

gcc cgc gag gtt cat cac ctg gcg atg ctc att ggt ttt ggt gcc gat  
2131

Ala Arg Glu Val His His Leu Ala Met Leu Ile Gly Phe Gly Ala Asp  
665 670 675

gcg atc aac ccg tac atg gca ttt gaa acc atc gat gag ctg cgc atg  
2179

Ala Ile Asn Pro Tyr Met Ala Phe Glu Thr Ile Asp Glu Leu Arg Met  
680 685 690

aag ggt cag ttg ggt gat ctt tct ttg gat gag gca tcc cga aac tac  
2227

Lys Gly Gln Leu Gly Asp Leu Ser Leu Asp Glu Ala Ser Arg Asn Tyr  
695 700 705

atc aag gca gcc acc act ggt gtg ctg aag gtg atg tcc aag atg ggc  
2275

Ile Lys Ala Ala Thr Thr Gly Val Leu Lys Val Met Ser Lys Met Gly  
710 715 720 725

att gca acg gtg tct tcg tac cgt ggc gcg cag ctt gcc gat gtc act  
2323

Ile Ala Thr Val Ser Ser Tyr Arg Gly Ala Gln Leu Ala Asp Val Thr  
730 735 740

ggt ctg cac cag gat ctc ctg gac aac tac ttc ggt ggt att gct tca  
2371

Gly Leu His Gln Asp Leu Leu Asp Asn Tyr Phe Gly Gly Ile Ala Ser  
745 750 755

cca att tct ggc atc ggt ctg gat gaa gtt gca gct gac gta gaa gct  
2419

Pro Ile Ser Gly Ile Gly Leu Asp Glu Val Ala Ala Asp Val Glu Ala  
760 765 770

cgt cac cgc agc gca ttt ttg cca cgc cct gaa gag cac gct cac cgt  
2467

Arg His Arg Ser Ala Phe Leu Pro Arg Pro Glu Glu His Ala His Arg  
775 780 785

gaa ttg gat ttg ggt ggt gaa tac aag tgg cgc cgc gaa ggt gaa tac  
2515

Glu Leu Asp Leu Gly Gly Glu Tyr Lys Trp Arg Arg Glu Gly Glu Tyr  
790 795 800 805



agc gaa gcg cag cca tat ggt gag tgg att cgc gat aat ttt gtg cat  
1411

Ser Glu Ala Gln Pro Tyr Gly Glu Trp Ile Arg Asp Asn Phe Val His  
425 430 435

ctg gat cgt ctg cct cag aca cgc tac aac tac atg gcg cac tct cgt  
1459

Leu Asp Arg Leu Pro Gln Thr Arg Tyr Asn Tyr Met Ala His Ser Arg  
440 445 450

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1507

Ala Val Leu Arg Gln Arg Val Phe Gly Ile Thr Glu Glu Asp Val Asp  
455 460 465

ttg ttg ctg ctg ccg atg gcc cgc cag ggt gct gag gcg att ggt tcc  
1555

Leu Leu Leu Leu Pro Met Ala Arg Gln Gly Ala Glu Ala Ile Gly Ser  
470 475 480 485

atg ggt tcg gat acg cca att gcg gcg cta tcc cag cga cca cgc atg  
1603

Met Gly Ser Asp Thr Pro Ile Ala Ala Leu Ser Gln Arg Pro Arg Met  
490 495 500

ctt tat gat ttc ttc gcg cag cgc ttt gct cag gtg aca aac cca ccg  
1651

Leu Tyr Asp Phe Phe Ala Gln Arg Phe Ala Gln Val Thr Asn Pro Pro  
505 510 515

ttg gac tct atc cgc gaa aag cct gtg acc agc atg ttc act ttg ttg  
1699

Leu Asp Ser Ile Arg Glu Lys Pro Val Thr Ser Met Phe Thr Leu Leu  
520 525 530

ggt gcg cag tct gac gtg ctc aat ccg ggt cct gat gcg gcg cga cgt  
1747

Gly Ala Gln Ser Asp Val Leu Asn Pro Gly Pro Asp Ala Ala Arg Arg  
535 540 545

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1795

Ile Arg Leu Glu Ser Pro Ile Ile Asp Asn His Glu Leu Ala Thr Leu  
550 555 560 565

atc aat gcc aac gcg cat ggt gag tgg gat tcc ttt ggt gct gct gta  
1843

Ile Asn Ala Asn Ala His Gly Glu Trp Asp Ser Phe Gly Ala Ala Val  
570 575 580

att tct ggt ttg tac cca gtg gct cac cat ggt gcc ggc atg aag gct  
1891

Ile Ser Gly Leu Tyr Pro Val Ala His His Gly Ala Gly Met Lys Ala  
585 590 595

gcg att gct cgt gtg cgc cgc gag gtt tct gaa gca atc cgc aat ggc  
1939

Ala Ile Ala Arg Val Arg Arg Glu Val Ser Glu Ala Ile Arg Asn Gly  
600 605 610

200	205	210	
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Ser Ala Ile Ala Ile Val His	Ser Arg Phe Ser Thr Asn Thr Phe Pro		
215	220	225	
agc tgg ccg ctg gcg cac ccg tac cgt ttc gtt gcc cac aac ggt gag			835
Ser Trp Pro Leu Ala His Pro Tyr Arg Phe Val Ala His Asn Gly Glu			
230	235	240	245
atc aac act gtg cgt ggc aat gaa aac tgg atg cgc gcc cgc gag gcg			883
Ile Asn Thr Val Arg Gly Asn Glu Asn Trp Met Arg Ala Arg Glu Ala			
250	255	260	
ctt atc aaa aac gac aag ctg ggc aat ttg agc agc gtg ctg cct atc			931
Leu Ile Lys Asn Asp Lys Leu Gly Asn Leu Ser Ser Val Leu Pro Ile			
265	270	275	
tgc acc ccg gag ggc tcg gat acc gcg cgt ttc gac gag gct ttg gag			979
Cys Thr Pro Glu Gly Ser Asp Thr Ala Arg Phe Asp Glu Ala Leu Glu			
280	285	290	
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1027			
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295	300	305	
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310	315	320	325
gat ttc tac gaa tac cac tct tgt ctg atg gag cca tgg gat ggt cct			
1123			
Asp Phe Tyr Glu Tyr His Ser Cys Leu Met Glu Pro Trp Asp Gly Pro			
330	335	340	
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1171			
Ala Ala Leu Ala Phe Thr Asp Gly Arg Phe Val Gly Ala Val Leu Asp			
345	350	355	
cgt aat ggc ctg cga cct ggg cga atc acc att act gat tcg ggt ttg			
1219			
Arg Asn Gly Leu Arg Pro Gly Arg Ile Thr Ile Thr Asp Ser Gly Leu			
360	365	370	
gtt gtg atg gct tct gaa tcg gga gtg ttg gac ttg agg gag gag agc			
1267			
Val Val Met Ala Ser Glu Ser Gly Val Leu Asp Leu Arg Glu Glu Ser			
375	380	385	
gtc gta aag cgt act cgc gta cag cct gga cgc atg ttc ctt gtt gac			
1315			
Val Val Lys Arg Thr Arg Val Gln Pro Gly Arg Met Phe Leu Val Asp			
390	395	400	405
act gcc gag ggc cgc atc gtt gaa gac gag gaa atc aag cag aaa tta			
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                                   Met Lys Pro Gln Gly
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Leu Tyr Asn Pro Ala His Glu His Asp Ala Cys Gly Val Ala Phe Ile
                                   10      15      20

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Ala Asp Ile His Gly Arg Pro Ser Arg Ser Ile Val Asp Arg Ala Leu
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gag gcg ctt cgc aac att gac cac cga ggt gcc gcc ggt gca gag aag 259
Glu Ala Leu Arg Asn Ile Asp His Arg Gly Ala Ala Gly Ala Glu Lys
                                   40      45      50

aac act ggc gat ggt gcg ggc atc ctc atg cag att ccg gac ggc ttt 307
Asn Thr Gly Asp Gly Ala Gly Ile Leu Met Gln Ile Pro Asp Gly Phe
                                   55      60      65

tat cgt gaa gta tct ggc att gag ctt cct gag gca ggg gag tat gcc 355
Tyr Arg Glu Val Ser Gly Ile Glu Leu Pro Glu Ala Gly Glu Tyr Ala
                                   70      75      80      85

act ggt att gcg ttc ttg cct cgc ggt cgc atg gcg atg atg gat gct 403
Thr Gly Ile Ala Phe Leu Pro Arg Gly Arg Met Ala Met Met Asp Ala
                                   90      95      100

cag aag gaa att gag cgc atc gca aag caa gaa ggt gcc gat gtg ctt 451
Gln Lys Glu Ile Glu Arg Ile Ala Lys Gln Glu Gly Ala Asp Val Leu
                                   105      110      115

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Gly Trp Arg Met Val Pro Phe Asp Ser Arg Asp Leu Gly Ser Met Ala
                                   120      125      130

gag gag gcg atg cct agt ttc gcg cag att ttc ctt act gtg cct gga 547
Glu Glu Ala Met Pro Ser Phe Ala Gln Ile Phe Leu Thr Val Pro Gly
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aaa tct ggt gaa gat ctt gac cgt gtg atg ttc ttt atc cgt aag cgt 595
Lys Ser Gly Glu Asp Leu Asp Arg Val Met Phe Phe Ile Arg Lys Arg
                                   150      155      160      165

tgt gag cgt gag ctg ggc acc acc aat ggt cgc gat acg gtg tat ttc 643
Cys Glu Arg Glu Leu Gly Thr Thr Asn Gly Arg Asp Thr Val Tyr Phe
                                   170      175      180

ccg tcg cta tct tca cgc acc atc att tac aaa ggc atg ttg acc act 691
Pro Ser Leu Ser Ser Arg Thr Ile Ile Tyr Lys Gly Met Leu Thr Thr
                                   185      190      195

ctg cag ctt gag ggc ttc ttt gag gat ctg ggt gat gct cgc ctg gag 739
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                1                      5                      10

gat cct tac cgc atg gtt cag cag ctg cgc cgc aag ctc tct cgc ttc 161
Asp Pro Tyr Arg Met Val Gln Gln Leu Arg Arg Lys Leu Ser Arg Phe
                15                      20                      25

gtc gag cag aag tgg aag cgc cag ccg gtc atc atg cca acc gtc att 209
Val Glu Gln Lys Trp Lys Arg Gln Pro Val Ile Met Pro Thr Val Ile
                30                      35                      40

ccg atg act gcg gaa acc acg cac atc ggt gac gat gag gtt cgc gct 257
Pro Met Thr Ala Glu Thr Thr His Ile Gly Asp Asp Glu Val Arg Ala
                45                      50                      55

tca cgc gag tcc ctg taaaagcatt tcgcttttcg acg 295
Ser Arg Glu Ser Leu
        60

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<210> 70
<211> 63
<212> PRT
<213> Corynebacterium glutamicum
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<400> 70
Met Asn Asp Leu Ala Ala Glu Gly Glu Asn Asp Pro Tyr Arg Met Val
  1                               10                      15

Gln Gln Leu Arg Arg Lys Leu Ser Arg Phe Val Glu Gln Lys Trp Lys
      20                      25                      30

Arg Gln Pro Val Ile Met Pro Thr Val Ile Pro Met Thr Ala Glu Thr
      35                      40                      45

Thr His Ile Gly Asp Asp Glu Val Arg Ala Ser Arg Glu Ser Leu
      50                      55                      60

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<210> 71
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<212> DNA
<213> Corynebacterium glutamicum
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Gln Ser Leu Val Ala Met Leu Pro Met Leu Ile Gly Asn Val Val Lys						
	165			170		175
Leu Val Leu Thr Leu Val Ile Met Leu Ala Ile Ser Pro Pro Leu Thr						
	180			185		190
Ile Ile Ala Ala Val Leu Val Pro Leu Leu Leu Trp Ala Val Ala Tyr						
	195			200		205
Ser Arg Lys Ala Leu Phe Ala Ser Thr Trp Ser Ala Gln Gln Lys Ala						
	210			215		220
Ala Asp Leu Thr Thr His Val Glu Glu Thr Val Thr Gly Ile Arg Val						
	225			230		240
Val Lys Ala Phe Ala Gln Glu Asp Arg Glu Thr Asp Lys Leu Asp Leu						
		245		250		255
Thr Ala Arg Glu Leu Phe Ala Gln Arg Met Arg Thr Ala Arg Leu Thr						
		260		265		270
Ala Lys Phe Ile Pro Met Val Glu Gln Leu Pro Gln Leu Ala Leu Val						
		275		280		285
Val Asn Ile Val Gly Gly Gly Tyr Leu Ala Met Thr Gly His Ile Thr						
		290		295		300
Val Gly Thr Phe Val Ala Phe Ser Ser Tyr Leu Thr Ser Leu Ser Ala						
		305		310		315
Val Ala Arg Ser Leu Ser Gly Met Leu Met Arg Val Gln Leu Ala Leu						
		325		330		335
Ser Ser Val Glu Arg Ile Phe Glu Val Ile Asp Leu Gln Pro Glu Arg						
		340		345		350
Thr Asp Pro Ala His Pro Leu Ser Leu Pro Asp Thr Pro Leu Gly Leu						
		355		360		365
Ser Phe Asn Asn Val Asp Phe Arg Gly Ile Leu Asn Gly Phe Glu Leu						
		370		375		380
Gly Val Gln Ala Gly Glu Thr Val Val Leu Val Gly Pro Pro Gly Ser						
		385		390		395
Gly Lys Thr Met Ala Val Gln Leu Ala Gly Asn Phe Tyr Gln Pro Asp						
		405		410		415
Ser Gly His Ile Ala Phe Asp Ser Asn Gly His Arg Thr Arg Phe Asp						
		420		425		430
Asp Leu Thr His Ser Asp Ile Arg Arg Asn Leu Ile Ala Val Phe Asp						
		435		440		445
Glu Pro Phe Leu Tyr Ser Ser Ser Ile Pro Arg Glu His Leu Asp Gly						
		450		455		460
Phe Gly Cys Gln						
465						

Glu Thr Val Val Leu Val Gly Pro Pro Gly Ser Gly Lys Thr Met Ala  
 390 395 400 405  
 gtg cag ctt gct gga aac ttt tat caa cca gac agc ggc cac atc gcc  
 1363  
 Val Gln Leu Ala Gly Asn Phe Tyr Gln Pro Asp Ser Gly His Ile Ala  
 410 415 420  
 ttt gat agc aac ggc cat cgc act cgc ttc gac gac ctc acc cac agc  
 1411  
 Phe Asp Ser Asn Gly His Arg Thr Arg Phe Asp Asp Leu Thr His Ser  
 425 430 435  
 gat atc cgc agg aat ctc atc gcg gtt ttt gat gag ccg ttc ttg tac  
 1459  
 Asp Ile Arg Arg Asn Leu Ile Ala Val Phe Asp Glu Pro Phe Leu Tyr  
 440 445 450  
 tcc tcc tcc ata ccg cga gaa cat ctc gat ggg ttt gga tgt cag  
 1504  
 Ser Ser Ser Ile Pro Arg Glu His Leu Asp Gly Phe Gly Cys Gln  
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 tgatgagcag atcgaacacg cag  
 1527

<210> 68  
 <211> 468  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 68  
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 Pro Glu Lys Pro Gln Arg Ile Arg Gln Leu Ile Ser Val Ala Trp Gln  
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 Arg Pro Trp Leu Thr Ser Phe Thr Val Ile Ser Ala Leu Ala Ala Thr  
 35 40 45  
 Leu Phe Glu Leu Thr Leu Pro Leu Leu Thr Gly Gly Ala Ile Asp Ile  
 50 55 60  
 Ala Leu Gly Asn Thr Gly Asp Thr Leu Thr Thr Asp Leu Leu Asp Arg  
 65 70 75 80  
 Phe Thr Pro Ser Gly Leu Ser Val Leu Thr Ser Val Ile Ala Leu Ile  
 85 90 95  
 Val Leu Leu Ala Leu Leu Arg Tyr Ala Ser Gln Phe Gly Arg Arg Tyr  
 100 105 110  
 Thr Ala Gly Lys Leu Ser Met Gly Val Gln His Asp Val Arg Leu Lys  
 115 120 125  
 Thr Met Arg Ser Leu Gln Asn Leu Asp Gly Pro Gly Gln Asp Ser Ile  
 130 135 140  
 Arg Thr Gly Gln Val Val Ser Arg Ser Ile Ser Asp Ile Asn Met Val

gtg atc atg ctg gct att tcc ccg ccg ctg acc atc atc gct gca gtg 691  
 Val Ile Met Leu Ala Ile Ser Pro Pro Leu Thr Ile Ile Ala Ala Val  
 185 190 195

ttg gtg cct ttg ctg ttg tgg gcc gtg gcc tat tcg cga aaa gcg ctt 739  
 Leu Val Pro Leu Leu Leu Trp Ala Val Ala Tyr Ser Arg Lys Ala Leu  
 200 205 210

ttt gcg tcc acg tgg tcg gcc cag caa aag gct gcg gat ctg acc act 787  
 Phe Ala Ser Thr Trp Ser Ala Gln Gln Lys Ala Ala Asp Leu Thr Thr  
 215 220 225

cat gtg gaa gaa act gtc acg ggt atc cgc gtg gtc aag gca ttt gcg 835  
 His Val Glu Glu Thr Val Thr Gly Ile Arg Val Val Lys Ala Phe Ala  
 230 235 240 245

cag gaa gac cgc gag acc gac aaa ttg gat ctc acc gca cgt gag tta 883  
 Gln Glu Asp Arg Glu Thr Asp Lys Leu Asp Leu Thr Ala Arg Glu Leu  
 250 255 260

ttt gcc cag cgc atg cgc act gca cgt ctg acg gca aag ttc atc ccc 931  
 Phe Ala Gln Arg Met Arg Thr Ala Arg Leu Thr Ala Lys Phe Ile Pro  
 265 270 275

atg gtt gag cag ctt ccg cag ctt gct ttg gtg gtc aac att gtt ggc 979  
 Met Val Glu Gln Leu Pro Gln Leu Ala Leu Val Val Asn Ile Val Gly  
 280 285 290

ggt ggc tat ttg gcc atg act ggt cac atc acg gtg ggc acg ttt gtg  
 1027  
 Gly Gly Tyr Leu Ala Met Thr Gly His Ile Thr Val Gly Thr Phe Val  
 295 300 305

gcg ttt tct tcc tat ctc act agc ttg tcg gcg gtg gct agg tcc ctg  
 1075  
 Ala Phe Ser Ser Tyr Leu Thr Ser Leu Ser Ala Val Ala Arg Ser Leu  
 310 315 320 325

tcg ggc atg ctc atg cgc gtg cag ttg gcg ctg tct tct gtg gag cgc  
 1123  
 Ser Gly Met Leu Met Arg Val Gln Leu Ala Leu Ser Ser Val Glu Arg  
 330 335 340

atc ttt gaa gtc att gat ctt cag cct gaa cgc acc gat cct gca cac  
 1171  
 Ile Phe Glu Val Ile Asp Leu Gln Pro Glu Arg Thr Asp Pro Ala His  
 345 350 355

ccc ctg tca ctt ccc gac act ccc ctg ggt ctg tcg ttc aac aac gta  
 1219  
 Pro Leu Ser Leu Pro Asp Thr Pro Leu Gly Leu Ser Phe Asn Asn Val  
 360 365 370

gat ttc cgt ggg att ctc aac ggt ttt gag ctg ggt gtt cag gcc ggt  
 1267  
 Asp Phe Arg Gly Ile Leu Asn Gly Phe Glu Leu Gly Val Gln Ala Gly  
 375 380 385

gaa acc gtt gtg ttg gtg ggc cct cca ggt tca ggc aag acc atg gct  
 1315

<400> 67																		60
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tactccccca acagggtcaa aaatactgaa aggctcacgc																		115
Met Lys Thr Glu Gln																		
1 5																		
tcc caa aaa gca caa tta gcc cct aag aaa gca cct gaa aag cca caa																		163
Ser Gln Lys Ala Gln Leu Ala Pro Lys Lys Ala Pro Glu Lys Pro Gln																		
10 15 20																		
cgc atc cgc caa ctt att tcc gtg gcg tgg cag cga cct tgg ctc acc																		211
Arg Ile Arg Gln Leu Ile Ser Val Ala Trp Gln Arg Pro Trp Leu Thr																		
25 30 35																		
tca ttc acc gta atc agc gct tta gct gca acg ttg ttt gaa ctt aca																		259
Ser Phe Thr Val Ile Ser Ala Leu Ala Ala Thr Leu Phe Glu Leu Thr																		
40 45 50																		
ctt cct ctt ttg acc ggt ggc gcc atc gat atc gcg ctc gga aat acc																		307
Leu Pro Leu Leu Thr Gly Gly Ala Ile Asp Ile Ala Leu Gly Asn Thr																		
55 60 65																		
gga gat act tta acc act gac ctg ctg gac cgg ttc act ccg agt gga																		355
Gly Asp Thr Leu Thr Thr Asp Leu Leu Asp Arg Phe Thr Pro Ser Gly																		
70 75 80 85																		
tta agc gtg ttg acc agc gtc att gcc ctt atc gtg ctt ctc gcg ttg																		403
Leu Ser Val Leu Thr Ser Val Ile Ala Leu Ile Val Leu Leu Ala Leu																		
90 95 100																		
ctt cgc tat gcc agt caa ttt gga cgg cga tac acc gca ggc aag ctc																		451
Leu Arg Tyr Ala Ser Gln Phe Gly Arg Arg Tyr Thr Ala Gly Lys Leu																		
105 110 115																		
agc atg ggg gta cag cat gat gtc cgg ctt aaa acg atg cgc tca ttg																		499
Ser Met Gly Val Gln His Asp Val Arg Leu Lys Thr Met Arg Ser Leu																		
120 125 130																		
cag aac ctc gat ggg cca ggt cag gac tct att cgc aca ggc caa gta																		547
Gln Asn Leu Asp Gly Pro Gly Gln Asp Ser Ile Arg Thr Gly Gln Val																		
135 140 145																		
gtc agt cgg tcc att tcg gat atc aac atg gtg caa agc ctt gtg gcg																		595
Val Ser Arg Ser Ile Ser Asp Ile Asn Met Val Gln Ser Leu Val Ala																		
150 155 160 165																		
atg ttg ccg atg ttg atc gga aat gtg gtc aag ctt gtg ctc act ttg																		643
Met Leu Pro Met Leu Ile Gly Asn Val Val Lys Leu Val Leu Thr Leu																		
170 175 180																		



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Leu Leu Ile Arg Asn Glu Glu Arg Glu Val Phe Val Asp Leu Phe Glu
      25              30              35

caa atg cct gca ccg ttc gga ctc atc cgt tac ggc gtt gct cca gac   259
Gln Met Pro Ala Pro Phe Gly Leu Ile Arg Tyr Gly Val Ala Pro Asp
      40              45              50

cac cca cgc atc aag ggc atc gtt aag tcc ctg cac aac gtg ttg gac   307
His Pro Arg Ile Lys Gly Ile Val Lys Ser Leu His Asn Val Leu Asp
      55              60              65

aag cca cgc ctg cgc ctg ctc ggt aac att gaa atc ggc aaa gac atc   355
Lys Pro Arg Leu Arg Leu Leu Gly Asn Ile Glu Ile Gly Lys Asp Ile
      70              75              80              85

acc gtc gaa gaa ctc cgc gac tac tac gat gca gtc gtg ttc tcc acc   403
Thr Val Glu Glu Leu Arg Asp Tyr Tyr Asp Ala Val Val Phe Ser Thr
      90              95              100

ggc gca gtt gca gac cgc gac ctc aac atc ccc gga att gaa gca gaa   451
Gly Ala Val Ala Asp Arg Asp Leu Asn Ile Pro Gly Ile Glu Ala Glu
      105              110              115

ggc tcc ttc ggt gcc ggc gag ttc gtt ggc ttc tac gac ggc aac cca   499
Gly Ser Phe Gly Ala Gly Glu Phe Val Gly Phe Tyr Asp Gly Asn Pro
      120              125              130

cgc ttc gag cgc tcc tgg gat ctg tct gca cag tcc gtc gct gtt atc   547
Arg Phe Glu Arg Ser Trp Asp Leu Ser Ala Gln Ser Val Ala Val Ile
      135              140              145

ggc gtt ggt aac gtc ggc ctc gac gta gcc cgc atc ctg gct aag aca   595
Gly Val Gly Asn Val Gly Leu Asp Val Ala Arg Ile Leu Ala Lys Thr
      150              155              160              165

ggc gac gag ctc aaa gtc acc gaa att tcc gac aac gtc tac gac tcc   643
Gly Asp Glu Leu Lys Val Thr Glu Ile Ser Asp Asn Val Tyr Asp Ser
      170              175              180

ctc aaa gaa aac aag gyc wct gaa gtg cac gtt ttc gga cgt cgg tgg   691
Leu Lys Glu Asn Lys Xaa Xaa Glu Val His Val Phe Gly Arg Arg Trp
      185              190              195

ccc agc aca ggt caa gtt cac ccc aca gga act maa aga act cgr cca   739
Pro Ser Thr Gly Gln Val His Pro Thr Gly Thr Xaa Arg Thr Xaa Pro
      200              205              210

ctc ccc cac cat caa cgt ggt tgt tgatccagaa gacatcgact acg       786
Leu Pro His His Gln Arg Gly Cys
      215              220

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&lt;210&gt; 82

&lt;211&gt; 221

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 82

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<210> 81
<211> 786
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
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<222> (101)..(763)  
<223> FRXA00075
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tgtttccata aaagggctca cgaaaggcaa cttcaaacac atg aca act ccc ctg 115  
Met Thr Thr Pro Leu  
1 5

cgc gta gcc gtc atc gga gct ggc cct gct ggc att tac gca tcc gac 163  
 Arg Val Ala Val Ile Gly Ala Gly Pro Ala Gly Ile Tyr Ala Ser Asp  
 10 15 20

ctc ctc atc cgc aat gaa gag cgc gaa gtg ttc gtt gac ctt ttc gag 211

cca gca att gtc taaattgttt taacgcgtga agc

1494

Pro Ala Ile Val

455

<210> 80

<211> 457

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 80

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20 25 30

Val Asp Leu Phe Glu Gln Met Pro Ala Pro Phe Gly Leu Ile Arg Tyr  
35 40 45

Gly Val Ala Pro Asp His Pro Arg Ile Lys Gly Ile Val Lys Ser Leu  
50 55 60

His Asn Val Leu Asp Lys Pro Arg Leu Arg Leu Leu Gly Asn Ile Glu  
65 70 75 80

Ile Gly Lys Asp Ile Thr Val Glu Glu Leu Arg Asp Tyr Tyr Asp Ala  
85 90 95

Val Val Phe Ser Thr Gly Ala Val Ala Asp Arg Asp Leu Asn Ile Pro  
100 105 110

Gly Ile Glu Ala Glu Gly Ser Phe Gly Ala Gly Glu Phe Val Gly Phe  
115 120 125

Tyr Asp Gly Asn Pro Arg Phe Glu Arg Ser Trp Asp Leu Ser Ala Gln  
130 135 140

Ser Val Ala Val Ile Gly Val Gly Asn Val Gly Leu Asp Val Ala Arg  
145 150 155 160

Ile Leu Ala Lys Thr Gly Asp Glu Leu Lys Val Thr Glu Ile Ser Asp  
165 170 175

Asn Val Tyr Asp Ser Leu Lys Glu Asn Lys Ala Thr Glu Val His Val  
180 185 190

Phe Gly Arg Arg Gly Pro Ala Gln Val Lys Phe Thr Pro Gln Glu Leu  
195 200 205

Lys Glu Leu Asp His Ser Pro Thr Ile Asn Val Val Val Asp Pro Glu  
210 215 220

Asp Ile Asp Tyr Asp Gly Ala Ser Glu Glu Ala Arg Arg Ala Ser Lys  
225 230 235 240

Ser Gln Asp Leu Val Cys Gln Ile Leu Glu Gln Tyr Ala Ile Arg Glu  
245 250 255

Pro Lys Asp Ala Pro His Thr Leu Gln Ile His Leu Phe Glu Asn Pro

Cys Gln Ile Leu Glu Gln Tyr Ala Ile Arg Glu Pro Lys Asp Ala Pro  
 250 255 260

cac acc ctg cag atc cac ctc ttt gaa aac cca gtt gag gtt ctt caa 931  
 His Thr Leu Gln Ile His Leu Phe Glu Asn Pro Val Glu Val Leu Gln  
 265 270 275

aag gac ggc aag gtt gtt ggc ctg cgc acc gaa cgc acc tca ctt gat 979  
 Lys Asp Gly Lys Val Val Gly Leu Arg Thr Glu Arg Thr Ser Leu Asp  
 280 285 290

ggc aac ggc ggc gta aac gga acc ggc gaa ttc aag gac tgg cca gtc  
 1027  
 Gly Asn Gly Gly Val Asn Gly Thr Gly Glu Phe Lys Asp Trp Pro Val  
 295 300 305

cag gct gtc tac cgc gca gtc ggc tac aag tcc gac ccc atc gac ggc  
 1075  
 Gln Ala Val Tyr Arg Ala Val Gly Tyr Lys Ser Asp Pro Ile Asp Gly  
 310 315 320 325

gtc cca ttc gat gag aac aag cac gtc atc cct aat gac ggc gga cat  
 1123  
 Val Pro Phe Asp Glu Asn Lys His Val Ile Pro Asn Asp Gly Gly His  
 330 335 340

gtc ctc acc gct cca ggc gca gaa cca gta cca ggc ctc tat gca acc  
 1171  
 Val Leu Thr Ala Pro Gly Ala Glu Pro Val Pro Gly Leu Tyr Ala Thr  
 345 350 355

ggc tgg atc aag cgt gga cca atc ggt cta atc ggc aac acc aag tcc  
 1219  
 Gly Trp Ile Lys Arg Gly Pro Ile Gly Leu Ile Gly Asn Thr Lys Ser  
 360 365 370

gac gcc aag gaa acc acc gac atc ctc atc aag gat gcc gtc gcc ggt  
 1267  
 Asp Ala Lys Glu Thr Thr Asp Ile Leu Ile Lys Asp Ala Val Ala Gly  
 375 380 385

gta ctt gaa gct cca aag cac cag ggc gaa gaa gcc atc atc gag ctt  
 1315  
 Val Leu Glu Ala Pro Lys His Gln Gly Glu Glu Ala Ile Ile Glu Leu  
 390 395 400 405

ctc gat tcc cgc aac atc cca ttc acc acc tgg gaa ggc tgg tac aaa  
 1363  
 Leu Asp Ser Arg Asn Ile Pro Phe Thr Thr Trp Glu Gly Trp Tyr Lys  
 410 415 420

ctc gac gca gca gag cgc gca ctc ggt gaa gcc gaa ggc cgc gag cgc  
 1411  
 Leu Asp Ala Ala Glu Arg Ala Leu Gly Glu Ala Glu Gly Arg Glu Arg  
 425 430 435

aag aag att gtt gat tgg gaa gaa atg gtc cgc cag gcc cgc gaa gct  
 1459  
 Lys Lys Ile Val Asp Trp Glu Glu Met Val Arg Gln Ala Arg Glu Ala  
 440 445 450

cgc gta gcc gtc atc gga gct ggc cct gct ggc att tac gca tcc gac	163
Arg Val Ala Val Ile Gly Ala Gly Pro Ala Gly Ile Tyr Ala Ser Asp	
10 15 20	
ctc ctc atc cgc aat gaa gag cgc gaa gtg ttc gtt gac ctt ttc gag	211
Leu Leu Ile Arg Asn Glu Glu Arg Glu Val Phe Val Asp Leu Phe Glu	
25 30 35	
caa atg cct gca ccg ttc gga ctc atc cgt tac ggc gtt gct cca gac	259
Gln Met Pro Ala Pro Phe Gly Leu Ile Arg Tyr Gly Val Ala Pro Asp	
40 45 50	
cac cca cgc atc aag ggc atc gtt aag tcc ctg cac aac gtg ttg gac	307
His Pro Arg Ile Lys Gly Ile Val Lys Ser Leu His Asn Val Leu Asp	
55 60 65	
aag cca cgc ctg cgc ctg ctc ggt aac att gaa atc ggc aaa gac atc	355
Lys Pro Arg Leu Arg Leu Leu Gly Asn Ile Glu Ile Gly Lys Asp Ile	
70 75 80 85	
acc gtc gaa gaa ctc cgc gac tac tac gat gca gtc gtg ttc tcc acc	403
Thr Val Glu Glu Leu Arg Asp Tyr Tyr Asp Ala Val Val Phe Ser Thr	
90 95 100	
ggc gca gtt gca gac cgc gac ctc aac atc ccc gga att gaa gca gaa	451
Gly Ala Val Ala Asp Arg Asp Leu Asn Ile Pro Gly Ile Glu Ala Glu	
105 110 115	
ggc tcc ttc ggt gcc ggc gag ttc gtt ggc ttc tac gac ggc aac cca	499
Gly Ser Phe Gly Ala Gly Glu Phe Val Gly Phe Tyr Asp Gly Asn Pro	
120 125 130	
cgc ttc gag cgc tcc tgg gat ctg tct gca cag tcc gtc gct gtt atc	547
Arg Phe Glu Arg Ser Trp Asp Leu Ser Ala Gln Ser Val Ala Val Ile	
135 140 145	
ggc gtt ggt aac gtc ggc ctc gac gta gcc cgc atc ctg gct aag aca	595
Gly Val Gly Asn Val Gly Leu Asp Val Ala Arg Ile Leu Ala Lys Thr	
150 155 160 165	
ggc gac gag ctc aaa gtc acc gaa att tcc gac aac gtc tac gac tcc	643
Gly Asp Glu Leu Lys Val Thr Glu Ile Ser Asp Asn Val Tyr Asp Ser	
170 175 180	
ctc aaa gaa aac aag gcc act gaa gtg cac gtt ttc gga cgt cgt ggc	691
Leu Lys Glu Asn Lys Ala Thr Glu Val His Val Phe Gly Arg Arg Gly	
185 190 195	
cca gca cag gtc aag ttc acc cca cag gaa ctc aaa gaa ctc gac cac	739
Pro Ala Gln Val Lys Phe Thr Pro Gln Glu Leu Lys Glu Leu Asp His	
200 205 210	
tcc ccc acc atc aac gtg gtt gtt gat cca gaa gac atc gac tac gac	787
Ser Pro Thr Ile Asn Val Val Val Asp Pro Glu Asp Ile Asp Tyr Asp	
215 220 225	
ggc gcc tct gaa gaa gcc cgc cgc gca tcc aag tcc cag gac ctg gtc	835
Gly Ala Ser Glu Glu Ala Arg Arg Ala Ser Lys Ser Gln Asp Leu Val	
230 235 240 245	
tgc cag atc ctg gaa cag tac gca atc cgc gag cca aag gac gct ccg	883

Ile Thr Leu Asn Leu Gln Gly Cys Ala Gly Asn Ser Phe Gly Ala Phe  
65 70 75 80

Ile Pro Arg Gly Ile Thr Ile Asn Leu Thr Gly Asp Ala Asn Asp Phe  
85 90 95

Val Gly Lys Gly Leu Ser Gly Gly Lys Ile Val Ile Lys Pro Ser Ala  
100 105 110

Gln Ala Pro Lys Gln Leu Lys Asn Asn Pro Asn Ile Ile Ala Gly Asn  
115 120 125

Val Leu Gly Tyr Gly Ala Thr Ser Gly Glu Leu Phe Ile Arg Gly Gln  
130 135 140

Val Gly Glu Arg Phe Cys Val Arg Asn Ser Gly Ala Thr Ala Val Val  
145 150 155 160

Glu Gly Ile Gly Asn His Gly Cys Glu Tyr Met Thr Gly Gly Arg Val  
165 170 175

Leu Val Leu Gly Pro Val Gly Glu Asn Phe Gly Ala Gly Met Ser Gly  
180 185 190

Gly Ile Ala Tyr Leu Ala Asn Ser Pro Asp Leu Asn Gln Lys Ile Asn  
195 200 205

Gly Glu Leu Val Asp Val Val Pro Leu Ser Ala Asp Asp Leu Thr Trp  
210 215 220

Ala Asp Glu Leu Ile Ala Arg His Arg Glu Leu Thr Gly Ser Glu Thr  
225 230 235 240

Lys Leu Arg Ala Gln Asp Leu Val Lys Ile Met Pro Arg Asp Phe Gln  
245 250 255

Lys Val Leu Asn Ile Ile Glu Thr Ala His Ala Glu Gly Gln Asp Pro  
260 265 270

Ala Ile Lys Ile Met Glu Ala Val Ser  
275 280

<210> 79

<211> 1494

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1471)

<223> RXN00076

<400> 79

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Met Thr Thr Pro Leu

1

5

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Val Leu Gly Tyr Gly Ala Thr Ser Gly Glu Leu Phe Ile Arg Gly Gln  
130 135 140

gtc ggc gaa cgt ttc tgc gtc cgt aac tct ggc gcc acc gca gtg gtt 480  
Val Gly Glu Arg Phe Cys Val Arg Asn Ser Gly Ala Thr Ala Val Val  
145 150 155 160

gaa ggt atc gga aac cac ggt tgt gag tac atg act ggc ggc cga gtc 528  
Glu Gly Ile Gly Asn His Gly Cys Glu Tyr Met Thr Gly Gly Arg Val  
165 170 175

ctg gtt ttg ggc ccg gtt ggt gag aac ttt ggt gcc ggc atg tct ggt 576  
Leu Val Leu Gly Pro Val Gly Glu Asn Phe Gly Ala Gly Met Ser Gly  
180 185 190

ggc att gca tac ctg gct aat tcc ccg gac cta aac cag aag atc aat 624  
Gly Ile Ala Tyr Leu Ala Asn Ser Pro Asp Leu Asn Gln Lys Ile Asn  
195 200 205

ggc gaa ttg gtg gat gtt gtt cca ctg agc gct gac gat ctg acg tgg 672  
Gly Glu Leu Val Asp Val Val Pro Leu Ser Ala Asp Asp Leu Thr Trp  
210 215 220

gct gat gag ctc att gct cgc cac cgc gaa ctc acc gga tcc gag acc 720  
Ala Asp Glu Leu Ile Ala Arg His Arg Glu Leu Thr Gly Ser Glu Thr  
225 230 235 240

aag ctg cgt gca caa gat ttg gtg aaa atc atg ccg cgc gat ttc caa 768  
Lys Leu Arg Ala Gln Asp Leu Val Lys Ile Met Pro Arg Asp Phe Gln  
245 250 255

aaa gta ctc aac atc atc gaa acg gcc cac gct gag ggc caa gac cca 816  
Lys Val Leu Asn Ile Ile Glu Thr Ala His Ala Glu Gly Gln Asp Pro  
260 265 270

gca atc aag atc atg gag gca gtg agc taatggccga cccacaagga 863  
Ala Ile Lys Ile Met Glu Ala Val Ser  
275 280

ttc 866

&lt;210&gt; 78

&lt;211&gt; 281

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 78

His Ser Leu Glu Lys Ala Leu Asp Asn Ala Phe Ile Asp Lys Ala Ser  
1 5 10 15

Asp Thr Ile Thr Arg Ala Ala Ala Gly Val Glu Thr Ser Ile Val Ile  
20 25 30

Asp Ser Ser Ile Ser Asn Val Asn Arg Ser Val Gly Thr Met Leu Gly  
35 40 45

Ser Ala Val Ser Arg Val Ala Gly Ala Gln Gly Leu Pro Asp Gly Thr  
50 55 60

Pro Leu Val Val Glu Gly Cys Ile Met Met Arg Val Cys His Leu Asp  
 340 345 350

Thr Cys Pro Val Gly Ile Ala Thr Gln Asn Pro Asp Leu Arg Ser Lys  
 355 360 365

Phe Thr Gly Lys Ala Glu His Val Val Asn Phe Phe Thr Phe Ile Ala  
 370 375 380

Gln Glu Val Arg Glu Tyr Leu Ala Gln Leu Gly Phe Arg Ser Ile Asp  
 385 390 395 400

Glu Ala Val Gly Gln Ala Gln Val Leu Arg Lys Arg Ser Gly Ile Pro  
 405 410 415

Ala Asp Ser Arg Ala Ala His Leu Asp Leu Ser Pro Ile Phe Ile  
 420 425 430

<210> 77  
 <211> 866  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(843)  
 <223> FRXA00367

<400> 77

cac agc cta gaa aaa gcc ctg gac aac gca ttt att gat aag gct tcg	48
His Ser Leu Glu Lys Ala Leu Asp Asn Ala Phe Ile Asp Lys Ala Ser	
1 5 10 15	
gac acg atc acc cgt gcc gca gcg ggt gtg gaa acc agc att gtt att	96
Asp Thr Ile Thr Arg Ala Ala Ala Gly Val Glu Thr Ser Ile Val Ile	
20 25 30	
gat agc tcc atc agc aac gtc aac cgt tca gtt ggc acg atg ctg ggt	144
Asp Ser Ser Ile Ser Asn Val Asn Arg Ser Val Gly Thr Met Leu Gly	
35 40 45	
tct gca gtc agc cgc gtg gct ggt gcc caa ggt ttg cca gac ggc acc	192
Ser Ala Val Ser Arg Val Ala Gly Ala Gln Gly Leu Pro Asp Gly Thr	
50 55 60	
atc acc ttg aat ctt caa ggc tgc gcc ggt aac tcc ttt ggc gcg ttc	240
Ile Thr Leu Asn Leu Gln Gly Cys Ala Gly Asn Ser Phe Gly Ala Phe	
65 70 75 80	
atc cca cga ggc atc acc atc aac ctc acc ggc gat gcc aat gac ttt	288
Ile Pro Arg Gly Ile Thr Ile Asn Leu Thr Gly Asp Ala Asn Asp Phe	
85 90 95	
gtg ggc aag gga tta tct ggc gga aag att gtg atc aag cct tcc gct	336
Val Gly Lys Gly Leu Ser Gly Gly Lys Ile Val Ile Lys Pro Ser Ala	
100 105 110	
cag gct ccg aag cag ctg aag aac aat cca aat atc att gcc gga aac	384
Gln Ala Pro Lys Gln Leu Lys Asn Asn Pro Asn Ile Ile Ala Gly Asn	
115 120 125	



Glu Tyr Lys Trp Arg Arg Glu Gly Glu Tyr His Leu Phe Asn Pro Glu  
 20 25 30  
 Thr Ile Phe Lys Leu Gln His Ala Thr Arg Ser Gly Ser Tyr Glu Ile  
 35 40 45  
 Phe Lys Asp Tyr Thr Arg Lys Val Asp Asp Gln Ser Thr Arg Leu Gly  
 50 55 60  
 Thr Ile Arg Gly Leu Phe Glu Phe Ser Thr Asp Arg Lys Pro Ile Ser  
 65 70 75 80  
 Val Ser Glu Val Glu Pro Val Ser Glu Ile Val Lys Arg Phe Ser Thr  
 85 90 95  
 Gly Ala Met Ser Tyr Gly Ser Ile Ser Ala Glu Ala His Glu Val Leu  
 100 105 110  
 Ala Ile Ala Met Asn Arg Leu Gly Gly Met Ser Asn Ser Gly Glu Gly  
 115 120 125  
 Gly Glu Asp Ala Arg Arg Phe Asp Val Glu Pro Asn Gly Asp Trp Lys  
 130 135 140  
 Arg Ser Ala Ile Lys Gln Val Ala Ser Gly Arg Phe Gly Val Thr Ser  
 145 150 155 160  
 His Tyr Leu Asn Asn Cys Thr Asp Ile Gln Ile Lys Met Ala Gln Gly  
 165 170 175  
 Ala Lys Pro Gly Glu Gly Gly Gln Leu Pro Pro Asn Lys Val Tyr Pro  
 180 185 190  
 Trp Val Ala Glu Val Arg Ile Thr Thr Pro Gly Val Gly Leu Ile Ser  
 195 200 205  
 Pro Pro Pro His His Asp Ile Tyr Ser Ile Glu Asp Leu Ala Gln Leu  
 210 215 220  
 Ile His Asp Leu Lys Asn Ala Asn Pro Arg Ala Arg Ile His Val Lys  
 225 230 235 240  
 Leu Val Ala Glu Gln Gly Val Gly Thr Val Ala Ala Gly Val Ser Lys  
 245 250 255  
 Ala His Ala Asp Val Val Leu Ile Ser Gly His Asp Gly Gly Thr Gly  
 260 265 270  
 Ala Ser Pro Leu Thr Ser Leu Lys His Ala Gly Gly Pro Trp Glu Leu  
 275 280 285  
 Gly Leu Ala Glu Thr Gln Gln Thr Leu Leu Leu Asn Gly Leu Arg Asp  
 290 295 300  
 Arg Ile Arg Val Gln Cys Asp Gly Gln Leu Lys Thr Gly Arg Asp Val  
 305 310 315 320  
 Val Ile Ala Ala Leu Leu Gly Ala Glu Glu Phe Gly Phe Ala Thr Ala  
 325 330 335

Thr Gly Ala Ser Pro Leu Thr Ser Leu Lys His Ala Gly Gly Pro Trp  
 275 280 285  
 gag ttg ggc ttg gct gaa acc cag caa acg ttg ctg ctc aac ggc ctg 975  
 Glu Leu Gly Leu Ala Glu Thr Gln Gln Thr Leu Leu Leu Asn Gly Leu  
 290 295 300  
 cgc gat cgt att cgc gtg cag tgc gat ggt cag ctg aaa act ggc cga  
 1023  
 Arg Asp Arg Ile Arg Val Gln Cys Asp Gly Gln Leu Lys Thr Gly Arg  
 305 310 315  
 gac gtg gtt atc gca gct ctt ctc ggt gcc gaa gaa ttc ggt ttt gcc  
 1071  
 Asp Val Val Ile Ala Ala Leu Leu Gly Ala Glu Glu Phe Gly Phe Ala  
 320 325 330  
 acc gca ccg ctg gtg gtt gaa ggc tgc atc atg atg cgc gtc tgc cac  
 1119  
 Thr Ala Pro Leu Val Val Glu Gly Cys Ile Met Met Arg Val Cys His  
 335 340 345 350  
 ctg gac acc tgc ccg gtg ggt atc gct acc cag aac ccg gat ttg cgt  
 1167  
 Leu Asp Thr Cys Pro Val Gly Ile Ala Thr Gln Asn Pro Asp Leu Arg  
 355 360 365  
 tcc aag ttc acc ggc aag gct gaa cac gtg gtc aac ttc ttc acc ttc  
 1215  
 Ser Lys Phe Thr Gly Lys Ala Glu His Val Val Asn Phe Phe Thr Phe  
 370 375 380  
 atc gcc cag gaa gtc cgt gag tac ttg gca cag ctt ggt ttc cgc tct  
 1263  
 Ile Ala Gln Glu Val Arg Glu Tyr Leu Ala Gln Leu Gly Phe Arg Ser  
 385 390 395  
 att gat gaa gcc gtc gga caa gcc cag gtg ctg cgc aag cgt tcc gga  
 1311  
 Ile Asp Glu Ala Val Gly Gln Ala Gln Val Leu Arg Lys Arg Ser Gly  
 400 405 410  
 atc cca gct gat tcc cgc gca gca cac ctg gat ttg agc cca att ttc  
 1359  
 Ile Pro Ala Asp Ser Arg Ala Ala His Leu Asp Leu Ser Pro Ile Phe  
 415 420 425 430  
 atc  
 1362  
 Ile

<210> 76  
 <211> 431  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 76  
 Leu Pro Arg Pro Glu Glu His Ala His Arg Glu Leu Asp Leu Gly Gly  
 1 5 10 15

cca gaa acc atc ttc aag ctg cag cat gca acg cgt tct ggc agc tac	207
Pro Glu Thr Ile Phe Lys Leu Gln His Ala Thr Arg Ser Gly Ser Tyr	
35 40 45	
gag att ttc aag gat tac acc cgc aag gtt gat gat caa tcc act cgc	255
Glu Ile Phe Lys Asp Tyr Thr Arg Lys Val Asp Asp Gln Ser Thr Arg	
50 55 60	
ttg ggt act att cgt gga ctg ttt gag ttc agc acg gac cgc aag cca	303
Leu Gly Thr Ile Arg Gly Leu Phe Glu Phe Ser Thr Asp Arg Lys Pro	
65 70 75	
att tcg gtg tct gag gtg gag ccg gtc agt gag atc gtg aag cgt ttc	351
Ile Ser Val Ser Glu Val Glu Pro Val Ser Glu Ile Val Lys Arg Phe	
80 85 90	
tcc act ggt gcg atg tct tat ggc tcg att tct gct gaa gcc cat gag	399
Ser Thr Gly Ala Met Ser Tyr Gly Ser Ile Ser Ala Glu Ala His Glu	
95 100 105 110	
gtc ttg gcc atc gcc atg aac cga ctg ggc ggt atg tcc aac tcc ggc	447
Val Leu Ala Ile Ala Met Asn Arg Leu Gly Gly Met Ser Asn Ser Gly	
115 120 125	
gaa ggt ggc gag gac gcc cgc cga ttt gat gtg gaa ccc aac ggt gac	495
Glu Gly Gly Glu Asp Ala Arg Arg Phe Asp Val Glu Pro Asn Gly Asp	
130 135 140	
tgg aag cgc tct gcc att aag cag gtg gcc tcg gga cgt ttc ggc gtg	543
Trp Lys Arg Ser Ala Ile Lys Gln Val Ala Ser Gly Arg Phe Gly Val	
145 150 155	
acc agc cac tac ttg aac aac tgc acc gat att cag atc aag atg gca	591
Thr Ser His Tyr Leu Asn Asn Cys Thr Asp Ile Gln Ile Lys Met Ala	
160 165 170	
cag ggc gca aag ccc ggt gaa ggt ggc cag ctg cca cca aac aag gtg	639
Gln Gly Ala Lys Pro Gly Glu Gly Gly Gln Leu Pro Pro Asn Lys Val	
175 180 185 190	
tac cca tgg gtt gca gaa gtc cgc atc acc acc cca ggc gtt ggt ctg	687
Tyr Pro Trp Val Ala Glu Val Arg Ile Thr Thr Pro Gly Val Gly Leu	
195 200 205	
att tcc cct cca cca cac cac gat att tac tcc att gag gat ctg gct	735
Ile Ser Pro Pro Pro His His Asp Ile Tyr Ser Ile Glu Asp Leu Ala	
210 215 220	
cag ctg atc cac gac ctg aag aac gct aac cca cgc gca cga atc cac	783
Gln Leu Ile His Asp Leu Lys Asn Ala Asn Pro Arg Ala Arg Ile His	
225 230 235	
gtg aag cta gtg gca gaa caa ggc gtg ggc acc gtt gcc gca ggt gtg	831
Val Lys Leu Val Ala Glu Gln Gly Val Gly Thr Val Ala Ala Gly Val	
240 245 250	
tcc aaa gca cac gct gat gtg gtg ctt att tcc ggc cac gat ggc gga	879
Ser Lys Ala His Ala Asp Val Val Leu Ile Ser Gly His Asp Gly Gly	
255 260 265 270	
act ggc gca tct cct ttg acc tcc ctg aag cat gcc ggt ggt cca tgg	927

Met Phe Leu Val Asp Thr Ala Glu Gly Arg Ile Val Glu Asp Glu Glu  
 405 410 415

Ile Lys Gln Lys Leu Ser Glu Ala Gln Pro Tyr Gly Glu Trp Ile Arg  
 420 425 430

Asp Asn Phe Val His Leu Asp Arg Leu Pro Gln Thr Arg Tyr Asn Tyr  
 435 440 445

Met Ala His Ser Arg Ala Val Leu Arg Gln Arg Val Phe Gly Ile Thr  
 450 455 460

Glu Glu Asp Val Asp Leu Leu Leu Leu Pro Met Ala Arg Gln Gly Ala  
 465 470 475 480

Glu Ala Ile Gly Ser Met Gly Ser Asp Thr Pro Ile Ala Ala Leu Ser  
 485 490 495

Gln Arg Pro Arg Met Leu Tyr Asp Phe Phe Ala Gln Arg Phe Ala Gln  
 500 505 510

Val Thr Asn Pro Pro Leu Asp Ser Ile Arg Glu Lys Pro Val Thr Ser  
 515 520 525

Met Phe Thr Leu Leu Gly Ala Gln Ser Asp Val Leu Asn Pro Gly Pro  
 530 535 540

Asp Ala Ala Arg Arg Ile Arg Leu Glu Ser Pro Ile Ile Asp Asn His  
 545 550 555 560

Glu Leu Ala Thr Leu Ile Asn Ala Asn Ala His Gly Glu Trp Asp Ser  
 565 570 575

Phe Gly Ala Ala Val Ile Ser Gly Leu Tyr Pro Val Ala His His Gly  
 580 585 590

Ala Gly Met Lys Ala Ala Ile Ala Arg Val  
 595 600

<210> 75  
 <211> 1362  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (70)..(1362)  
 <223> FRXA00364

<400> 75  
 accaatttct ggcacgggtc tggatgaagt tgcagctgac gtagaaagct cgtcaccgca 60  
 gcgcattttttg cca cgc cct gaa gag cac gct cac cgt gaa ttg gat ttg 111  
 Leu Pro Arg Pro Glu Glu His Ala His Arg Glu Leu Asp Leu  
 1 5 10  
 ggt ggt gaa tac aag tgg cgc cgc gaa ggt gaa tac cac ctg ttc aac 159  
 Gly Gly Glu Tyr Lys Trp Arg Arg Glu Gly Glu Tyr His Leu Phe Asn  
 15 20 25 30

117

atg ggt tcg gat acg cca att gcg gcg cta tcc cag cga cca cgc atg  
1603

Met Gly Ser Asp Thr Pro Ile Ala Ala Leu Ser Gln Arg Pro Arg Met  
490 495 500

ctt tat gat ttc ttc gcg cag cgc ttt gct cag gtg aca aac cca ccg  
1651

Leu Tyr Asp Phe Phe Ala Gln Arg Phe Ala Gln Val Thr Asn Pro Pro  
505 510 515

ttg gac tct atc cgc gaa aag cct gtg acc agc atg ttc act ttg ttg  
1699

Leu Asp Ser Ile Arg Glu Lys Pro Val Thr Ser Met Phe Thr Leu Leu  
520 525 530

ggg gcg cag tct gac gtg ctc aat ccg ggt cct gat gcg gcg cga cgt  
1747

Gly Ala Gln Ser Asp Val Leu Asn Pro Gly Pro Asp Ala Ala Arg Arg  
535 540 545

att cgt ttg gaa tcg ccg atc att gat aac cat gag ctg gcc acc ttg  
1795

Ile Arg Leu Glu Ser Pro Ile Ile Asp Asn His Glu Leu Ala Thr Leu  
550 555 560 565

atc aat gcc aac gcg cat ggt gag tgg gat tcc ttt ggt gct gct gta  
1843

Ile Asn Ala Asn Ala His Gly Glu Trp Asp Ser Phe Gly Ala Ala Val  
570 575 580

att tct ggt ttg tac cca gtg gct cac cat ggt gcc ggc atg aag gct  
1891

Ile Ser Gly Leu Tyr Pro Val Ala His His Gly Ala Gly Met Lys Ala  
585 590 595

gcg att gct cgt gtg  
1906

Ala Ile Ala Arg Val  
600

<210> 74

<211> 602

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 74

Met Lys Pro Gln Gly Leu Tyr Asn Pro Ala His Glu His Asp Ala Cys  
1 5 10 15

Gly Val Ala Phe Ile Ala Asp Ile His Gly Arg Pro Ser Arg Ser Ile  
20 25 30

Val Asp Arg Ala Leu Glu Ala Leu Arg Asn Ile Asp His Arg Gly Ala  
35 40 45

Ala Gly Ala Glu Lys Asn Thr Gly Asp Gly Ala Gly Ile Leu Met Gln  
50 55 60

Ile Pro Asp Gly Phe Tyr Arg Glu Val Ser Gly Ile Glu Leu Pro Glu  
65 70 75 80

ctt ttg cac ctg ggc gga tac tca ctt ccg cat gct gtt gcg atg atg  
 1027  
 Leu Leu His Leu Gly Gly Tyr Ser Leu Pro His Ala Val Ala Met Met  
 295 300 305

atc cct cag gcg tgg gaa cac aac aag acg ctg agc cct gag ctg cgt  
 1075  
 Ile Pro Gln Ala Trp Glu His Asn Lys Thr Leu Ser Pro Glu Leu Arg  
 310 315 320 325

gat ttc tac gaa tac cac tct tgt ctg atg gag cca tgg gat ggt cct  
 1123  
 Asp Phe Tyr Glu Tyr His Ser Cys Leu Met Glu Pro Trp Asp Gly Pro  
 330 335 340

gca gcg ctg gca ttt act gac ggt cgt ttt gtg ggt gcc gtg ctg gac  
 1171  
 Ala Ala Leu Ala Phe Thr Asp Gly Arg Phe Val Gly Ala Val Leu Asp  
 345 350 355

cgt aat ggc ctg cga cct ggg cga atc acc att act gat tcg ggt ttg  
 1219  
 Arg Asn Gly Leu Arg Pro Gly Arg Ile Thr Ile Thr Asp Ser Gly Leu  
 360 365 370

gtt gtg atg gct tct gaa tcg gga gtg ttg gac ttg agg gag gag agc  
 1267  
 Val Val Met Ala Ser Glu Ser Gly Val Leu Asp Leu Arg Glu Glu Ser  
 375 380 385

gtc gta aag cgt act cgc gta cag cct gga cgc atg ttc ctt gtt gac  
 1315  
 Val Val Lys Arg Thr Arg Val Gln Pro Gly Arg Met Phe Leu Val Asp  
 390 395 400 405

act gcc gag ggc cgc atc gtt gaa gac gag gaa atc aag cag aaa tta  
 1363  
 Thr Ala Glu Gly Arg Ile Val Glu Asp Glu Glu Ile Lys Gln Lys Leu  
 410 415 420

agc gaa gcg cag cca tat ggt gag tgg att cgc gat aat ttt gtg cat  
 1411  
 Ser Glu Ala Gln Pro Tyr Gly Glu Trp Ile Arg Asp Asn Phe Val His  
 425 430 435

ctg gat cgt ctg cct cag aca cgc tac aac tac atg gcg cac tct cgt  
 1459  
 Leu Asp Arg Leu Pro Gln Thr Arg Tyr Asn Tyr Met Ala His Ser Arg  
 440 445 450

gct gtg ttg cgt cag cgt gtt ttc gga atc act gaa gaa gat gtg gat  
 1507  
 Ala Val Leu Arg Gln Arg Val Phe Gly Ile Thr Glu Glu Asp Val Asp  
 455 460 465

ttg ttg ctg ctg ccg atg gcc cgc cag ggt gct gag gcg att ggt tcc  
 1555  
 Leu Leu Leu Leu Pro Met Ala Arg Gln Gly Ala Glu Ala Ile Gly Ser  
 470 475 480 485

aac act ggc gat ggt gcg ggc atc ctc atg cag att ccg gac ggc ttt 307  
 Asn Thr Gly Asp Gly Ala Gly Ile Leu Met Gln Ile Pro Asp Gly Phe  
 55 60 65

tat cgt gaa gta tct ggc att gag ctt cct gag gca ggg gag tat gcc 355  
 Tyr Arg Glu Val Ser Gly Ile Glu Leu Pro Glu Ala Gly Glu Tyr Ala  
 70 75 80 85

act ggt att gcg ttc ttg cct cgc ggt cgc atg gcg atg atg gat gct 403  
 Thr Gly Ile Ala Phe Leu Pro Arg Gly Arg Met Ala Met Met Asp Ala  
 90 95 100

cag aag gaa att gag cgc atc gca aag caa gaa ggt gcc gat gtg ctt 451  
 Gln Lys Glu Ile Glu Arg Ile Ala Lys Gln Glu Gly Ala Asp Val Leu  
 105 110 115

ggt tgg cgc atg gtt cct ttt gat tct cgt gat ttg ggt tcc atg gct 499  
 Gly Trp Arg Met Val Pro Phe Asp Ser Arg Asp Leu Gly Ser Met Ala  
 120 125 130

gag gag gcg atg cct agt ttc gcg cag att ttc ctt act gtg cct gga 547  
 Glu Glu Ala Met Pro Ser Phe Ala Gln Ile Phe Leu Thr Val Pro Gly  
 135 140 145

aaa tct ggt gaa gat ctt gac cgt gtg atg ttc ttt atc cgt aag cgt 595  
 Lys Ser Gly Glu Asp Leu Asp Arg Val Met Phe Phe Ile Arg Lys Arg  
 150 155 160 165

tgt gag cgt gag ctg ggc acc acc aat ggt cgc gat acg gtg tat ttc 643  
 Cys Glu Arg Glu Leu Gly Thr Thr Asn Gly Arg Asp Thr Val Tyr Phe  
 170 175 180

ccg tcg cta tct tca cgc acc atc att tac aaa ggc atg ttg acc act 691  
 Pro Ser Leu Ser Ser Arg Thr Ile Ile Tyr Lys Gly Met Leu Thr Thr  
 185 190 195

ctg cag ctt gag ggc ttc ttt gag gat ctg ggt gat gct cgc ctg gag 739  
 Leu Gln Leu Glu Gly Phe Phe Glu Asp Leu Gly Asp Ala Arg Leu Glu  
 200 205 210

tcg gcc att gct att gtg cac tcg cgt ttc tcc acg aac act ttc cca 787  
 Ser Ala Ile Ala Ile Val His Ser Arg Phe Ser Thr Asn Thr Phe Pro  
 215 220 225

agc tgg ccg ctg gcg cac ccg tac cgt ttc gtt gcc cac aac ggt gag 835  
 Ser Trp Pro Leu Ala His Pro Tyr Arg Phe Val Ala His Asn Gly Glu  
 230 235 240 245

atc aac act gtg cgt ggc aat gaa aac tgg atg cgc gcc cgc gag gcg 883  
 Ile Asn Thr Val Arg Gly Asn Glu Asn Trp Met Arg Ala Arg Glu Ala  
 250 255 260

ctt atc aaa aac gac aag ctg ggc aat ttg agc agc gtg ctg cct atc 931  
 Leu Ile Lys Asn Asp Lys Leu Gly Asn Leu Ser Ser Val Leu Pro Ile  
 265 270 275

tgc acc ccg gag ggc tcg gat acc gcg cgt ttc gac gag gct ttg gag 979  
 Cys Thr Pro Glu Gly Ser Asp Thr Ala Arg Phe Asp Glu Ala Leu Glu  
 280 285 290



1345	1350	1355	1360
Tyr Gly Ala Thr Ser Gly Glu Leu Phe Ile Arg Gly Gln Val Gly Glu			
1365	1370	1375	
Arg Phe Cys Val Arg Asn Ser Gly Ala Thr Ala Val Val Glu Gly Ile			
1380	1385	1390	
Gly Asn His Gly Cys Glu Tyr Met Thr Gly Gly Arg Val Leu Val Leu			
1395	1400	1405	
Gly Pro Val Gly Glu Asn Phe Gly Ala Gly Met Ser Gly Gly Ile Ala			
1410	1415	1420	
Tyr Leu Ala Asn Ser Pro Asp Leu Asn Gln Lys Ile Asn Gly Glu Leu			
1425	1430	1435	1440
Val Asp Val Val Pro Leu Ser Ala Asp Asp Leu Thr Trp Ala Asp Glu			
1445	1450	1455	
Leu Ile Ala Arg His Arg Glu Leu Thr Gly Ser Glu Thr Lys Leu Arg			
1460	1465	1470	
Ala Gln Asp Leu Val Lys Ile Met Pro Arg Asp Phe Gln Lys Val Leu			
1475	1480	1485	
Asn Ile Ile Glu Thr Ala His Ala Glu Gly Gln Asp Pro Ala Ile Lys			
1490	1495	1500	
Ile Met Glu Ala Val Ser			
1505	1510		

&lt;210&gt; 73

&lt;211&gt; 1906

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1906)

&lt;223&gt; FRXA00007

&lt;400&gt; 73

atcgaaagta acccttttgt tacttgcgtt gcaggtagtgc tccctgattt tcttattatc 60

gaacgattga tagaaacagg attaaagtga ggtatccgc	atg aaa cca caa gga	115
	Met Lys Pro Gln Gly	
	1 5	

ctc tac aac cct gcg cat gaa cat gac gcc tgc ggt gtg gcg ttt att	163
Leu Tyr Asn Pro Ala His Glu His Asp Ala Cys Gly Val Ala Phe Ile	
10 15 20	

gcg gat atc cac ggt cga ccc agc cgc agc att gtt gat cgt gca ctt	211
Ala Asp Ile His Gly Arg Pro Ser Arg Ser Ile Val Asp Arg Ala Leu	
25 30 35	

gag gcg ctt cgc aac att gac cac cga ggt gcc gcc ggt gca gag aag	259
Glu Ala Leu Arg Asn Ile Asp His Arg Gly Ala Ala Gly Ala Glu Lys	
40 45 50	

Gly Val Gly Thr Val Ala Ala Gly Val Ser Lys Ala His Ala Asp Val  
 1025 1030 1035 1040  
 Val Leu Ile Ser Gly His Asp Gly Gly Thr Gly Ala Ser Pro Leu Thr  
 1045 1050 1055  
 Ser Leu Lys His Ala Gly Gly Pro Trp Glu Leu Gly Leu Ala Glu Thr  
 1060 1065 1070  
 Gln Gln Thr Leu Leu Leu Asn Gly Leu Arg Asp Arg Ile Arg Val Gln  
 1075 1080 1085  
 Cys Asp Gly Gln Leu Lys Thr Gly Arg Asp Val Val Ile Ala Ala Leu  
 1090 1095 1100  
 Leu Gly Ala Glu Glu Phe Gly Phe Ala Thr Ala Pro Leu Val Val Glu  
 1105 1110 1115 1120  
 Gly Cys Ile Met Met Arg Val Cys His Leu Asp Thr Cys Pro Val Gly  
 1125 1130 1135  
 Ile Ala Thr Gln Asn Pro Asp Leu Arg Ser Lys Phe Thr Gly Lys Ala  
 1140 1145 1150  
 Glu His Val Val Asn Phe Phe Thr Phe Ile Ala Gln Glu Val Arg Glu  
 1155 1160 1165  
 Tyr Leu Ala Gln Leu Gly Phe Arg Ser Ile Asp Glu Ala Val Gly Gln  
 1170 1175 1180  
 Ala Gln Val Leu Arg Lys Arg Ser Gly Ile Pro Ala Asp Ser Arg Ala  
 1185 1190 1195 1200  
 Ala His Leu Asp Leu Ser Pro Ile Phe His Arg Pro Glu Thr Pro His  
 1205 1210 1215  
 Phe Pro Thr Gln Asp Val Arg Cys Thr Lys Thr Gln Glu His Ser Leu  
 1220 1225 1230  
 Glu Lys Ala Leu Asp Asn Ala Phe Ile Asp Lys Ala Ser Asp Thr Ile  
 1235 1240 1245  
 Thr Arg Ala Ala Ala Gly Val Glu Thr Ser Ile Val Ile Asp Ser Ser  
 1250 1255 1260  
 Ile Ser Asn Val Asn Arg Ser Val Gly Thr Met Leu Gly Ser Ala Val  
 1265 1270 1275 1280  
 Ser Arg Val Ala Gly Ala Gln Gly Leu Pro Asp Gly Thr Ile Thr Leu  
 1285 1290 1295  
 Asn Leu Gln Gly Cys Ala Gly Asn Ser Phe Gly Ala Phe Ile Pro Arg  
 1300 1305 1310  
 Gly Ile Thr Ile Asn Leu Thr Gly Asp Ala Asn Asp Phe Val Gly Lys  
 1315 1320 1325  
 Gly Leu Ser Gly Gly Lys Ile Val Ile Lys Pro Ser Ala Gln Ala Pro  
 1330 1335 1340  
 Lys Gln Leu Lys Asn Asn Pro Asn Ile Ile Ala Gly Asn Val Leu Gly

Met Asn Ser Glu Gln Glu Phe Val Leu Ser Ala Ile Glu Glu Arg Asp  
 1 5 10 15  
 Ile Lys Phe Val Arg Leu Trp Phe Thr Asp Ile Leu Gly His Leu Lys  
 20 25 30  
 Ser Val Val Val Ala Pro Ala Glu Leu Glu Ser Ala Leu Glu Glu Gly  
 35 40 45  
 Ile Gly Phe Asp Gly Ser Ala Ile Glu Gly Tyr Ala Arg Ile Ser Glu  
 50 55 60  
 Ala Asp Thr Ile Ala Arg Pro Asp Pro Ser Thr Phe Gln Val Leu Pro  
 65 70 75 80  
 Leu Glu Ala Gly Ile Ser Lys Leu Gln Ala Ala Arg Leu Phe Cys Asp  
 85 90 95  
 Val Thr Met Pro Asp Gly Gln Pro Ser Phe Ser Asp Pro Arg Gln Val  
 100 105 110  
 Leu Arg Arg Gln Val Gln Leu Ala Ala Asp Glu Gly Leu Thr Cys Met  
 115 120 125  
 Ile Ser Pro Glu Ile Glu Phe Tyr Leu Val Gln Ser Leu Arg Thr Asn  
 130 135 140  
 Gly Leu Pro Pro Val Pro Thr Asp Asn Gly Gly Tyr Phe Asp Gln Ala  
 145 150 155 160  
 Thr Phe Asn Glu Ala Pro Asn Phe Arg Arg Asn Ala Met Val Ala Leu  
 165 170 175  
 Glu Glu Leu Gly Ile Pro Val Glu Phe Ser His His Glu Thr Ala Pro  
 180 185 190  
 Gly Gln Gln Glu Ile Asp Leu Arg His Ala Asp Ala Leu Thr Met Ala  
 195 200 205  
 Asp Asn Ile Met Thr Phe Arg Tyr Ile Met Lys Gln Val Ala Arg Asp  
 210 215 220  
 Gln Gly Val Gly Ala Ser Phe Met Pro Lys Pro Phe Gln Glu His Ala  
 225 230 235 240  
 Gly Ser Ala Met His Thr His Met Ser Leu Phe Glu Gly Asp Thr Asn  
 245 250 255  
 Ala Phe His Asp Pro Asp Asp Ser Tyr Met Leu Ser Lys Thr Ala Lys  
 260 265 270  
 Gln Phe Ile Ala Gly Ile Leu His His Ala Pro Glu Phe Thr Ala Val  
 275 280 285  
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Asn Ser Tyr Lys Arg Ile Val Tyr Gly Asn Glu Ala Pro Thr Ala Ala  
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1075

Thr Trp Gly Val Ser Asn Arg Ser Ala Leu Val Arg Val Pro Thr Tyr  
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1123

Arg Leu Asn Lys Glu Glu Ser Arg Arg Val Glu Val Arg Leu Pro Asp  
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1171

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1219

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1267

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1315

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1363

Glu Leu Val Ala Asp Ile Leu Gly Glu His Val Phe Glu Phe Phe Leu  
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1411

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425 430 435

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gat tta cgc cat gcg gat gcg ctc acc atg gcc gac aac atc atg acc Asp Leu Arg His Ala Asp Ala Leu Thr Met Ala Asp Asn Ile Met Thr 200 205 210			739
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gac gat tct tac atg ctg tcc aaa acc gca aaa cag ttc atc gct gga Asp Asp Ser Tyr Met Leu Ser Lys Thr Ala Lys Gln Phe Ile Ala Gly 265 270 275			931
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 Thr Asp Gly Ser Ile Trp Asp Leu Lys Cys Asp Ile Ala Leu Pro Cys  
 305 310 315 320  
 Ala Thr Gln Asn Glu Leu Asn Gly Glu Asn Ala Lys Thr Leu Ala Asp  
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 Glu Ala Val Glu Val Phe Arg Glu Arg Asp Ile Arg Phe Gly Pro Gly  
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 Lys Ala Ala Asn Ala Gly Gly Val Ala Thr Ser Ala Leu Glu Met Gln  
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 Gln Asn Ala Ser Arg Asp Ser Trp Ser Phe Glu Tyr Thr Asp Glu Arg  
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 Met Asn Ser Glu Gln  
 1 5  
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 Glu Phe Val Leu Ser Ala Ile Glu Glu Arg Asp Ile Lys Phe Val Arg  
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1464

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Val	Pro	Trp	Val	Asp	Asp	Gln	Gly	Gln	Val	His	Val	Asn	Arg	Gly	Phe
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Tyr	Arg	Asp	Val	Pro	Ala	Gly	Asn	Ile	Gly	Val	Gly	Gly	His	Glu	Ile
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Gly	Val	Leu	Thr	Gly	Lys	Gly	Leu	Thr	Trp	Gly	Gly	Ser	Leu	Val	Arg
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Lys	Ala	Lys	Gly	Glu	Ser	Ile	Ser	Gly	Gln	Lys	Ile	Ile	Val	Ser	Gly
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Ser	Gly	Asn	Val	Ala	Thr	Tyr	Ala	Ile	Glu	Lys	Ala	Gln	Glu	Leu	Gly
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Phe Ser Asp Ser Ser Gly Trp Val His Thr Pro Asn Gly Val Asp Val			
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gct aag ctc cgc gaa atc aag gaa gtt cgt cgc gca cgc gta tcc gtg			979
Ala Lys Leu Arg Glu Ile Lys Glu Val Arg Arg Ala Arg Val Ser Val			
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Tyr Ala Asp Glu Val Glu Gly Ala Thr Tyr His Thr Asp Gly Ser Ile			
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1123			
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1219			
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425	430	435	
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1461			
Ala Asp Ala Met Leu Ala Gln Gly Val Ile			
440	445		



Gln	Val	Ser	Asn	Tyr	Tyr	Asp	Met	Leu	Leu	Lys	Arg	Asn	Ala	Gly	Glu		
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Pro	Glu	Phe	His	Gln	Ala	Val	Ala	Glu	Val	Leu	Glu	Ser	Leu	Lys	Ile		
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Val	Leu	Glu	Lys	Asp	Pro	His	Tyr	Ala	Asp	Tyr	Gly	Leu	Ile	Gln	Arg		
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Leu	Cys	Glu	Pro	Glu	Arg	Gln	Leu	Ile	Phe	Arg	Val	Pro	Trp	Val	Asp		
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Ser	Ala	Leu	Gly	Pro	Tyr	Lys	Gly	Gly	Leu	Arg	Phe	His	Pro	Ser	Val		
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Asn	Leu	Gly	Ile	Val	Lys	Phe	Leu	Gly	Phe	Glu	Gln	Ile	Phe	Lys	Asn		
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Ser	Leu	Thr	Gly	Leu	Pro	Ile	Gly	Gly	Gly	Lys	Gly	Gly	Ser	Asp	Phe		
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gac	cct	aag	ggc	aag	tcc	gat	ctg	gaa	atc	atg	cgt	ttc	tgc	cag	tcc	547	
Asp	Pro	Lys	Gly	Lys	Ser	Asp	Leu	Glu	Ile	Met	Arg	Phe	Cys	Gln	Ser		
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Phe	Met	Thr	Glu	Leu	His	Arg	His	Ile	Gly	Glu	Tyr	Arg	Asp	Val	Pro		
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Ala	Gly	Asn	Ile	Gly	Val	Gly	Gly	His	Glu	Ile	Gly	Tyr	Leu	Phe	Gly		
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His	Tyr	Arg	Arg	Met	Ala	Asn	Gln	His	Glu	Ser	Gly	Val	Leu	Thr	Gly		
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Lys	Gly	Leu	Thr	Trp	Gly	Gly	Ser	Leu	Val	Arg	Thr	Glu	Ala	Thr	Gly		
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Tyr	Gly	Cys	Val	Tyr	Phe	Val	Ser	Glu	Met	Ile	Lys	Ala	Lys	Gly	Glu		
	215					220					225						
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Ser	Ile	Ser	Gly	Gln	Lys	Ile	Ile	Val	Ser	Gly	Ser	Gly	Asn	Val	Ala		
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Thr	Tyr	Ala	Ile	Glu	Lys	Ala	Gln	Glu	Leu	Gly	Ala	Thr	Val	Ile	Gly		

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 Lys Ala Pro Ala Gly Gln Ile Glu Glu Gln Ala Ala Arg Cys Met Asp  
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 Cys Gly Val Pro Phe Cys His Glu Gly Cys Pro Leu Gly Asn Ile Ile  
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 Pro Glu Trp Asn Asp Leu Val Arg Gln Gly Arg Trp Lys Glu Ala Tyr  
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 Asp Arg Leu His Ala Thr Asn Asn Phe Pro Glu Phe Thr Gly Arg Leu  
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   Met Thr Val Asp Glu  
   1                            5  
 cag gtc tct aac tat tac gac atg ctt ctg aag cgc aat gct ggc gag 163

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Tyr	Leu	Thr	Ala	Gln	Asn	Arg	Ile	Asn	Glu	Gly	Asp	Gly	Glu	Val	Ser
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Pro	Ile	Asn	Ala	Lys	Gly	Lys	Lys	Val	Val	Ile	Ile	Gly	Gly	Gly	Asp
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Gln Ile Glu Glu Gln Ala Ala Arg Cys Met Asp Cys Gly Val Pro Phe																
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70 75 80 85																
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Val Gly Thr Ser Pro Arg Ala Ala	Glu Leu Ala Leu Phe Asp Ala Ile			
	105	110	115	
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Leu Leu Ala Thr Gly Thr Pro Val Ala Arg Glu Leu Ser Val Pro Gly				
	120	125	130	
cac gat ctc aac ggc atc cat gcg gca atg gat tac ctc acc gcc caa			547	
His Asp Leu Asn Gly Ile His Ala Ala Met Asp Tyr Leu Thr Ala Gln				
	135	140	145	
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	170	175	180	
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Phe Gly Thr Ala Leu Arg Gln Gly Ala Glu Ser Val Thr Gln Phe Asp				
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Ala Gln Gln Leu Thr Arg Ala Gly His Ser Val Thr Val Phe Glu Arg				
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Asp Asp Arg Leu Gly Gly Leu Met Arg Tyr Gly Val Pro Glu Tyr Lys				
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Met Glu Asn Arg Trp Ile Asp Arg Arg Ile Glu Gln Met Glu Ala Glu				
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Gly Thr Thr Phe Gln Val Gly Thr Ser Pro Arg Ala Ala Glu Leu Ala				
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 115 120 125  
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 Tyr Leu Thr Ala Gln Asn Arg Ile Asn Glu Gly Asp Gly Glu Val Ser  
 145 150 155 160  
 Pro Ile Asn Ala Lys Gly Lys Lys Val Val Ile Ile Gly Gly Gly Asp  
 165 170 175  
 Thr Gly Thr Asp Cys Phe Gly Thr Ala Leu Arg Gln Gly Ala Glu Ser  
 180 185 190  
 Val Thr Gln Phe Asp Ile Arg Pro Arg Ala Pro Phe Gln Arg Ala Asp  
 195 200 205  
 Ser

<210> 89  
 <211> 727  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(727)  
 <223> FRXA00365

<400> 89  
 gaagcctacg atcgcttgca cgcgaccaac aatttccccg agttcaccgg ccgtttgtgc 60  
 cccgcaccct gcgaaggcgc ctgcgtgctc ggtatcaacg atg att ctg tca cca 115  
 Met Ile Leu Ser Pro  
 1 5  
 tca aaa acg ttt gag ctg gaa atc gtc gaa aaa gca ttc cgc gaa ggc 163  
 Ser Lys Thr Phe Glu Leu Glu Ile Val Glu Lys Ala Phe Arg Glu Gly  
 10 15 20  
 tgg gtg caa cca gta atc cca tcc atg tct acc ggg ctg tca gtc gcc 211  
 Trp Val Gln Pro Val Ile Pro Ser Met Ser Thr Gly Leu Ser Val Ala  
 25 30 35  
 gtc gtc ggt tcc ggc ccc gct ggc ctt gcc gcc gcg cag cag ctc acc 259  
 Val Val Gly Ser Gly Pro Ala Gly Leu Ala Ala Ala Gln Leu Thr  
 40 45 50  
 cgc gca ggc cac agc gtt acc gtc ttt gaa cgc gac gac cgc ctc ggc 307  
 Arg Ala Gly His Ser Val Thr Val Phe Glu Arg Asp Asp Arg Leu Gly  
 55 60 65  
 ggc ctc atg cgc tac ggc gtg cca gaa tac aaa atg gag aac cgc tgg 355  
 Gly Leu Met Arg Tyr Gly Val Pro Glu Tyr Lys Met Glu Asn Arg Trp

ggc ctc atg cgc tac ggc gtg cca gaa tac aaa atg gag aac cgc tgg 355  
 Gly Leu Met Arg Tyr Gly Val Pro Glu Tyr Lys Met Glu Asn Arg Trp  
 70 75 80 85

atc gac cgc cgc atc gag caa atg gaa gca gag ggc aca act ttc cag 403  
 Ile Asp Arg Arg Ile Glu Gln Met Glu Ala Glu Gly Thr Thr Phe Gln  
 90 95 100

gta ggc acc tcg ccg cgc gcc gct gaa cta gcg ctt ttc gac gcg atc 451  
 Val Gly Thr Ser Pro Arg Ala Ala Glu Leu Ala Leu Phe Asp Ala Ile  
 105 110 115

ctc ctc gca acc ggc acc cca gtg gcc cgc gaa ctc tca gtt cca ggc 499  
 Leu Leu Ala Thr Gly Thr Pro Val Ala Arg Glu Leu Ser Val Pro Gly  
 120 125 130

cac gat ctc aac ggc atc cat gcg gca atg gat tac ctc acc gcc caa 547  
 His Asp Leu Asn Gly Ile His Ala Ala Met Asp Tyr Leu Thr Ala Gln  
 135 140 145

aac cgc atc aac gaa ggc gac ggt gaa gtc tct cca atc aac gcc aaa 595  
 Asn Arg Ile Asn Glu Gly Asp Gly Glu Val Ser Pro Ile Asn Ala Lys  
 150 155 160 165

ggc aag aaa gtt gtc atc atc ggt ggc ggc gac acc ggc acc gac tgc 643  
 Gly Lys Lys Val Val Ile Ile Gly Gly Gly Asp Thr Gly Thr Asp Cys  
 170 175 180

ttc ggc acc gca ctg cgc caa gga gca gaa tca gtc acc caa ttt gat 691  
 Phe Gly Thr Ala Leu Arg Gln Gly Ala Glu Ser Val Thr Gln Phe Asp  
 185 190 195

atc cgc ccc cgc gct cct ttc cag cgc gcc gat tcc 727  
 Ile Arg Pro Arg Ala Pro Phe Gln Arg Ala Asp Ser  
 200 205

<210> 88  
 <211> 209  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 88  
 Met Ile Leu Ser Pro Ser Lys Thr Phe Glu Leu Glu Ile Val Glu Lys  
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 Ala Phe Arg Glu Gly Trp Val Gln Pro Val Ile Pro Ser Met Ser Thr  
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 Gly Leu Ser Val Ala Val Val Gly Ser Gly Pro Ala Gly Leu Ala Ala  
 35 40 45  
 Ala Gln Gln Leu Thr Arg Ala Gly His Ser Val Thr Val Phe Glu Arg  
 50 55 60  
 Asp Asp Arg Leu Gly Gly Leu Met Arg Tyr Gly Val Pro Glu Tyr Lys  
 65 70 75 80  
 Met Glu Asn Arg Trp Ile Asp Arg Arg Ile Glu Gln Met Glu Ala Glu  
 85 90 95

tagcttgggt agaaaatgct aga

305

&lt;210&gt; 86

&lt;211&gt; 94

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 86

Leu Val Leu Val Ala Leu Gly Phe Thr Gly Ala Glu Gln Gly Gly Leu  
 1 5 10 15

Ala His Glu Leu Gly Val Gly Phe Asp Asp Arg Gly Arg Ile Leu Arg  
 20 25 30

Asp Ser Glu Tyr Arg Ser Pro Thr Asn Ser Arg Val Tyr Ile Ala Gly  
 35 40 45

Asp Asn Gly Arg Gly Gln Ser Leu Ile Val Trp Ala Ile Ala Glu Gly  
 50 55 60

Arg Ala Cys Ala Ala Ala Ile Asp Ala Asp Leu Met Gly Glu Thr Ala  
 65 70 75 80

Leu Pro Val Ala Val Ala Pro Gln Asp Val Pro Leu Ala Val  
 85 90

&lt;210&gt; 87

&lt;211&gt; 727

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(727)

&lt;223&gt; RXN00365

&lt;400&gt; 87

gaagcctacg atcgcttgca cgcgaccaac aatttccccg agttcaccgg ccgtttgtgc 60

cccgccacct gcgaaggcgc ctgcgtgctc ggtatcaacg atg att ctg tca cca 115  
 Met Ile Leu Ser Pro  
 1 5

tca aaa acg ttt gag ctg gaa atc gtc gaa aaa gca ttc cgc gaa ggc 163  
 Ser Lys Thr Phe Glu Leu Glu Ile Val Glu Lys Ala Phe Arg Glu Gly  
 10 15 20

tgg gtg caa cca gta atc cca tcc atg tct acc ggg ctg tca gtc gcc 211  
 Trp Val Gln Pro Val Ile Pro Ser Met Ser Thr Gly Leu Ser Val Ala  
 25 30 35

gtc gtc ggt tcc ggc ccc gct ggc ctt gcc gcc gcg cag cag ctc acc 259  
 Val Val Gly Ser Gly Pro Ala Gly Leu Ala Ala Ala Gln Gln Leu Thr  
 40 45 50

cgc gca ggc cac agc gtt acc gtc ttt gaa cgc gac gac cgc ctc ggc 307  
 Arg Ala Gly His Ser Val Thr Val Phe Glu Arg Asp Asp Arg Leu Gly  
 55 60 65

50                      55                      60  
 Thr Gly Asn Gln Ile Arg Val Val Asn Gly Lys Arg Glu Pro Ile Glu  
 65                      70                      75                      80  
 Gly Thr Glu Phe Pro Phe Glu Ala Asp Leu Val Leu Val Ala Leu Gly  
 85                      90                      95  
 Phe Thr Gly Ala Glu Gln Gly Gly Leu Ala His Glu Leu Gly Val Gly  
 100                      105                      110  
 Phe Asp Asp Arg Gly Arg Ile Leu Arg Asp Ser Glu Tyr Arg Ser Pro  
 115                      120                      125  
 Thr Asn Ser Arg Val Tyr Ile Ala Gly Asp Asn Gly Arg Gly Gln Ser  
 130                      135                      140  
 Leu Ile Val Trp Ala Ile Ala Glu Gly Arg Ala Cys Ala Ala Ala Ile  
 145                      150                      155                      160  
 Asp Ala Asp Leu Met Gly Glu Thr Ala Leu Pro Val Ala Val Ala Pro  
 165                      170                      175  
 Gln Asp Val Pro Leu Ala Val  
 180

<210> 85  
 <211> 305  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(282)  
 <223> FRXA00198

<400> 85  
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 Leu Val Leu Val Ala Leu Gly Phe Thr Gly Ala Glu Gln Gly Gly Leu  
 1                      5                      10                      15  
 gca cac gaa cta ggc gta ggt ttc gac gac cgg ggc cgc atc ctc cgc 96  
 Ala His Glu Leu Gly Val Gly Phe Asp Asp Arg Gly Arg Ile Leu Arg  
 20                      25                      30  
 gat tcc gaa tac cgc agc ccc acc aac tcc cgc gtt tac atc gca ggc 144  
 Asp Ser Glu Tyr Arg Ser Pro Thr Asn Ser Arg Val Tyr Ile Ala Gly  
 35                      40                      45  
 gac aac ggc cgt ggc cag tcc ctg atc gtg tgg gca atc gcc gaa ggc 192  
 Asp Asn Gly Arg Gly Gln Ser Leu Ile Val Trp Ala Ile Ala Glu Gly  
 50                      55                      60  
 cgc gca tgc gcc gca gct atc gac gcc gat ctc atg ggt gaa act gca 240  
 Arg Ala Cys Ala Ala Ala Ile Asp Ala Asp Leu Met Gly Glu Thr Ala  
 65                      70                      75                      80  
 ctc cct gta gca gtt gca cca cag gac gtg ccg ctg gct gtc 282  
 Leu Pro Val Ala Val Ala Pro Gln Asp Val Pro Leu Ala Val  
 85                      90



gat gaa tca gcc gat gaa atc gca gcc ctg ggc ctc gcc gaa cgt gcc 211  
Asp Glu Ser Ala Asp Glu Ile Ala Ala Leu Gly Leu Ala Glu Arg Ala  
25 30 35

gca ggc tcc acg ctt ggt gaa cgt aaa ttt gct gtc aac acc gtg gaa 259  
Ala Gly Ser Thr Leu Gly Glu Arg Lys Phe Ala Val Asn Thr Val Glu  
40 45 50

ttc cac ggc aac aac ggc cac gtc acc gga ctc acc ggc aac caa atc 307  
Phe His Gly Asn Asn Gly His Val Thr Gly Leu Thr Gly Asn Gln Ile  
55 60 65

cga gtt gtc aac ggc aaa cgt gaa cca atc gaa ggc acc gaa ttc ccc 355  
Arg Val Val Asn Gly Lys Arg Glu Pro Ile Glu Gly Thr Glu Phe Pro  
70 75 80 85

ttc gaa gca gac ctc gtt ctt gtt gca ctt ggc ttc acc ggc gca gaa 403  
Phe Glu Ala Asp Leu Val Leu Val Ala Leu Gly Phe Thr Gly Ala Glu  
90 95 100

caa ggc gga ttg gca cac gaa cta ggc gta ggt ttc gac gac cgg ggc 451  
Gln Gly Gly Leu Ala His Glu Leu Gly Val Gly Phe Asp Asp Arg Gly  
105 110 115

cgc atc ctc cgc gat tcc gaa tac cgc agc ccc acc aac tcc cgc gtt 499  
Arg Ile Leu Arg Asp Ser Glu Tyr Arg Ser Pro Thr Asn Ser Arg Val  
120 125 130

tac atc gca ggc gac aac ggc cgt ggc cag tcc ctg atc gtg tgg gca 547  
Tyr Ile Ala Gly Asp Asn Gly Arg Gly Gln Ser Leu Ile Val Trp Ala  
135 140 145

atc gcc gaa ggc cgc gca tgc gcc gca gct atc gac gcc gat ctc atg 595  
Ile Ala Glu Gly Arg Ala Cys Ala Ala Ala Ile Asp Ala Asp Leu Met  
150 155 160 165

ggg gaa act gca ctc cct gta gca gtt gca cca cag gac gtg ccg ctg 643  
Gly Glu Thr Ala Leu Pro Val Ala Val Ala Pro Gln Asp Val Pro Leu  
170 175 180

gct gtc tagcttgggt agaaaatgct aga 672  
Ala Val

&lt;210&gt; 84

&lt;211&gt; 183

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 84

Met Tyr Pro Asn Leu Phe Arg Thr Ala Thr Ala His Glu Glu Gly Glu  
1 5 10 15

Tyr Ile Ile Thr Gly Asp Glu Ser Ala Asp Glu Ile Ala Ala Leu Gly  
20 25 30

Leu Ala Glu Arg Ala Ala Gly Ser Thr Leu Gly Glu Arg Lys Phe Ala  
35 40 45

Val Asn Thr Val Glu Phe His Gly Asn Asn Gly His Val Thr Gly Leu

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Ile Tyr Ala Ser Asp Leu Leu Ile Arg Asn Glu Glu Arg Glu Val Phe
      20              25              30
Val Asp Leu Phe Glu Gln Met Pro Ala Pro Phe Gly Leu Ile Arg Tyr
      35              40              45
Gly Val Ala Pro Asp His Pro Arg Ile Lys Gly Ile Val Lys Ser Leu
      50              55              60
His Asn Val Leu Asp Lys Pro Arg Leu Arg Leu Leu Gly Asn Ile Glu
      65              70              75              80
Ile Gly Lys Asp Ile Thr Val Glu Glu Leu Arg Asp Tyr Tyr Asp Ala
      85              90              95
Val Val Phe Ser Thr Gly Ala Val Ala Asp Arg Asp Leu Asn Ile Pro
      100             105             110
Gly Ile Glu Ala Glu Gly Ser Phe Gly Ala Gly Glu Phe Val Gly Phe
      115             120             125
Tyr Asp Gly Asn Pro Arg Phe Glu Arg Ser Trp Asp Leu Ser Ala Gln
      130             135             140
Ser Val Ala Val Ile Gly Val Gly Asn Val Gly Leu Asp Val Ala Arg
      145             150             155             160
Ile Leu Ala Lys Thr Gly Asp Glu Leu Lys Val Thr Glu Ile Ser Asp
      165             170             175
Asn Val Tyr Asp Ser Leu Lys Glu Asn Lys Xaa Xaa Glu Val His Val
      180             185             190
Phe Gly Arg Arg Trp Pro Ser Thr Gly Gln Val His Pro Thr Gly Thr
      195             200             205
Xaa Arg Thr Xaa Pro Leu Pro His His Gln Arg Gly Cys
      210             215             220

<210> 83
<211> 672
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(649)
<223> RXN00198

<400> 83
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                        Met Tyr Pro Asn Leu
                        1              5

ttc cgc acc gca acg gct cac gaa gaa ggc gaa tac atc atc act ggc 163
Phe Arg Thr Ala Thr Ala His Glu Glu Gly Glu Tyr Ile Ile Thr Gly
      10              15              20

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Gly Val Met Gly Leu Glu Phe Ser Pro Gln Glu Gln Asp Phe Ser Leu  
 100 105 110  
 Ile Leu Pro Ser Val Gln Ala Gly Thr Leu Asp Ile Gly Ala Ser Gly  
 115 120 125  
 Phe Thr Asp Asn Glu Glu Arg Arg Glu Asn Phe Asp Phe Ile Asp Phe  
 130 135 140  
 Leu Phe Ala Gly Val Gln Trp Ala Gln Ala Thr Asp Arg Glu Thr Pro  
 145 150 155 160  
 Ile Asp Pro Glu Asn Ala Cys Gly Leu Thr Val Ala Val Gln Arg Thr  
 165 170 175  
 Thr Val Ala Glu Thr Asp Asp Val Arg Pro Arg Ser Ala Gln Cys Glu  
 180 185 190  
 Ala Glu Gly Lys Glu Pro Ile Thr Ile Leu Ser Tyr Glu Thr Ala Asp  
 195 200 205  
 Thr Ala Ala Thr Ala Leu Ile Leu Gly Arg Ala Asp Ala Leu Ala Ala  
 210 215 220  
 Asp Ser Pro Val Ser Ala Trp Ala Ala Glu Arg Ser Glu Gly Arg Ile  
 225 230 235 240  
 Glu Val Val Gly Asp Met Tyr Leu Ala Ala Pro Phe Gly Phe Ala Phe  
 245 250 255  
 Pro Leu Glu Ser Asp Leu Thr Pro Ala Ala Ala Ala Phe Gln His  
 260 265 270  
 Leu Ile Asp Thr Gly Asp Tyr Gln Arg Ile Met Ala Gln Trp Gly Ile  
 275 280 285  
 Glu Glu Gly Leu Leu Asp Glu Ala Leu Ile Asn Glu Gln Pro Leu Asn  
 290 295 300

<210> 109  
 <211> 1962  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1939)  
 <223> RXA02139

<400> 109  
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 Met Arg His Arg Gly  
 1 5  
 cct gac gat gcc ggc act tgg cat gac gcc gat gca gcg ttt gga ttc 163

gac gat gtc cgt cct cgc tca gct caa tgt gaa gcc gaa ggc aaa gag 691  
 Asp Asp Val Arg Pro Arg Ser Ala Gln Cys Glu Ala Glu Gly Lys Glu  
 185 190 195

ccg atc acc att ttg tct tat gaa acc gca gat act gca gct acc gca 739  
 Pro Ile Thr Ile Leu Ser Tyr Glu Thr Ala Asp Thr Ala Ala Thr Ala  
 200 205 210

ttg atc ctg gga cgc gca gac gca ctt gct gcg gac tcc cct gtt tca 787  
 Leu Ile Leu Gly Arg Ala Asp Ala Leu Ala Ala Asp Ser Pro Val Ser  
 215 220 225

gct tgg gct gca gag cgc tcc gaa ggc cgc atc gaa gtt gtg ggc gat 835  
 Ala Trp Ala Ala Glu Arg Ser Glu Gly Arg Ile Glu Val Val Gly Asp  
 230 235 240 245

atg tac ttg gct gcg cca ttt ggt ttc gca ttc ccg ttg gaa tct gac 883  
 Met Tyr Leu Ala Ala Pro Phe Gly Phe Ala Phe Pro Leu Glu Ser Asp  
 250 255 260

ctc acc cca gca gca gct gcg gcg ttc caa cac ttg att gac acc ggc 931  
 Leu Thr Pro Ala Ala Ala Ala Phe Gln His Leu Ile Asp Thr Gly  
 265 270 275

gat tac cag cgc atc atg gcg caa tgg ggc att gaa gaa ggc ctt ctt 979  
 Asp Tyr Gln Arg Ile Met Ala Gln Trp Gly Ile Glu Glu Gly Leu Leu  
 280 285 290

gat gag gcc ctg atc aac gaa cag cca ctc aac tagagccttc cagcaactaa  
 1032  
 Asp Glu Ala Leu Ile Asn Glu Gln Pro Leu Asn  
 295 300

aaa  
 1035

<210> 108  
 <211> 304  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 108  
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 Ile Val Ala Thr Ser Phe Thr Leu Ala Ser Cys Val Thr Asn Glu Glu  
 20 25 30  
 Gln Gly Asn Pro Asp Gly Trp Glu Gln Ile Val Pro Asp Pro Val Pro  
 35 40 45  
 Glu Ile Gln Ala Met Val Pro Glu Ala Leu Ala Gln Arg Gly Val Leu  
 50 55 60  
 Thr Ala Gly Ala Asn Pro Pro Phe Pro Phe Glu Phe Lys Asp Ser  
 65 70 75 80  
 Asp Gly Gln Ile Ile Gly Val Glu Met Asp Leu Val Arg Ala Met Ala  
 85 90 95

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<220>
<221> CDS
<222> (101)..(1012)
<223> RXA00727
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167

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 Leu Pro Pro Asp Ser Ser Ile Glu Ala Pro Gly Glu Lys Glu Pro Ile  
 50 55 60  
 Val Glu Val Ile Glu Asn Trp Pro Gly Ser Leu Arg Pro Asp Asp Leu  
 65 70 75 80  
 Thr Pro Glu Glu Arg Val Pro Gly Ile Val Asn Arg Gly Arg Ile Ile  
 85 90 95  
 Val Gly Val Asp Gln Ser Gln Asn Leu Leu Ser Phe Arg Asp Pro Val  
 100 105 110  
 Thr Gly Glu Leu Arg Gly Phe Glu Val Glu Leu Ala Arg Glu Ile Ser  
 115 120 125  
 Arg Asp Ile Phe Gly Asp Pro Asn Lys Val Asp Phe Arg Phe Val Gly  
 130 135 140  
 Ser Ser Asp Arg Leu Arg Ser Leu Asp Gln Gly Asp Val Asp Ile Val  
 145 150 155 160  
 Ile Arg Ser Val Thr Ile Thr Asp Glu Arg Ala Lys Leu Val Glu Phe  
 165 170 175  
 Ser Thr Pro Tyr Leu Arg Thr Gln Thr Arg Met Leu Thr Met Glu Ser  
 180 185 190  
 Ser Gly Ile Thr Ser Ile Ala Asp Leu Pro Gly His Thr Ile Cys Val  
 195 200 205  
 Thr Asp Gly Ser Thr Ser Leu Gln Arg Ala Arg Thr Ile Ala Pro Glu  
 210 215 220  
 Ala Ser Ile Leu Lys Thr Arg Asn Trp Ser Asp Cys Leu Met Ala Leu  
 225 230 235 240  
 Gln Gln His Gln Ala Gln Val Ile Leu Gly Asp Asp Val Ile Leu Ser  
 245 250 255  
 Gly Ile Ala Ala Gln Asp Pro Tyr Thr Glu Ile Leu Asp Thr Ser Leu  
 260 265 270  
 Asp Ser His Ser Tyr Gly Val Ala Ala Ala Ser Thr Thr Ala Glu Thr  
 275 280 285  
 Asp Ser Ser Gly Leu Ile Arg Gln Val Asn Tyr Thr Ile Glu Arg Ile  
 290 295 300  
 Arg Thr Asp Arg Met Trp Trp Thr Met Phe Asp Asp Trp Phe Gly Pro  
 305 310 315 320  
 Tyr Leu Trp Ser Tyr Gly Pro Pro Gln Leu Gln Tyr Met Pro Glu Glu  
 325 330 335  
 Glu Gly Thr Glu Asn Asp Glu Gly  
 340

cgc acc caa acc cgc atg ttg acc atg gaa tct tca gga atc acg tcc 691  
 Arg Thr Gln Thr Arg Met Leu Thr Met Glu Ser Ser Gly Ile Thr Ser  
 185 190 195  
  
 atc gca gat cta ccc ggc cac acc att tgt gtc acc gat ggc tcc act 739  
 Ile Ala Asp Leu Pro Gly His Thr Ile Cys Val Thr Asp Gly Ser Thr  
 200 205 210  
  
 tca ttg cag cga gcc cgc acc att gcg ccg gag gcc tca atc tta aaa 787  
 Ser Leu Gln Arg Ala Arg Thr Ile Ala Pro Glu Ala Ser Ile Leu Lys  
 215 220 225  
  
 act cgc aat tgg tcc gat tgt ctc atg gcg ttg cag cag cat cag gct 835  
 Thr Arg Asn Trp Ser Asp Cys Leu Met Ala Leu Gln Gln His Gln Ala  
 230 235 240 245  
  
 cag gtc att ttg ggc gat gat gtc att ttg tcc ggc atc gca gca cag 883  
 Gln Val Ile Leu Gly Asp Asp Val Ile Leu Ser Gly Ile Ala Ala Gln  
 250 255 260  
  
 gat ccc tac acc gag att ctt gat acc tcc ctc gat tcc cat tcc tat 931  
 Asp Pro Tyr Thr Glu Ile Leu Asp Thr Ser Leu Asp Ser His Ser Tyr  
 265 270 275  
  
 gga gtg gca gcg gca tcg acc act gct gaa aca gac tct tcg ggg ttg 979  
 Gly Val Ala Ala Ala Ser Thr Thr Ala Glu Thr Asp Ser Ser Gly Leu  
 280 285 290  
  
 att cgg cag gta aac tac aca att gaa cgg atc cgc aca gac cgc atg  
 1027  
 Ile Arg Gln Val Asn Tyr Thr Ile Glu Arg Ile Arg Thr Asp Arg Met  
 295 300 305  
  
 tgg tgg aca atg ttc gac gat tgg ttc gga cct tat ctc tgg tcc tac  
 1075  
 Trp Trp Thr Met Phe Asp Asp Trp Phe Gly Pro Tyr Leu Trp Ser Tyr  
 310 315 320 325  
  
 ggt cca cca cag ctg cag tac atg cca gag gaa gaa ggg aca gaa aac  
 1123  
 Gly Pro Pro Gln Leu Gln Tyr Met Pro Glu Glu Glu Gly Thr Glu Asn  
 330 335 340  
  
 gat gaa gga taatgaagat ttcgatccag att  
 1155  
 Asp Glu Gly

&lt;210&gt; 106

&lt;211&gt; 344

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 106

Met His Ala Phe Arg Arg Pro Pro Pro Leu Thr Thr Arg Val Gly Ala  
 1 5 10 15

Ala Leu Leu Ala Ala Thr Leu Leu Ala Ser Cys Thr Pro Thr Pro Val  
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<220>
<221> CDS
<222> (101)..(1132)
<223> RXA00278
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				Met His Ala Phe Arg		
				1 5		
cgc ccc cct cca ctc acc acg cga gtc ggc gct gca ttg ctg gcc gca	163					
Arg Pro Pro Pro Leu Thr Thr Arg Val Gly Ala Ala Leu Leu Ala Ala						
10 15 20						
acg ctg ctt gct tcc tgc act cca aca cct gtg gaa ccg gca gaa acc	211					
Thr Leu Leu Ala Ser Cys Thr Pro Thr Pro Val Glu Pro Ala Glu Thr						
25 30 35						
ttg act gct ttg gat ccc gat gcc ggt cca cca ctg cca ccg gat tct	259					
Leu Thr Ala Leu Asp Pro Asp Ala Gly Pro Pro Leu Pro Pro Asp Ser						
40 45 50						
tcg att gaa gct ccc ggt gaa aaa gag ccc att gtg gaa gta ata gag	307					
Ser Ile Glu Ala Pro Gly Glu Lys Glu Pro Ile Val Glu Val Ile Glu						
55 60 65						
aat tgg cca ggt tct tta cgc ccg gat gat ctg acc cct gag gag cgg	355					
Asn Trp Pro Gly Ser Leu Arg Pro Asp Asp Leu Thr Pro Glu Glu Arg						
70 75 80 85						
gta cct ggc atc gtc aac cgg ggt cgc atc att gtg ggt gtg gat caa	403					
Val Pro Gly Ile Val Asn Arg Gly Arg Ile Ile Val Gly Val Asp Gln						
90 95 100						
tcg caa aac ttg ctc agt ttc cgt gat ccg gtg act ggt gag ctg cgc	451					
Ser Gln Asn Leu Leu Ser Phe Arg Asp Pro Val Thr Gly Glu Leu Arg						
105 110 115						
ggt ttt gaa gtg gaa tta gcg agg gaa att tcc cgc gac att ttc ggt	499					
Gly Phe Glu Val Glu Leu Ala Arg Glu Ile Ser Arg Asp Ile Phe Gly						
120 125 130						
rac ccc aat aag gtg gat ttc cga ttc gtc ggc tcg tcc gac cgt ctg	547					
asp Pro Asn Lys Val Asp Phe Arg Phe Val Gly Ser Ser Asp Arg Leu						
135 140 145						
gt tcc ctt gac caa ggt gat gta gat att gtg att cgt tcc gtc acg	595					
arg Ser Leu Asp Gln Gly Asp Val Asp Ile Val Ile Arg Ser Val Thr						
50 155 160 165						
tc acc gac gaa cgc gcc aaa ttg gtg gaa ttt tcc aca ccg tac ctg	643					
le Thr Asp Glu Arg Ala Lys Leu Val Glu Phe Ser Thr Pro Tyr Leu						
170 175 180						



&lt;210&gt; 104

&lt;211&gt; 287

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 104

Glu Leu Ala Asp Tyr Ile Pro Glu Leu Lys Ser Ala Asp Pro Asn Pro  
 1 5 10 15

Leu Ala Val Ala Leu Cys Thr Val Asn Gly His Ile Tyr Ser Ala Gly  
 20 25 30

Asp Asp Asp Ile Glu Phe Thr Met Gln Ser Ile Ser Lys Pro Phe Ala  
 35 40 45

Tyr Ala Leu Ala Leu Gln Glu Cys Gly Phe Asp Glu Val Ser Ala Ser  
 50 55 60

Val Ala Leu Glu Pro Ser Gly Glu Ala Phe Asn Glu Leu Ser Leu Asp  
 65 70 75 80

Gly Glu Asn Arg Pro Met Asn Pro Met Ile Asn Ala Gly Ala Ile Ala  
 85 90 95

Ile Asn Gln Leu Ile Asn Gly Ser Asp Ser Thr Val Glu Asp Arg Val  
 100 105 110

Glu Lys Ile Arg His Tyr Phe Ser Glu Leu Ala Gly Arg Glu Leu Thr  
 115 120 125

Ile Asp Arg Val Leu Ala Glu Ser Glu Leu Ala Gly Ala Asp Arg Asn  
 130 135 140

Leu Ser Ile Ala His Met Leu Arg Asn Tyr Gly Val Ile Glu Asp Glu  
 145 150 155 160

Ala His Asp Ala Val Leu Ser Tyr Thr Leu Gln Cys Ala Ile Lys Val  
 165 170 175

Thr Thr Arg Asp Leu Ala Val Met Thr Ala Thr Leu Ala Ala Gly Gly  
 180 185 190

Thr His Pro Ile Thr Gly Lys Lys Leu Leu Asp Ala Arg Val Cys Arg  
 195 200 205

Leu Thr Leu Ser Val Met Ala Ser Ala Gly Met Tyr Asp Glu Ala Gly  
 210 215 220

Gln Trp Leu Ser Thr Val Gly Ile Pro Ala Lys Ser Gly Val Ala Gly  
 225 230 235 240

Gly Leu Ile Gly Ile Leu Pro Gly Gln Leu Gly Ile Ala Thr Phe Ser  
 245 250 255

Pro Arg Leu Asn Pro Lys Gly Asn Ser Val Arg Gly Val Lys Ile Phe  
 260 265 270

Lys Gln Leu Ser Asp Asp Met Gly Leu His Leu Met Ser Thr Glu  
 275 280 285

tac gca ctc gca ctc caa gaa tgc ggc ttt gat gag gtc tct gca tcc	192
Tyr Ala Leu Ala Leu Gln Glu Cys Gly Phe Asp Glu Val Ser Ala Ser	
50 55 60	
gtg gcc ttg gag ccc tcc ggt gag gcc ttc aac gaa ctt tcc ctc gac	240
Val Ala Leu Glu Pro Ser Gly Glu Ala Phe Asn Glu Leu Ser Leu Asp	
65 70 75 80	
ggc gaa aac cgc ccc atg aac ccc atg atc aac gcc ggc gcg atc gcc	288
Gly Glu Asn Arg Pro Met Asn Pro Met Ile Asn Ala Gly Ala Ile Ala	
85 90 95	
atc aac cag ctg atc aac ggc tcc gat tcc acc gtg gaa gac cgc gtg	336
Ile Asn Gln Leu Ile Asn Gly Ser Asp Ser Thr Val Glu Asp Arg Val	
100 105 110	
gaa aaa atc cga cac tac ttc tct gaa ctt gct gga cgc gaa ctc acc	384
Glu Lys Ile Arg His Tyr Phe Ser Glu Leu Ala Gly Arg Glu Leu Thr	
115 120 125	
atc gac cgc gtg ctt gcc gaa tcc gaa ctc gcc ggc gcc gac cgc aac	432
Ile Asp Arg Val Leu Ala Glu Ser Glu Leu Ala Gly Ala Asp Arg Asn	
130 135 140	
ctc tcc atc gcc cac atg ctg cgc aat tac ggc gtc atc gaa gac gaa	480
Leu Ser Ile Ala His Met Leu Arg Asn Tyr Gly Val Ile Glu Asp Glu	
145 150 155 160	
gcc cac gac gcc gtc ctc agc tac acg ctg caa tgc gcc atc aaa gta	528
Ala His Asp Ala Val Leu Ser Tyr Thr Leu Gln Cys Ala Ile Lys Val	
165 170 175	
acc acg cgc gac ctc gca gtc atg acc gcc acg ctc gcc gcc ggc ggc	576
Thr Thr Arg Asp Leu Ala Val Met Thr Ala Thr Leu Ala Ala Gly Gly	
180 185 190	
aca cac cca att acc ggc aag aag ctt ctc gac gcc cgc gtc tgc cgc	624
Thr His Pro Ile Thr Gly Lys Lys Leu Leu Asp Ala Arg Val Cys Arg	
195 200 205	
ctc acc ctc tcc gtc atg gct tca gca ggc atg tac gac gag gca ggg	672
Leu Thr Leu Ser Val Met Ala Ser Ala Gly Met Tyr Asp Glu Ala Gly	
210 215 220	
cag tgg ctc tcc acc gta ggc atc ccc gcg aaa tca gga gtc gcc ggc	720
Gln Trp Leu Ser Thr Val Gly Ile Pro Ala Lys Ser Gly Val Ala Gly	
225 230 235 240	
gga ctc atc ggc att ctg cca ggt cag ctg ggc atc gcc aca ttt tcc	768
Gly Leu Ile Gly Ile Leu Pro Gly Gln Leu Gly Ile Ala Thr Phe Ser	
245 250 255	
cca cgc ctg aac ccc aaa ggc aac agc gtg cgc ggc gta aaa ata ttc	816
Pro Arg Leu Asn Pro Lys Gly Asn Ser Val Arg Gly Val Lys Ile Phe	
260 265 270	
aaa cag ctt tcc gac gac atg ggc ctc cac ctc atg tcc acc gag	861
Lys Gln Leu Ser Asp Asp Met Gly Leu His Leu Met Ser Thr Glu	
275 280 285	

Ile Asn Gln Leu Ile Asn Gly Ser Asp Ser Thr Val Glu Asp Arg Val  
 100 105 110  
 Glu Lys Ile Arg His Tyr Phe Ser Glu Leu Ala Gly Arg Glu Leu Thr  
 115 120 125  
 Ile Asp Arg Val Leu Ala Glu Ser Glu Leu Ala Gly Ala Asp Arg Asn  
 130 135 140  
 Leu Ser Ile Ala His Met Leu Arg Asn Tyr Gly Val Ile Glu Asp Glu  
 145 150 155 160  
 Ala His Asp Ala Val Leu Ser Tyr Thr Leu Gln Cys Ala Ile Lys Val  
 165 170 175  
 Thr Thr Arg Asp Leu Ala Val Met Thr Ala Thr Leu Ala Ala Gly Gly  
 180 185 190  
 Thr His Pro Ile Thr Gly Lys Lys Leu Leu Asp Ala Arg Val Cys Arg  
 195 200 205  
 Leu Thr Leu Ser Val Met Ala Ser Ala Gly Met Tyr Asp Glu Ala Gly  
 210 215 220  
 Gln Trp Leu Ser Thr Val Gly Ile Pro Ala Lys Ser Gly Val Ala Gly  
 225 230 235 240  
 Gly Leu Ile Gly Ile Leu Pro Gly Gln Leu Gly Ile Ala Thr Phe Ser  
 245 250 255  
 Pro Arg Leu Asn Pro Lys Gly Asn Ser Val Arg Gly Val Lys Ile Phe  
 260 265 270  
 Lys Gln Leu Ser Asp Asp Met Gly Leu His Leu Met Ser Thr Glu  
 275 280 285

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 <213> Corynebacterium glutamicum

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 Glu Leu Ala Asp Tyr Ile Pro Glu Leu Lys Ser Ala Asp Pro Asn Pro  
 1 5 10 15  
 ctg gca gta gcc ctg tgc acc gtt aac gga cac atc tac agc gca ggc 96  
 Leu Ala Val Ala Leu Cys Thr Val Asn Gly His Ile Tyr Ser Ala Gly  
 20 25 30  
 gat gac gac atc gaa ttc acc atg caa agt att tcc aag cca ttt gcc 144  
 Asp Asp Asp Ile Glu Phe Thr Met Gln Ser Ile Ser Lys Pro Phe Ala  
 35 40 45

ctc tcc atc gcc cac atg ctg cgc aat tac ggc gtc atc gaa gac gaa 480  
 Leu Ser Ile Ala His Met Leu Arg Asn Tyr Gly Val Ile Glu Asp Glu  
 145 150 155 160  
 gcc cac gac gcc gtc ctc agc tac acg ctg caa tgc gcc atc aaa gta 528  
 Ala His Asp Ala Val Leu Ser Tyr Thr Leu Gln Cys Ala Ile Lys Val  
 165 170 175  
 acc acg cgc gac ctc gca gtc atg acc gcc acg ctc gcc gcc ggc ggc 576  
 Thr Thr Arg Asp Leu Ala Val Met Thr Ala Thr Leu Ala Ala Gly Gly  
 180 185 190  
 aca cac cca att acc ggc aag aag ctt ctc gac gcc cgc gtc tgc cgc 624  
 Thr His Pro Ile Thr Gly Lys Lys Leu Leu Asp Ala Arg Val Cys Arg  
 195 200 205  
 ctc acc ctc tcc gtc atg gct tca gca ggc atg tac gac gag gca ggc 672  
 Leu Thr Leu Ser Val Met Ala Ser Ala Gly Met Tyr Asp Glu Ala Gly  
 210 215 220  
 cag tgg ctc tcc acc gta ggc atc ccc gcg aaa tca gga gtc gcc ggc 720  
 Gln Trp Leu Ser Thr Val Gly Ile Pro Ala Lys Ser Gly Val Ala Gly  
 225 230 235 240  
 gga ctc atc ggc att ctg cca ggt cag ctg ggc atc gcc aca ttt tcc 768  
 Gly Leu Ile Gly Ile Leu Pro Gly Gln Leu Gly Ile Ala Thr Phe Ser  
 245 250 255  
 cca cgc ctg aac ccc aaa ggc aac agc gtg cgc ggc gta aaa ata ttc 816  
 Pro Arg Leu Asn Pro Lys Gly Asn Ser Val Arg Gly Val Lys Ile Phe  
 260 265 270  
 aaa cag ctt tcc gac gac atg ggc ctc cac ctc atg tcc acc gag 861  
 Lys Gln Leu Ser Asp Asp Met Gly Leu His Leu Met Ser Thr Glu  
 275 280 285

&lt;210&gt; 102

&lt;211&gt; 287

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 102

Glu Leu Ala Asp Tyr Ile Pro Glu Leu Lys Ser Ala Asp Pro Asn Pro  
 1 5 10 15  
 Leu Ala Val Ala Leu Cys Thr Val Asn Gly His Ile Tyr Ser Ala Gly  
 20 25 30  
 Asp Asp Asp Ile Glu Phe Thr Met Gln Ser Ile Ser Lys Pro Phe Ala  
 35 40 45  
 Tyr Ala Leu Ala Leu Gln Glu Cys Gly Phe Asp Glu Val Ser Ala Ser  
 50 55 60  
 Val Ala Leu Glu Pro Ser Gly Glu Ala Phe Asn Glu Leu Ser Leu Asp  
 65 70 75 80  
 Gly Glu Asn Arg Pro Met Asn Pro Met Ile Asn Ala Gly Ala Ile Ala  
 85 90 95

980	985	990	
Thr Pro Gly Pro His Leu Ala Gln Val Ala Gly Ala Ser Gly Trp Asp			
995	1000	1005	
Pro Asn Glu Tyr Gln Glu Tyr Leu Glu Asn Tyr Leu Lys Val Thr Arg			
1010	1015	1020	
Lys Ser Arg Gln Val Val Asp Glu Val Phe Trp Gly Val Asp Ser Met			
1025	1030	1035	1040
Glu Gln Arg Glu Phe			
1045			
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Glu Leu Ala Asp Tyr Ile Pro Glu Leu Lys Ser Ala Asp Pro Asn Pro			
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ctg gca gta gcc ctg tgc acc gtt aac gga cac atc tac agc gca ggc 96			
Leu Ala Val Ala Leu Cys Thr Val Asn Gly His Ile Tyr Ser Ala Gly			
	20	25	30
gat gac gac atc gaa ttc acc atg caa agt att tcc aag cca ttt gcc 144			
Asp Asp Asp Ile Glu Phe Thr Met Gln Ser Ile Ser Lys Pro Phe Ala			
	35	40	45
tac gca ctc gca ctc caa gaa tgc ggc ttt gat gag gtc tct gca tcc 192			
Tyr Ala Leu Ala Leu Gln Glu Cys Gly Phe Asp Glu Val Ser Ala Ser			
50		55	60
gtg gcc ttg gag ccc tcc ggt gag gcc ttc aac gaa ctt tcc ctc gac 240			
Val Ala Leu Glu Pro Ser Gly Glu Ala Phe Asn Glu Leu Ser Leu Asp			
65	70	75	80
ggc gaa aac cgc ccc atg aac ccc atg atc aac gcc ggc gcg atc gcc 288			
Gly Glu Asn Arg Pro Met Asn Pro Met Ile Asn Ala Gly Ala Ile Ala			
	85	90	95
atc aac cag ctg atc aac ggc tcc gat tcc acc gtg gaa gac cgc gtg 336			
Ile Asn Gln Leu Ile Asn Gly Ser Asp Ser Thr Val Glu Asp Arg Val			
	100	105	110
gaa aaa atc cga cac tac ttc tct gaa ctt gct gga cgc gaa ctc acc 384			
Glu Lys Ile Arg His Tyr Phe Ser Glu Leu Ala Gly Arg Glu Leu Thr			
115	120	125	
atc gac cgc gtg ctt gcc gaa tcc gaa ctc gcc ggc gcc gac cgc aac 432			
Ile Asp Arg Val Leu Ala Glu Ser Glu Leu Ala Gly Ala Asp Arg Asn			
130	135	140	

Ala Ala Ser Gly Pro Lys Leu Leu Ala Thr Ala Pro Thr Gln Val Val  
 660 665 670  
 Lys Ala Ile Lys Ala Thr Val Ser Arg His Glu Ser Pro Asp Arg Ala  
 675 680 685  
 Ile Gln Ala Ala Arg Ser Leu Arg Arg Gln Glu Leu Ala Arg Ile Ala  
 690 695 700  
 Ser Ala Asp Leu Leu Asn Met Leu Thr Val Gln Glu Val Cys Gln Ser  
 705 710 715 720  
 Leu Ser Leu Val Trp Asp Ala Val Leu Asp Ala Ala Leu Asp Ala Glu  
 725 730 735  
 Ile Arg Ala Ala Leu Asn Asp Pro Gln Lys Pro Asp Gln Pro Leu Ala  
 740 745 750  
 Asn Ile Ser Val Ile Gly Met Gly Arg Leu Gly Gly Ala Glu Leu Gly  
 755 760 765  
 Tyr Gly Ser Asp Ala Asp Val Met Phe Val Cys Glu Pro Val Ala Gly  
 770 775 780  
 Val Glu Glu His Glu Ala Val Thr Trp Ser Ile Ala Ile Cys Asp Ser  
 785 790 795 800  
 Met Arg Ser Arg Leu Ala Gln Pro Ser Gly Asp Pro Pro Leu Glu Val  
 805 810 815  
 Asp Leu Gly Leu Arg Pro Glu Gly Arg Ser Gly Ala Ile Val Arg Thr  
 820 825 830  
 Val Asp Ser Tyr Val Lys Tyr Tyr Glu Lys Trp Gly Glu Thr Trp Glu  
 835 840 845  
 Ile Gln Ala Leu Leu Arg Ala Ala Trp Val Ala Gly Asp Arg Glu Leu  
 850 855 860  
 Gly Ile Lys Phe Leu Glu Ser Ile Asp Arg Phe Arg Tyr Pro Val Asp  
 865 870 875 880  
 Gly Ala Thr Gln Ala Gln Leu Arg Glu Val Arg Arg Ile Lys Ala Arg  
 885 890 895  
 Val Asp Asn Glu Arg Leu Pro Arg Gly Ala Asp Arg Asn Thr His Thr  
 900 905 910  
 Lys Leu Gly Arg Gly Ala Leu Thr Asp Ile Glu Trp Thr Val Gln Leu  
 915 920 925  
 Leu Thr Met Met His Ala His Glu Ile Pro Glu Leu His Asn Thr Ser  
 930 935 940  
 Thr Leu Glu Val Leu Glu Val Leu Glu Lys His Gln Ile Ile Asn Pro  
 945 950 955 960  
 Val Gln Val Gln Thr Leu Arg Glu Ala Trp Leu Thr Ala Thr Ala Ala  
 965 970 975  
 Arg Asn Ala Leu Val Leu Val Arg Gly Lys Arg Leu Asp Gln Leu Pro

Ala Leu Leu Lys Ala Arg Pro Met Thr Gly Asp Ile Asn Leu Gly Gln  
 340 345 350  
 Ser Tyr Val Asp Ala Leu Ser Pro Leu Ile Trp Thr Ala Ser Gln Arg  
 355 360 365  
 Glu Ser Phe Val Thr Asp Val Gln Ala Met Arg Arg Arg Val Leu Asp  
 370 375 380  
 Asn Val Pro Glu Asp Leu Arg Asp Arg Glu Leu Lys Leu Gly Arg Gly  
 385 390 395 400  
 Gly Leu Arg Asp Val Glu Phe Ala Val Gln Leu Leu Gln Met Val His  
 405 410 415  
 Gly Arg Ile Asp Glu Thr Leu Arg Val Arg Ser Thr Val Asn Ala Leu  
 420 425 430  
 His Val Leu Val Asp Gln Gly Tyr Val Gly Arg Glu Asp Gly His Asn  
 435 440 445  
 Leu Ile Glu Ser Tyr Glu Phe Leu Arg Leu Leu Glu His Arg Leu Gln  
 450 455 460  
 Leu Glu Arg Ile Lys Arg Thr His Leu Leu Pro Lys Pro Asp Asp Arg  
 465 470 475 480  
 Met Asn Met Arg Trp Leu Ala Arg Ala Ser Gly Phe Thr Gly Ser Met  
 485 490 495  
 Glu Gln Ser Ser Ala Lys Ala Met Glu Arg His Leu Arg Lys Val Arg  
 500 505 510  
 Leu Gln Ile Gln Ser Leu His Ser Gln Leu Phe Tyr Arg Pro Leu Leu  
 515 520 525  
 Asn Ser Val Val Asn Leu Ser Ala Asp Ala Ile Arg Leu Ser Pro Asp  
 530 535 540  
 Ala Ala Lys Leu Gln Leu Ala Ala Leu Gly Tyr Leu His Pro Ser Arg  
 545 550 555 560  
 Ala Tyr Glu His Leu Thr Ala Leu Ala Ser Gly Ala Ser Arg Lys Ala  
 565 570 575  
 Lys Ile Gln Ala Met Leu Leu Pro Thr Leu Met Glu Trp Leu Ser Gln  
 580 585 590  
 Thr Ala Glu Pro Asp Ala Gly Leu Leu Asn Tyr Arg Lys Leu Ser Asp  
 595 600 605  
 Ala Ser Tyr Asp Arg Ser Trp Phe Leu Arg Met Leu Arg Asp Glu Gly  
 610 615 620  
 Val Val Gly Gln Arg Leu Met Arg Ile Leu Gly Asn Ser Pro Tyr Ile  
 625 630 635 640  
 Ser Glu Leu Ile Ile Ser Thr Pro Asp Phe Met Lys Gln Leu Gly Asp  
 645 650 655

1	5	10	15
Asp Pro Leu	Pro Lys Val Gly Ser Leu	Ser Leu Lys Ser	Glu His Ala
	20	25	30
Gln Ala Asp	Leu Glu His Leu Gly Trp Arg Asn Val	Glu Ser Leu	Asp
	35	40	45
Leu Leu Trp	Gly Leu Ser Gly Ala Gly Asp Pro	Asp Val Ala Leu	Asn
	50	55	60
Leu Leu Ile	Arg Leu Tyr Gln Ala Leu Glu Ala Ile Gly Glu Asp Ala		
	65	70	75
Arg Asn Glu	Leu Asp Gln Glu Ile Arg Gln Asp Glu Lys Leu Arg Val		
	85	90	95
Arg Leu Phe	Ala Leu Leu Gly Gly Ser Ser Ala Val Gly Asp His Leu		
	100	105	110
Val Ala Asn	Pro Leu Gln Trp Lys Leu Leu Lys Leu Asp Ala Pro Ser		
	115	120	125
Arg Glu Glu	Met Phe Gln Ala Leu Leu Glu Ser Val Lys Ala Gln Pro		
	130	135	140
Ala Val Leu	Glu Val Glu Asp Phe Ser Asp Ala His Asn Ile Ala Arg		
	145	150	155
Asp Asp Leu	Ser Thr Pro Gly Phe Tyr Thr Ala Ser Val Thr Gly Pro		
	165	170	175
Glu Ala Glu	Arg Val Leu Lys Trp Thr Tyr Arg Thr Leu Leu Thr Arg		
	180	185	190
Ile Ala Ala	His Asp Leu Ala Gly Thr Tyr Pro Thr Asp Met Arg Arg		
	195	200	205
Lys Gly Gly	Asp Pro Val Pro Phe Ser Thr Val Thr Met Gln Leu Ser		
	210	215	220
Asp Leu Ala	Asp Ala Ala Leu Thr Ala Ala Leu Ala Val Ala Ile Ala		
	225	230	235
Asn Val Tyr	Gly Glu Lys Pro Val Asp Ser Ala Leu Ser Val Ile Ala		
	245	250	255
Met Gly Lys	Cys Gly Ala Gln Glu Leu Asn Tyr Ile Ser Asp Val Asp		
	260	265	270
Val Val Phe	Val Ala Glu Pro Ala Asn Ser Lys Ser Thr Arg Thr Ala		
	275	280	285
Ala Glu Leu	Ile Arg Ile Gly Ser Asn Ser Phe Phe Glu Val Asp Ala		
	290	295	300
Ala Leu Arg	Pro Glu Gly Lys Ser Gly Ala Leu Val Arg Ser Leu Asp		
	305	310	315
Ser His Met	Ala Tyr Tyr Lys Arg Trp Ala Glu Thr Trp Glu Phe Gln		
	325	330	335



cag ctt cgt gaa gtt cgt cga att aag gcg agg gtg gat aat gag agg  
 2803  
 Gln Leu Arg Glu Val Arg Arg Ile Lys Ala Arg Val Asp Asn Glu Arg  
 890 895 900  
 ctt ccg cgc ggg gct gat cga aat acc cat acc aag ctg ggt cgg gga  
 2851  
 Leu Pro Arg Gly Ala Asp Arg Asn Thr His Thr Lys Leu Gly Arg Gly  
 905 910 915  
 gcg tta act gac atc gag tgg act gtg cag ttg ttg acc atg atg cat  
 2899  
 Ala Leu Thr Asp Ile Glu Trp Thr Val Gln Leu Leu Thr Met Met His  
 920 925 930  
 gct cat gag att ccg gag ctg cac aat acg tcg acg ttg gaa gtt ctt  
 2947  
 Ala His Glu Ile Pro Glu Leu His Asn Thr Ser Thr Leu Glu Val Leu  
 935 940 945  
 gaa gtg ctg gaa aag cat cag att att aac cct gtg cag gtg cag acg  
 2995  
 Glu Val Leu Glu Lys His Gln Ile Ile Asn Pro Val Gln Val Gln Thr  
 950 955 960 965  
 ctt cgg gaa gcg tgg ctg acg gca acg gct gct agg aat gcg ctt gtg  
 3043  
 Leu Arg Glu Ala Trp Leu Thr Ala Thr Ala Ala Arg Asn Ala Leu Val  
 970 975 980  
 ctg gtc agg ggt aag aga tta gat cag tta cct act cct ggt ccg cac  
 3091  
 Leu Val Arg Gly Lys Arg Leu Asp Gln Leu Pro Thr Pro Gly Pro<sup>\*</sup>His  
 985 990 995  
 ctt gcg cag gtg gct ggt gcg tct ggt tgg gat cca aat gag tac cag  
 3139  
 Leu Ala Gln Val Ala Gly Ala Ser Gly Trp Asp Pro Asn Glu Tyr Gln  
 1000 1005 1010  
 gag tat ttg gaa aac tat ctg aaa gtg acc agg aag agt cgt cag gtt  
 3187  
 Glu Tyr Leu Glu Asn Tyr Leu Lys Val Thr Arg Lys Ser Arg Gln Val  
 1015 1020 1025  
 gtt gat gaa gtc ttc tgg ggt gtg gac tct atg gag caa cgt gag ttt  
 3235  
 Val Asp Glu Val Phe Trp Gly Val Asp Ser Met Glu Gln Arg Glu Phe  
 1030 1035 1040 1045  
 taggtaggtg gtgggagccc caa  
 3258

&lt;210&gt; 100

&lt;211&gt; 1045

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 100

Met Ser Gly Pro Leu Arg Ser Glu Arg Lys Val Val Gly Phe Val Arg

tcg ctg agg agg cag gag ctg gca cgc att gcc tct gct gat ttg ctc  
2227

Ser Leu Arg Arg Gln Glu Leu Ala Arg Ile Ala Ser Ala Asp Leu Leu  
695 700 705

aac atg ctc act gtt cag gaa gta tgc caa agc ttg tca cta gtc tgg  
2275

Asn Met Leu Thr Val Gln Glu Val Cys Gln Ser Leu Ser Leu Val Trp  
710 715 720 725

gat gcg gtg ttg gat gct gcc ttg gat gcg gaa atc cgt gct gca ctt  
2323

Asp Ala Val Leu Asp Ala Ala Leu Asp Ala Glu Ile Arg Ala Ala Leu  
730 735 740

aac gat cca cag aaa cca gat cag cct ctg gcc aat att tct gtg atc  
2371

Asn Asp Pro Gln Lys Pro Asp Gln Pro Leu Ala Asn Ile Ser Val Ile  
745 750 755

ggc atg ggc cgt ttg ggt gga gca gaa ctt gga tac ggt tct gat gcc  
2419

Gly Met Gly Arg Leu Gly Gly Ala Glu Leu Gly Tyr Gly Ser Asp Ala  
760 765 770

gat gtg atg ttt gta tgc gag ccg gta gcc ggt gtg gaa gag cat gag  
2467

Asp Val Met Phe Val Cys Glu Pro Val Ala Gly Val Glu Glu His Glu  
775 780 785

gcc gtc aca tgg tct att gct atc tgt gat tcc atg cgg tcg agg ctt  
2515

Ala Val Thr Trp Ser Ile Ala Ile Cys Asp Ser Met Arg Ser Arg Leu  
790 795 800 805

gcg cag cct tcc ggt gat cca cct ttg gag gtg gat ctg ggg ctg cgt  
2563

Ala Gln Pro Ser Gly Asp Pro Pro Leu Glu Val Asp Leu Gly Leu Arg  
810 815 820

cct gaa ggg aga tct ggt gcg att gtg cgc acc gtt gat tcc tat gtg  
2611

Pro Glu Gly Arg Ser Gly Ala Ile Val Arg Thr Val Asp Ser Tyr Val  
825 830 835

aag tac tac gaa aag tgg ggt gaa act tgg gag att cag gcg ctg ctg  
2659

Lys Tyr Tyr Glu Lys Trp Gly Glu Thr Trp Glu Ile Gln Ala Leu Leu  
840 845 850

agg gct gcg tgg gtt gct ggt gat cgt gag ctg ggt att aag ttc ttg  
2707

Arg Ala Ala Trp Val Ala Gly Asp Arg Glu Leu Gly Ile Lys Phe Leu  
855 860 865

gag tcg att gat cgt ttc cgc tac cca gtt gac ggg gca acg cag gcg  
2755

Glu Ser Ile Asp Arg Phe Arg Tyr Pro Val Asp Gly Ala Thr Gln Ala  
870 875 880 885

aaa gct atg gaa cgg cat ttg cgt aag gtt cgt ttg cag att cag tcg  
1651

Lys Ala Met Glu Arg His Leu Arg Lys Val Arg Leu Gln Ile Gln Ser  
505 510 515

ttg cat agt cag ctg ttt tat cgg cca ctg ctg aac tct gtg gtc aac  
1699

Leu His Ser Gln Leu Phe Tyr Arg Pro Leu Leu Asn Ser Val Val Asn  
520 525 530

ttg agc gcg gat gcc atc agg ttg tct ccg gat gct gca aag cta caa  
1747

Leu Ser Ala Asp Ala Ile Arg Leu Ser Pro Asp Ala Ala Lys Leu Gln  
535 540 545

ttg gcg gca ttg gga tac ctg cat cca tca cgt gct tat gaa cac ctg  
1795

Leu Ala Ala Leu Gly Tyr Leu His Pro Ser Arg Ala Tyr Glu His Leu  
550 555 560 565

act gct ctt gca tca gga gct agc cgt aaa gcc aag att cag gcg atg  
1843

Thr Ala Leu Ala Ser Gly Ala Ser Arg Lys Ala Lys Ile Gln Ala Met  
570 575 580

ttg ctg ccc acg ttg atg gag tgg ctg tct caa aca gct gaa cca gat  
1891

Leu Leu Pro Thr Leu Met Glu Trp Leu Ser Gln Thr Ala Glu Pro Asp  
585 590 595

gcg gga ttg ctg aat tac cgc aag ctt tct gat gct tcc tat gat cgc  
1939

Ala Gly Leu Leu Asn Tyr Arg Lys Leu Ser Asp Ala Ser Tyr Asp Arg  
600 605 610

agc tgg ttt ttg cgc atg ctg cgt gat gag ggc gta gtg ggg cag cgg  
1987

Ser Trp Phe Leu Arg Met Leu Arg Asp Glu Gly Val Val Gly Gln Arg  
615 620 625

ttg atg cgt att ttg gga aat tct ccc tat att tct gaa ctg att atc  
2035

Leu Met Arg Ile Leu Gly Asn Ser Pro Tyr Ile Ser Glu Leu Ile Ile  
630 635 640 645

tcc act ccg gac ttt atg aaa cag ctg ggt gat gcg gcg tct ggt cct  
2083

Ser Thr Pro Asp Phe Met Lys Gln Leu Gly Asp Ala Ala Ser Gly Pro  
650 655 660

aaa ttg ctt gct act gca ccg act cag gtt gtg aaa gca atc aag gca  
2131

Lys Leu Leu Ala Thr Ala Pro Thr Gln Val Val Lys Ala Ile Lys Ala  
665 670 675

acg gtg tcg cgt cat gag tca cct gat cgg gcg atc cag gct gca cga  
2179

Thr Val Ser Arg His Glu Ser Pro Asp Arg Ala Ile Gln Ala Ala Arg  
680 685 690

ggt aaa agt ggc gct ctt gtg cgc tct ttg gat tcc cat atg gcg tat  
 1075  
 Gly Lys Ser Gly Ala Leu Val Arg Ser Leu Asp Ser His Met Ala Tyr  
 310 315 320 325

tac aag cgc tgg gcg gaa acc tgg gag ttt cag gca ctg ctg aaa gct  
 1123  
 Tyr Lys Arg Trp Ala Glu Thr Trp Glu Phe Gln Ala Leu Leu Lys Ala  
 330 335 340

cgt ccc atg acg ggt gat att aac ctt ggg cag tcc tat gtg gat gct  
 1171  
 Arg Pro Met Thr Gly Asp Ile Asn Leu Gly Gln Ser Tyr Val Asp Ala  
 345 350 355

ctt tca ccg ttg att tgg acg gct agc cag cgg gaa tca ttt gtc aca  
 1219  
 Leu Ser Pro Leu Ile Trp Thr Ala Ser Gln Arg Glu Ser Phe Val Thr  
 360 365 370

gat gtc caa gct atg cgc cgt cga gtg ttg gac aat gtt ccg gaa gac  
 1267  
 Asp Val Gln Ala Met Arg Arg Arg Val Leu Asp Asn Val Pro Glu Asp  
 375 380 385

ttg cgt gat cgt gag ctg aag ctt ggt cgc ggt ggt ttg agg gat gtg  
 1315  
 Leu Arg Asp Arg Glu Leu Lys Leu Gly Arg Gly Gly Leu Arg Asp Val  
 390 395 400 405

gag ttt gct gtc cag ctc ctt cag atg gtg cat ggt cgc att gat gag  
 1363  
 Glu Phe Ala Val Gln Leu Leu Gln Met Val His Gly Arg Ile Asp Glu  
 410 415 420

acg ttg cgg gtt cgg tca acg gta aat gct ttg cat gtg ttg gtt gat  
 1411  
 Thr Leu Arg Val Arg Ser Thr Val Asn Ala Leu His Val Leu Val Asp  
 425 430 435

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 1459  
 Gln Gly Tyr Val Gly Arg Glu Asp Gly His Asn Leu Ile Glu Ser Tyr  
 440 445 450

gag ttt ttg cgt ctg ttg gag cat cgc ctt caa ttg gag cgg atc aag  
 1507  
 Glu Phe Leu Arg Leu Leu Glu His Arg Leu Gln Leu Glu Arg Ile Lys  
 455 460 465

cgc act cac ttg tta ccg aaa cct gat gac cga atg aat atg cgc tgg  
 1555  
 Arg Thr His Leu Leu Pro Lys Pro Asp Asp Arg Met Asn Met Arg Trp  
 470 475 480 485

ttg gcg cgc gct tct ggg ttt act ggt tcg atg gag caa agt tcg gcc  
 1603  
 Leu Ala Arg Ala Ser Gly Phe Thr Gly Ser Met Glu Gln Ser Ser Ala  
 490 495 500

Tyr	Gln	Ala	Leu	Glu	Ala	Ile	Gly	Glu	Asp	Ala	Arg	Asn	Glu	Leu	Asp	
70					75					80					85	
caa	gag	att	cgc	cag	gat	gaa	aaa	cta	cga	gtc	cgc	ctt	ttt	gca	ttg	403
Gln	Glu	Ile	Arg	Gln	Asp	Glu	Lys	Leu	Arg	Val	Arg	Leu	Phe	Ala	Leu	
				90					95					100		
ttg	ggt	ggt	tcc	tcg	gct	gtc	ggt	gat	cac	ttg	gtc	gcc	aat	cct	ttg	451
Leu	Gly	Gly	Ser	Ser	Ala	Val	Gly	Asp	His	Leu	Val	Ala	Asn	Pro	Leu	
			105					110					115			
cag	tgg	aaa	ctc	tta	aaa	ctt	gat	gcg	cca	tcg	agg	gaa	gag	atg	ttt	499
Gln	Trp	Lys	Leu	Leu	Lys	Leu	Asp	Ala	Pro	Ser	Arg	Glu	Glu	Met	Phe	
		120					125					130				
cag	gcg	ctg	ctg	gaa	tct	gtg	aaa	gct	cag	cct	gct	gtg	ctt	gag	gtt	547
Gln	Ala	Leu	Leu	Glu	Ser	Val	Lys	Ala	Gln	Pro	Ala	Val	Leu	Glu	Val	
		135				140					145					
gag	gat	ttc	agc	gat	gca	cac	aac	att	gcc	cga	gac	gat	ttg	agc	acg	595
Glu	Asp	Phe	Ser	Asp	Ala	His	Asn	Ile	Ala	Arg	Asp	Asp	Leu	Ser	Thr	
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cct	ggt	ttt	tac	acg	gct	agt	gtt	acc	ggg	cct	gaa	gca	gag	cga	gtc	643
Pro	Gly	Phe	Tyr	Thr	Ala	Ser	Val	Thr	Gly	Pro	Glu	Ala	Glu	Arg	Val	
				170					175					180		
ttg	aaa	tgg	act	tat	cgc	acg	ttg	ctg	acc	cgg	att	gct	gcg	cat	gat	691
Leu	Lys	Trp	Thr	Tyr	Arg	Thr	Leu	Leu	Thr	Arg	Ile	Ala	Ala	His	Asp	
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Leu	Ala	Gly	Thr	Tyr	Pro	Thr	Asp	Met	Arg	Arg	Lys	Gly	Gly	Asp	Pro	
		200					205					210				
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Val	Pro	Phe	Ser	Thr	Val	Thr	Met	Gln	Leu	Ser	Asp	Leu	Ala	Asp	Ala	
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gct	ttg	act	gct	gct	tta	gct	gtg	gca	att	gcc	aat	gtt	tat	ggt	gaa	835
Ala	Leu	Thr	Ala	Ala	Leu	Ala	Val	Ala	Ile	Ala	Asn	Val	Tyr	Gly	Glu	
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Lys	Pro	Val	Asp	Ser	Ala	Leu	Ser	Val	Ile	Ala	Met	Gly	Lys	Cys	Gly	
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gcg	cag	gaa	ttg	aac	tac	att	tca	gat	gtg	gac	gtg	gtg	ttt	gtt	gca	931
Ala	Gln	Glu	Leu	Asn	Tyr	Ile	Ser	Asp	Val	Asp	Val	Val	Phe	Val	Ala	
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gag	ccg	gca	aac	tct	aaa	tca	aca	cgc	acc	gca	gca	gag	ctc	att	cgc	979
Glu	Pro	Ala	Asn	Ser	Lys	Ser	Thr	Arg	Thr	Ala	Ala	Glu	Leu	Ile	Arg	
		280					285					290				
atc	ggt	agc	aac	tcg	ttc	ttt	gag	gtg	gat	gca	gca	ctt	cgc	cca	gaa	
1027																
Ile	Gly	Ser	Asn	Ser	Phe	Phe	Glu	Val	Asp	Ala	Ala	Leu	Arg	Pro	Glu	
		295				300					305					

340	345	350
Pro Ile Thr Gly Ser Asn Pro Lys Ala Lys Arg Ile Glu Phe Arg Ala 355 360 365		
Pro Asp Pro Ser Gly Asn Pro Tyr Leu Gly Phe Ala Ala Met Met Met 370 375 380		
Ala Gly Leu Asp Gly Ile Lys Asn Arg Ile Glu Pro His Ala Pro Val 385 390 395 400		
Asp Lys Asp Leu Tyr Glu Leu Pro Pro Glu Glu Ala Ala Ser Ile Pro 405 410 415		
Gln Ala Pro Thr Ser Leu Glu Ala Ser Leu Lys Ala Leu Gln Glu Asp 420 425 430		
Thr Asp Phe Leu Thr Glu Ser Asp Val Phe Thr Glu Asp Leu Ile Glu 435 440 445		
Ala Tyr Ile Gln Tyr Lys Tyr Asp Asn Glu Ile Ser Pro Val Arg Leu 450 455 460		
Arg Pro Thr Pro Gln Glu Phe Glu Leu Tyr Phe Asp Cys 465 470 475		
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	Met Ser Gly Pro Leu	
	1 5	
aga agt gaa cgt aaa gtc gtt ggc ttt gtc aga gac cca ctg cca aaa		163
Arg Ser Glu Arg Lys Val Val Gly Phe Val Arg Asp Pro Leu Pro Lys		
10 15 20		
gtt ggt tct tta tcg ctg aaa tct gag cat gcc caa gca gat cta gag		211
Val Gly Ser Leu Ser Leu Lys Ser Glu His Ala Gln Ala Asp Leu Glu		
25 30 35		
cat ttg ggt tgg cgc aat gtt gag tct ttg gat ttg ttg tgg ggc ttg		259
His Leu Gly Trp Arg Asn Val Glu Ser Leu Asp Leu Leu Trp Gly Leu		
40 45 50		
tca ggt gca ggc gat ccc gat gtc gcg ctg aac ctt ctt att cgg ctg		307
Ser Gly Ala Gly Asp Pro Asp Val Ala Leu Asn Leu Leu Ile Arg Leu		
55 60 65		
tat cag gca ctt gaa gca atc ggc gag gat gct cga aac gag ctt gat		355

Asn Val Glu Phe Val Asp Val Arg Phe Thr Asp Leu Pro Gly Thr Glu  
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 Gln His Phe Ser Ile Pro Ala Ala Ser Phe Asp Ala Asp Thr Ile Glu  
 35 40 45  
 Glu Gly Leu Ala Phe Asp Gly Ser Ser Ile Arg Gly Phe Thr Thr Ile  
 50 55 60  
 Asp Glu Ser Asp Met Asn Leu Leu Pro Asp Leu Gly Thr Ala Thr Leu  
 65 70 75 80  
 Asp Pro Phe Arg Lys Ala Lys Thr Leu Asn Val Lys Phe Phe Val His  
 85 90 95  
 Asp Pro Phe Thr Arg Glu Ala Phe Ser Arg Asp Pro Arg Asn Val Ala  
 100 105 110  
 Arg Lys Ala Glu Gln Tyr Leu Ala Ser Thr Gly Ile Ala Asp Thr Cys  
 115 120 125  
 Asn Phe Gly Ala Glu Ala Glu Phe Tyr Leu Phe Asp Ser Val Arg Tyr  
 130 135 140  
 Ser Thr Glu Met Asn Ser Gly Phe Tyr Glu Val Asp Thr Glu Glu Gly  
 145 150 155 160  
 Trp Trp Asn Arg Gly Lys Glu Thr Asn Leu Asp Gly Thr Pro Asn Leu  
 165 170 175  
 Gly Ala Lys Asn Arg Val Lys Gly Gly Tyr Phe Pro Val Ala Pro Tyr  
 180 185 190  
 Asp Gln Thr Val Asp Val Arg Asp Asp Met Val Arg Asn Leu Ala Ala  
 195 200 205  
 Ser Gly Phe Ala Leu Glu Arg Phe His His Glu Val Gly Gly Gly Gln  
 210 215 220  
 Gln Glu Ile Asn Tyr Arg Phe Asn Thr Met Leu His Ala Ala Asp Asp  
 225 230 235 240  
 Ile Gln Thr Phe Lys Tyr Ile Ile Lys Asn Thr Ala Arg Leu His Gly  
 245 250 255  
 Lys Ala Ala Thr Phe Met Pro Lys Pro Leu Ala Gly Asp Asn Gly Ser  
 260 265 270  
 Gly Met His Ala His Gln Ser Leu Trp Lys Asp Gly Lys Pro Leu Phe  
 275 280 285  
 His Asp Glu Ser Gly Tyr Ala Gly Leu Ser Asp Ile Ala Arg Tyr Tyr  
 290 295 300  
 Ile Gly Gly Ile Leu His His Ala Gly Ala Val Leu Ala Phe Thr Asn  
 305 310 315 320  
 Ala Thr Leu Asn Ser Tyr His Arg Leu Val Pro Gly Phe Glu Ala Pro  
 325 330 335  
 Ile Asn Leu Val Tyr Ser Gln Arg Asn Arg Ser Ala Ala Val Arg Ile

tac cac cgt ctg gtt cca ggc ttc gag gct cca atc aac ctg gtg tac  
1123

Tyr His Arg Leu Val Pro Gly Phe Glu Ala Pro Ile Asn Leu Val Tyr  
330 335 340

tca cag cgc aac cgt tcc gct gct gtc cgt atc cca atc acc gga tcc  
1171

Ser Gln Arg Asn Arg Ser Ala Ala Val Arg Ile Pro Ile Thr Gly Ser  
345 350 355

aac ccg aag gca aag cgc atc gaa ttc cgc gct cca gac cca tca ggc  
1219

Asn Pro Lys Ala Lys Arg Ile Glu Phe Arg Ala Pro Asp Pro Ser Gly  
360 365 370

aac cca tac ctg ggc ttt gca gcg atg atg atg gcc ggc ctc gac ggc  
1267

Asn Pro Tyr Leu Gly Phe Ala Ala Met Met Met Ala Gly Leu Asp Gly  
375 380 385

atc aag aac cgc atc gag cca cac gct cca gtg gac aag gac ctc tac  
1315

Ile Lys Asn Arg Ile Glu Pro His Ala Pro Val Asp Lys Asp Leu Tyr  
390 395 400 405

gaa cta cca cca gag gaa gct gca tcc att cca cag gca cca acc tcc  
1363

Glu Leu Pro Pro Glu Glu Ala Ala Ser Ile Pro Gln Ala Pro Thr Ser  
410 415 420

ctg gaa gca tcc ctg aag gca ctg cag gaa gac acc gac ttc ctc acc  
1411

Leu Glu Ala Ser Leu Lys Ala Leu Gln Glu Asp Thr Asp Phe Leu Thr  
425 430 435

gag tct gac gtc ttc acc gag gat ctc atc gag gcg tac atc cag tac  
1459

Glu Ser Asp Val Phe Thr Glu Asp Leu Ile Glu Ala Tyr Ile Gln Tyr  
440 445 450

aag tac gac aac gag atc tcc cca gtt cgc ctg cgc cca acc ccg cag  
1507

Lys Tyr Asp Asn Glu Ile Ser Pro Val Arg Leu Arg Pro Thr Pro Gln  
455 460 465

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1554

Glu Phe Glu Leu Tyr Phe Asp Cys  
470 475

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<211> 477

<212> PRT

<213> Corynebacterium glutamicum

<400> 98

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Ala Lys Thr Leu Asn Val Lys Phe Phe Val His Asp Pro Phe Thr Arg	
90 95 100	
gag gca ttc tcc cgc gac cca cgc aac gtg gca cgc aag gca gag cag	451
Glu Ala Phe Ser Arg Asp Pro Arg Asn Val Ala Arg Lys Ala Glu Gln	
105 110 115	
tac ctg gca tcc acc ggc att gca gac acc tgc aac ttc ggc gcc gag	499
Tyr Leu Ala Ser Thr Gly Ile Ala Asp Thr Cys Asn Phe Gly Ala Glu	
120 125 130	
gct gag ttc tac ctc ttc gac tcc gtt cgc tac tcc acc gag atg aac	547
Ala Glu Phe Tyr Leu Phe Asp Ser Val Arg Tyr Ser Thr Glu Met Asn	
135 140 145	
tcc ggc ttc tac gaa gta gat acc gaa gaa ggc tgg tgg aac cgt ggc	595
Ser Gly Phe Tyr Glu Val Asp Thr Glu Glu Gly Trp Trp Asn Arg Gly	
150 155 160 165	
aag gaa acc aac ctc gac ggc acc cca aac ctg ggc gca aag aac cgc	643
Lys Glu Thr Asn Leu Asp Gly Thr Pro Asn Leu Gly Ala Lys Asn Arg	
170 175 180	
gtc aag ggt ggc tac ttc cca gta gca cca tac gac caa acc gtt gac	691
Val Lys Gly Gly Tyr Phe Pro Val Ala Pro Tyr Asp Gln Thr Val Asp	
185 190 195	
gtg cgc gat gac atg gtt cgc aac ctc gca gct tcc ggc ttc gct ctt	739
Val Arg Asp Asp Met Val Arg Asn Leu Ala Ala Ser Gly Phe Ala Leu	
200 205 210	
gag cgt ttc cac cac gaa gtc ggt ggc gga cag cag gaa atc aac tac	787
Glu Arg Phe His His Glu Val Gly Gly Gly Gln Gln Glu Ile Asn Tyr	
215 220 225	
cgc ttc aac acc atg ctc cac gcg gca gat gat atc cag acc ttc aag	835
Arg Phe Asn Thr Met Leu His Ala Ala Asp Asp Ile Gln Thr Phe Lys	
230 235 240 245	
tac atc atc aag aac acc gct cgc ctc cac ggc aag gct gca acc ttc	883
Tyr Ile Ile Lys Asn Thr Ala Arg Leu His Gly Lys Ala Ala Thr Phe	
250 255 260	
atg cct aag cca ctg gct ggc gac aac ggt tcc ggc atg cac gct cac	931
Met Pro Lys Pro Leu Ala Gly Asp Asn Gly Ser Gly Met His Ala His	
265 270 275	
cag tcc ctc tgg aag gac ggc aag cca ctc ttc cac gat gag tcc ggc	979
Gln Ser Leu Trp Lys Asp Gly Lys Pro Leu Phe His Asp Glu Ser Gly	
280 285 290	
tac gca ggc ctg tcc gac atc gcc cgc tac tac atc ggc ggc atc ctg	
1027	
Tyr Ala Gly Leu Ser Asp Ile Ala Arg Tyr Tyr Ile Gly Gly Ile Leu	
295 300 305	
cac cac gca ggc gct gtt ctg gcg ttc acc aac gca acc ctg aac tcc	
1075	
His His Ala Gly Ala Val Leu Ala Phe Thr Asn Ala Thr Leu Asn Ser	
310 315 320 325	

	325		330		335	
Val Arg Leu Pro Asp Thr Ala Cys Asn Pro Tyr Leu Ala Phe Ser Val						
	340		345		350	
Met Leu Gly Ala Gly Leu Lys Gly Ile Lys Glu Gly Tyr Glu Leu Asp						
	355		360		365	
Glu Pro Ala Glu Asp Asp Ile Ser Asn Leu Ser Phe Arg Glu Arg Arg						
	370		375		380	
Ala Met Gly Tyr Asn Asp Leu Pro Ser Ser Leu Asp Gln Ala Leu Arg						
	385		390		395	400
Gln Met Glu Lys Ser Glu Leu Val Ala Asp Ile Leu Gly Glu His Val						
	405		410		415	
Phe Glu Phe Phe Leu Arg Asn Lys Trp Arg Glu Trp Arg Asp Tyr Gln						
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Glu Gln Ile Thr Pro Trp Glu Leu Arg Asn Asn Leu Asp Tyr						
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1531)  
 <223> RXA00335

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 Val Ala Phe Glu Thr 5  
 1  
 ccg gaa gaa att gtc aag ttc atc aag gat gaa aac gtc gag ttc gtt 163  
 Pro Glu Glu Ile Val Lys Phe Ile Lys Asp Glu Asn Val Glu Phe Val 20  
 10 15  
 gac gtt cga ttc acc gac ctt ccc ggc acc gag cag cac ttc agc atc 211  
 Asp Val Arg Phe Thr Asp Leu Pro Gly Thr Glu Gln His Phe Ser Ile 35  
 25 30  
 cca gct gcc agc ttc gat gca gat aca atc gaa gaa ggt ctc gca ttc 259  
 Pro Ala Ala Ser Phe Asp Ala Asp Thr Ile Glu Glu Gly Leu Ala Phe 50  
 40 45  
 gac gga tcc tcg atc cgt ggc ttc acc acg atc gac gaa tct gac atg 307  
 Asp Gly Ser Ser Ile Arg Gly Phe Thr Thr Ile Asp Glu Ser Asp Met 65  
 55 60  
 aat ctc ctg cca gac ctc gga acg gcc acc ctt gat cca ttc cgc aag 355  
 Asn Leu Leu Pro Asp Leu Gly Thr Ala Thr Leu Asp Pro Phe Arg Lys 85  
 70 75 80

Asp Ile Lys Ser Lys Ile Ser Glu Lys Thr Lys Ala Ile Val Val Ile  
 195 200 205  
 Asn Pro Asn Asn Pro Thr Gly Ala Val Tyr Pro Arg Arg Val Leu Glu  
 210 215 220  
 Gln Ile Val Glu Ile Ala Arg Glu His Asp Leu Leu Ile Leu Ala Asp  
 225 230 235 240  
 Glu Ile Tyr Asp Arg Ile Leu Tyr Asp Asp Ala Glu His Ile Ser Leu  
 245 250 255  
 Ala Thr Leu Ala Pro Asp Leu Leu Cys Ile Thr Tyr Asn Gly Leu Ser  
 260 265 270  
 Lys Ala Tyr Arg Val Ala Gly Tyr Arg Ala Gly Trp Met Val Leu Thr  
 275 280 285  
 Gly Pro Lys Gln Tyr Ala Arg Gly Phe Ile Glu Gly Leu Glu Leu Leu  
 290 295 300  
 Ala Gly Thr Arg Leu Cys Pro Asn Val Pro Ala Gln His Ala Ile Gln  
 305 310 315 320  
 Val Ala Leu Gly Gly Arg Gln Ser Ile Tyr Asp Leu Thr Gly Glu His  
 325 330 335  
 Gly Arg Leu Leu Glu Gln Arg Asn Met Ala Trp Thr Lys Leu Asn Glu  
 340 345 350  
 Ile Pro Gly Val Ser Cys Val Lys Pro Met Gly Ala Leu Tyr Ala Phe  
 355 360 365  
 Pro Lys Leu Asp Pro Asn Val Tyr Glu Ile His Asp Asp Thr Gln Leu  
 370 375 380  
 Met Leu Asp Leu Leu Arg Ala Glu Lys Ile Leu Met Val Gln Gly Thr  
 385 390 395 400  
 Gly Phe Asn Trp Pro His His Asp His Phe Arg Val Val Thr Leu Pro  
 405 410 415  
 Trp Ala Ser Gln Leu Glu Asn Ala Ile Glu Arg Leu Gly Asn Phe Leu  
 420 425 430  
 Ser Thr Tyr Lys Gln  
 435

&lt;210&gt; 123

&lt;211&gt; 1701

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1678)

&lt;223&gt; RXA02193

&lt;400&gt; 123

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1315

Arg Ala Glu Lys Ile Leu Met Val Gln Gly Thr Gly Phe Asn Trp Pro  
390 395 400 405

cat cac gat cac ttc cga gtg gtc acc ctg cca tgg gca tcc cag ttg  
1363

His His Asp His Phe Arg Val Val Thr Leu Pro Trp Ala Ser Gln Leu  
410 415 420

gaa aac gca att gag cgc ctg ggt aac ttc ctg tcc act tac aag cag  
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1434

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<211> 437

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 122

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Arg Arg Ile Phe Asp Gln Ser Glu Lys Met Lys Asp Val Leu Tyr Glu  
35 40 45

Ile Arg Gly Pro Val Ala Ala Glu Ala Glu Arg Met Glu Leu Asp Gly  
50 55 60

His Asn Ile Leu Lys Leu Asn Thr Gly Asn Pro Ala Val Phe Gly Phe  
65 70 75 80

Asp Ala Pro Asp Val Ile Met Arg Asp Met Ile Ala Asn Leu Pro Thr  
85 90 95

Ser Gln Gly Tyr Ser Thr Ser Lys Gly Ile Ile Pro Ala Arg Arg Ala  
100 105 110

Val Val Thr Arg Tyr Glu Val Val Pro Gly Phe Pro His Phe Asp Val  
115 120 125

Asp Asp Val Phe Leu Gly Asn Gly Val Ser Glu Leu Ile Thr Met Thr  
130 135 140

Thr Gln Ala Leu Leu Asn Asp Gly Asp Glu Val Leu Ile Pro Ala Pro  
145 150 155 160

Asp Tyr Pro Leu Trp Thr Ala Ala Thr Ser Leu Ala Gly Gly Lys Pro  
165 170 175

Val His Tyr Leu Cys Asp Glu Glu Asp Asp Trp Asn Pro Ser Ile Glu  
180 185 190

170	175	180	
gat gag gaa gat gac tgg aac cca tcc atc gaa gac atc aag tcc aaa Asp Glu Glu Asp Asp Trp Asn Pro Ser Ile Glu Asp Ile Lys Ser Lys 185 190 195			691
atc tca gag aaa acc aaa gct att gtg gtg atc aac ccc aac aac ccc Ile Ser Glu Lys Thr Lys Ala Ile Val Val Ile Asn Pro Asn Asn Pro 200 205 210			739
acg gga gct gtc tac ccg cgc cgg gtg ttg gaa caa atc gtc gag att Thr Gly Ala Val Tyr Pro Arg Arg Val Leu Glu Gln Ile Val Glu Ile 215 220 225			787
gca cgc gag cat gac ctg ctg att ttg gcc gat gaa atc tac gac cgc Ala Arg Glu His Asp Leu Leu Ile Leu Ala Asp Glu Ile Tyr Asp Arg 230 235 240 245			835
att ctc tac gat gat gcc gag cac atc agc ctg gca acc ctt gca cca Ile Leu Tyr Asp Asp Ala Glu His Ile Ser Leu Ala Thr Leu Ala Pro 250 255 260			883
gat ctc ctt tgc atc aca tac aac ggt cta tcc aag gca tac cgc gtc Asp Leu Leu Cys Ile Thr Tyr Asn Gly Leu Ser Lys Ala Tyr Arg Val 265 270 275			931
gca gga tac cga gct ggc tgg atg gta ttg act gga cca aag caa tac Ala Gly Tyr Arg Ala Gly Trp Met Val Leu Thr Gly Pro Lys Gln Tyr 280 285 290			979
gca cgt gga ttt att gag ggc ctc gaa ctc ctc gca ggc act cga ctc 1027 Ala Arg Gly Phe Ile Glu Gly Leu Glu Leu Leu Ala Gly Thr Arg Leu 295 300 305			
tgc cca aat gtc cca gct cag cac gct att cag gta gct ctg ggt gga 1075 Cys Pro Asn Val Pro Ala Gln His Ala Ile Gln Val Ala Leu Gly Gly 310 315 320 325			
cgc cag tcc atc tac gac ctc act ggc gaa cac ggc cga ctc ctg gaa 1123 Arg Gln Ser Ile Tyr Asp Leu Thr Gly Glu His Gly Arg Leu Leu Glu 330 335 340			
cag cgc aac atg gca tgg acg aaa ctc aac gaa atc cca ggt gtc agc 1171 Gln Arg Asn Met Ala Trp Thr Lys Leu Asn Glu Ile Pro Gly Val Ser 345 350 355			
tgt gtg aaa cca atg gga gct cta tac gcg ttc ccc aag ctc gac ccc 1219 Cys Val Lys Pro Met Gly Ala Leu Tyr Ala Phe Pro Lys Leu Asp Pro 360 365 370			
aac gtg tac gaa atc cac gac gac acc caa ctc atg ctg gat ctt ctc 1267 Asn Val Tyr Glu Ile His Asp Asp Thr Gln Leu Met Leu Asp Leu Leu 375 380 385			



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&lt;221&gt; CDS

&lt;222&gt; (101)..(385)

&lt;223&gt; FRXA00627

&lt;400&gt; 119

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                                         Met Gln Met Leu Asp
                                         1           5

cga gtc cac cgt cgc agg cgc gaa ggc aaa gac acc tta atg ttc tgc 163
Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp Thr Leu Met Phe Cys
                10                15                20

gct ggc cag ccg tca act ggt gcg cca gaa gca gtc atc gaa gaa gca 211
Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala Val Ile Glu Glu Ala
                25                30                35

gag atc gct ctt cgc tcg ggt cct ttg gga tac acc gag gtg att ggt 259
Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr Thr Glu Val Ile Gly
                40                45                50

gat cgt gag ttc cgt gaa cgc atc gcc gat tgg cac tct gct act tat 307
Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp His Ser Ala Thr Tyr
                55                60                65

gac gta gac acc aac cct gac aat gtt att gtc acc acc ggt tct tca 355
Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val Thr Thr Gly Ser Ser
                70                75                80                85

ggt gga ttc gtg gca tcg ttt atc gcc acc 385
Gly Gly Phe Val Ala Ser Phe Ile Ala Thr
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&lt;210&gt; 120

&lt;211&gt; 95

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 120

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Thr Leu Met Phe Cys Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala
 20           25           30

Val Ile Glu Glu Ala Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr
 35           40           45

Thr Glu Val Ile Gly Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp
 50           55           60

His Ser Ala Thr Tyr Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val
 65           70           75           80

Thr Thr Gly Ser Ser Gly Gly Phe Val Ala Ser Phe Ile Ala Thr
 85           90           95

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Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe Asp Pro Glu Glu  
 135 140 145

ggc cac aag tgg att cgt ttg agc ctg tgc gcg tca aag gaa gac acc 595  
 Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser Lys Glu Asp Thr  
 150 155 160 165

att gaa ggt gtg cgc aaa atc gga gaa ttc atc aaa aaa tagcagcgac 644  
 Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys Lys  
 170 175

taggttagtt tcg 657

<210> 118  
 <211> 178  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 118  
 Met Ser Phe Gly Arg Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn  
 1 5 10 15

Ala Ile Val Val Gly Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp  
 20 25 30

Arg Val Gly Trp Ile Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu  
 35 40 45

Asn Leu Gln Ala Ser Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala  
 50 55 60

Ala Gly Arg Ala Ala Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala  
 65 70 75 80

His Val Glu Ala Tyr Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu  
 85 90 95

Pro Glu Ile Gly Leu Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr  
 100 105 110

Leu Trp Val Asp Val Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala  
 115 120 125

Leu Arg Leu Leu Asp Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp  
 130 135 140

Phe Asp Pro Glu Glu Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala  
 145 150 155 160

Ser Lys Glu Asp Thr Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile  
 165 170 175

Lys Lys

<210> 119  
 <211> 385  
 <212> DNA  
 <213> Corynebacterium glutamicum



Asp Pro Glu Glu Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser  
 340 345 350

Lys Glu Asp Thr Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys  
 355 360 365

Lys

<210> 117

<211> 657

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(634)

<223> FRXA00618

<400> 117

cccaacgggc accatcattg atccggaaga gctagagcgc atcgccaagt ggtgcatga 60

caatgatgct gttcttatct ctgatgagga ctaccacggc atg agc ttt ggt cgt 115  
 Met Ser Phe Gly Arg  
 1 5

ccg ctg gca act gcg cat cag ttt tcc aag aac gcc atc gtg gtg ggt 163  
 Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala Ile Val Val Gly  
 10 15 20

acc ttg tcc aag tac ttc tcc atg acg ggt tgg cgc gtg ggt tgg atc 211  
 Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg Val Gly Trp Ile  
 25 30 35

atc gtt cca gat gag ctg gtc aca ccg att gaa aac ctg cag gct tct 259  
 Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn Leu Gln Ala Ser  
 40 45 50

ctt tcc ttg tgt gct cct gcc atc ggg cag gct gcg gga cgc gca gcc 307  
 Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala Gly Arg Ala Ala  
 55 60 65

ttc act ttg gag gct ggg gcc gaa ctt gat gcc cac gtt gaa gcg tat 355  
 Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His Val Glu Ala Tyr  
 70 75 80 85

cgc gag gcc cgg gag gtg ttc gtc gat aag ctc cct gaa atc ggg ctt 403  
 Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro Glu Ile Gly Leu  
 90 95 100

ggc act ttc gcc gac ccg gat ggc ggc ctg tat ttg tgg gtc gat gtt 451  
 Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu Trp Val Asp Val  
 105 110 115

tct gca tac acc gat gat tca gag gaa tgg gca ttg cgt ttg ctc gat 499  
 Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu Arg Leu Leu Asp  
 120 125 130

gaa gcg ggc gtg gcc gtc gcg ccg ggt gtt gat ttt gat cct gag gaa 547

1	5	10	15
Thr Leu Met	Phe Cys Ala Gly Gln	Pro Ser Thr Gly Ala	Pro Glu Ala
	20	25	30
Val Ile Glu	Glu Ala Glu Ile Ala	Leu Arg Ser Gly	Pro Leu Gly Tyr
	35	40	45
Thr Glu Val	Ile Gly Asp Arg Glu	Phe Arg Glu Arg	Ile Ala Asp Trp
	50	55	60
His Ser Ala	Thr Tyr Asp Val Asp	Thr Asn Pro Asp	Asn Val Ile Val
	65	70	75
Thr Thr Gly	Ser Ser Gly Gly Phe	Val Ala Ser Phe	Ile Ala Thr Leu
	85	90	95
Asp His Gly	Asp Tyr Val Ala Met	Pro Thr Pro Gly	Tyr Pro Ala Tyr
	100	105	110
Arg Asn Ile	Leu Glu Ser Leu Gly	Ala Lys Val Leu	Asn Leu Arg Cys
	115	120	125
Thr Ala Glu	Thr Arg Phe Gln Pro	Thr Ala Gln Met	Leu Glu Glu Leu
	130	135	140
Pro His Lys	Pro Lys Ala Val Ile	Val Thr Ser Pro	Gly Asn Pro Thr
	145	150	155
Gly Thr Ile	Ile Asp Pro Glu Glu	Leu Glu Arg Ile	Ala Lys Trp Cys
	165	170	175
Asp Asp Asn	Asp Ala Val Leu Ile	Ser Asp Glu Asp	Tyr His Gly Met
	180	185	190
Ser Phe Gly	Arg Pro Leu Ala Thr	Ala His Gln Phe	Ser Lys Asn Ala
	195	200	205
Ile Val Val	Gly Thr Leu Ser Lys	Tyr Phe Ser Met	Thr Gly Trp Arg
	210	215	220
Val Gly Trp	Ile Ile Val Pro Asp	Glu Leu Val Thr	Pro Ile Glu Asn
	225	230	235
Leu Gln Ala	Ser Leu Ser Leu Cys	Ala Pro Ala Ile	Gly Gln Ala Ala
	245	250	255
Gly Arg Ala	Ala Phe Thr Leu Glu	Ala Gly Ala Glu	Leu Asp Ala His
	260	265	270
Val Glu Ala	Tyr Arg Glu Ala Arg	Glu Val Phe Val	Asp Lys Leu Pro
	275	280	285
Glu Ile Gly	Leu Gly Thr Phe Ala	Asp Pro Asp Gly	Gly Leu Tyr Leu
	290	295	300
Trp Val Asp	Val Ser Ala Tyr Thr	Asp Asp Ser Glu	Glu Trp Ala Leu
	305	310	315
Arg Leu Leu	Asp Glu Ala Gly Val	Ala Val Ala Pro	Gly Val Asp Phe
	325	330	335

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ctg gca act gcg cat cag ttt tcc aag aac gcc atc gtg gtg ggt acc 739
Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala Ile Val Val Gly Thr
      200                      205                      210

ttg tcc aag tac ttc tcc atg acg ggt tgg cgc gtg ggt tgg atc atc 787
Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg Val Gly Trp Ile Ile
      215                      220                      225

gtt cca gat gag ctg gtc aca ccg att gaa aac ctg cag gct tct ctt 835
Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn Leu Gln Ala Ser Leu
      230                      235                      240                      245

tcc ttg tgt gct cct gcc atc ggg cag gct gcg gga cgc gca gcc ttc 883
Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala Gly Arg Ala Ala Phe
      250                      255                      260

act ttg gag gct ggg gcc gaa ctt gat gcc cac gtt gaa gcg tat cgc 931
Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His Val Glu Ala Tyr Arg
      265                      270                      275

gag gcc cgg gag gtg ttc gtc gat aag ctc cct gaa atc ggg ctt ggc 979
Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro Glu Ile Gly Leu Gly
      280                      285                      290

act ttc gcc gac ccg gat ggc ggc ctg tat ttg tgg gtc gat gtt tct
1027
Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu Trp Val Asp Val Ser
      295                      300                      305

gca tac acc gat gat tca gag gaa tgg gca ttg cgt ttg ctc gat gaa
1075
Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu Arg Leu Leu Asp Glu
      310                      315                      320                      325

gcg ggc gtg gcc gtc gcg ccg ggt gtt gat ttt gat cct gag gaa ggc
1123
Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe Asp Pro Glu Glu Gly
      330                      335                      340

cac aag tgg att cgt ttg agc ctg tgc gcg tca aag gaa gac acc att
1171
His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser Lys Glu Asp Thr Ile
      345                      350                      355

gaa ggt gtg cgc aaa atc gga gaa ttc atc aaa aaa tagcagcgac
1217
Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys Lys
      360                      365

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taggttagtt tcg
1230

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<210> 116
<211> 369
<212> PRT
<213> Corynebacterium glutamicum

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<400> 116
Met Gln Met Leu Asp Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp

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&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1207)

&lt;223&gt; RXN00618

&lt;400&gt; 115

gctgcattag agggtcgtat ctcgatctaa aagcagtacg cagataggct tgtctcttat 60

gaagccaagc	actagaagca	atgttcagcc	gtttcgcgct	atg	cag	atg	ttg	gac	115
				Met	Gln	Met	Leu	Asp	
				1				5	

cga	gtc	cac	cgt	cgc	agg	cgc	gaa	ggc	aaa	gac	acc	tta	atg	ttc	tgc	163
Arg	Val	His	Arg	Arg	Arg	Arg	Glu	Gly	Lys	Asp	Thr	Leu	Met	Phe	Cys	
			10					15						20		

gct	ggc	cag	ccg	tca	act	ggt	gcg	cca	gaa	gca	gtc	atc	gaa	gaa	gca	211
Ala	Gly	Gln	Pro	Ser	Thr	Gly	Ala	Pro	Glu	Ala	Val	Ile	Glu	Glu	Ala	
			25					30					35			

gag	atc	gct	ctt	cgc	tcg	ggt	cct	ttg	gga	tac	acc	gag	gtg	att	ggt	259
Glu	Ile	Ala	Leu	Arg	Ser	Gly	Pro	Leu	Gly	Tyr	Thr	Glu	Val	Ile	Gly	
		40					45					50				

gat	cgt	gag	ttc	cgt	gaa	cgc	atc	gcc	gat	tgg	cac	tct	gct	act	tat	307
Asp	Arg	Glu	Phe	Arg	Glu	Arg	Ile	Ala	Asp	Trp	His	Ser	Ala	Thr	Tyr	
		55				60					65					

gac	gta	gac	acc	aac	cct	gac	aat	gtt	att	gtc	acc	acc	ggt	tct	tca	355
Asp	Val	Asp	Thr	Asn	Pro	Asp	Asn	Val	Ile	Val	Thr	Thr	Gly	Ser	Ser	
	70				75					80					85	

ggt	gga	ttc	gtg	gca	tcg	ttt	atc	gcc	acc	ttg	gat	cac	ggg	gat	tat	403
Gly	Gly	Phe	Val	Ala	Ser	Phe	Ile	Ala	Thr	Leu	Asp	His	Gly	Asp	Tyr	
			90					95						100		

gtg	gca	atg	cct	acc	ccg	ggg	tac	ccg	gca	tat	cgc	aat	att	ctg	gaa	451
Val	Ala	Met	Pro	Thr	Pro	Gly	Tyr	Pro	Ala	Tyr	Arg	Asn	Ile	Leu	Glu	
			105					110					115			

tct	ttg	ggg	gcg	aag	gtt	ctg	aac	ctg	cgc	tgt	act	gca	gag	act	cgt	499
Ser	Leu	Gly	Ala	Lys	Val	Leu	Asn	Leu	Arg	Cys	Thr	Ala	Glu	Thr	Arg	
		120					125					130				

ttc	cag	cca	acc	gct	caa	atg	ttg	gag	gaa	ctg	cca	cac	aag	ccg	aag	547
Phe	Gln	Pro	Thr	Ala	Gln	Met	Leu	Glu	Glu	Leu	Pro	His	Lys	Pro	Lys	
		135				140					145					

gct	gtt	att	gtc	acc	agc	cca	gga	aac	cca	acg	ggc	acc	atc	att	gat	595
Ala	Val	Ile	Val	Thr	Ser	Pro	Gly	Asn	Pro	Thr	Gly	Thr	Ile	Ile	Asp	
150					155					160					165	

ccg	gaa	gag	cta	gag	cgc	atc	gcc	aag	tgg	tgc	gat	gac	aat	gat	gct	643
Pro	Glu	Glu	Leu	Glu	Arg	Ile	Ala	Lys	Trp	Cys	Asp	Asp	Asn	Asp	Ala	
			170						175						180	

gtt	ctt	atc	tct	gat	gag	gac	tac	cac	ggc	atg	agc	ttt	ggt	cgt	ccg	691
Val	Leu	Ile	Ser	Asp	Glu	Asp	Tyr	His	Gly	Met	Ser	Phe	Gly	Arg	Pro	
			185					190					195			

gtg gcg gtt cct ttg cag gag gtg gag aac tcg tgg gat gtg gat gtc 499  
 Val Ala Val Pro Leu Gln Glu Val Glu Asn Ser Trp Asp Val Asp Val  
           120                          125                          130

gat aag ttg cat gcg gcg gtg act aag aag acg cgg atg att atc gtt 547  
 Asp Lys Leu His Ala Ala Val Thr Lys Lys Thr Arg Met Ile Ile Val  
           135                          140                          145

aat tcg ccg cat aat ccg acg ggt tcg gtg ttt tct aag aag gcg ttg 595  
 Asn Ser Pro His Asn Pro Thr Gly Ser Val Phe Ser Lys Lys Ala Leu  
           150                          155                          160                          165

aag cag ttg gcg 607  
 Lys Gln Leu Ala

<210> 114

<211> 169

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 114

Met Thr Gln Arg Ala Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly  
       1                          5                          10                          15

Phe Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu  
           20                          25                          30

Gln Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala  
           35                          40                          45

Ser Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu  
           50                          55                          60

Glu Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu  
           65                          70                          75                          80

Ala Ile Thr Ala Thr Val Leu Gly Leu Val Glu Pro Gly Asp Glu Val  
                           85                          90                          95

Ile Val Leu Glu Pro Tyr Tyr Asp Ala Tyr Ala Ala Ala Ile Ala Leu  
           100                          105                          110

Ala Gly Ala Thr Arg Val Ala Val Pro Leu Gln Glu Val Glu Asn Ser  
           115                          120                          125

Trp Asp Val Asp Val Asp Lys Leu His Ala Ala Val Thr Lys Lys Thr  
           130                          135                          140

Arg Met Ile Ile Val Asn Ser Pro His Asn Pro Thr Gly Ser Val Phe  
           145                          150                          155                          160

Ser Lys Lys Ala Leu Lys Gln Leu Ala  
           165

<210> 115

<211> 1230

<212> DNA

<400> 113																
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				Met	Thr	Gln	Arg	Ala								
					1			5								
gtt	gag	gcg	ggg	gca	atc	aat	ctt	ggg	cag	ggc	ttt	cct	gat	gag	gat	163
Val	Glu	Ala	Gly	Ala	Ile	Asn	Leu	Gly	Gln	Gly	Phe	Pro	Asp	Glu	Asp	
				10				15						20		
ggg	cct	cgt	cgg	atg	tta	gag	atc	gcg	tcg	gag	cag	att	ctc	ggg	gga	211
Gly	Pro	Arg	Arg	Met	Leu	Glu	Ile	Ala	Ser	Glu	Gln	Ile	Leu	Gly	Gly	
			25					30					35			
aat	aat	cag	tat	tcg	gcg	ggg	cgt	ggg	gat	gct	tcg	ttg	agg	gca	gct	259
Asn	Asn	Gln	Tyr	Ser	Ala	Gly	Arg	Gly	Asp	Ala	Ser	Leu	Arg	Ala	Ala	
		40					45					50				
gtg	gct	cgt	gat	cat	ttg	gag	agg	ttt	gat	ctg	gag	tac	aac	cct	gat	307
Val	Ala	Arg	Asp	His	Leu	Glu	Arg	Phe	Asp	Leu	Glu	Tyr	Asn	Pro	Asp	
	55				60					65						
tcg	gag	gtg	ttg	atc	acg	gtg	ggg	gcc	act	gag	gcg	att	acg	gcg	act	355
Ser	Glu	Val	Leu	Ile	Thr	Val	Gly	Ala	Thr	Glu	Ala	Ile	Thr	Ala	Thr	
70					75					80					85	
gtg	ttg	ggg	ttg	gtg	gag	cct	ggg	gat	gaa	gtg	atc	ggt	ttg	gaa	cgg	403
Val	Leu	Gly	Leu	Val	Glu	Pro	Gly	Asp	Glu	Val	Ile	Val	Leu	Glu	Pro	
				90				95					100			
tat	tac	gat	gcg	tat	gcg	gcg	gct	att	gcg	ttg	gcg	ggg	gcg	acg	cgg	451
Tyr	Tyr	Asp	Ala	Tyr	Ala	Ala	Ala	Ile	Ala	Leu	Ala	Gly	Ala	Thr	Arg	
			105					110					115			

&lt;400&gt; 112

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Met Ser Asn Asp Phe Val Val Ser Arg Leu Arg Pro Phe Gly Glu Thr
 1           5           10           15

Ile Phe Ala Thr Met Thr Gln Arg Ala Val Glu Ala Gly Ala Ile Asn
      20           25           30

Leu Gly Gln Gly Phe Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu
      35           40           45

Ile Ala Ser Glu Gln Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly
      50           55           60

Arg Gly Asp Ala Ser Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu
      65           70           75           80

Arg Phe Asp Leu Glu Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val
      85           90           95

Gly Ala Thr Glu Ala Ile Thr Ala Thr Val Leu Gly Leu Val Glu Pro
      100           105           110

Gly Asp Glu Val Ile Val Leu Glu Pro Tyr Tyr Asp Ala Tyr Ala Ala
      115           120           125

Ala Ile Ala Leu Ala Gly Ala Thr Arg Val Ala Val Pro Leu Gln Glu
      130           135           140

Val Glu Asn Ser Trp Asp Val Asp Val Asp Lys Leu His Ala Ala Val
      145           150           155           160

Thr Lys Lys Thr Arg Met Ile Ile Val Asn Ser Pro His Asn Pro Thr
      165           170           175

Gly Ser Val Phe Ser Lys Lys Ala Leu Lys Gln Leu Ala Gly Val Ala
      180           185           190

Arg Ala Tyr Asp Leu Leu Val Leu Ser Asp Glu Val Tyr Glu His Leu
      195           200           205

Val Phe Asp Asp Gln Lys His Val Ser Val Ala Lys Leu Pro Gly Met
      210           215           220

Trp Asp Arg Thr Val Thr Val Ser Ser Ala Ala Lys Thr Phe Asn Val
      225           230           235           240

Thr Gly Trp Lys Thr Gly Trp Ala Leu Ala Pro Glu Pro Leu Leu Glu
      245           250           255

Ala Val Leu Lys Ala Lys Gln Phe Met Ser Tyr Val Gly Ala Thr Pro
      260           265           270

Phe Gln Pro Ala Val Ala His Ala Ile Glu His Glu Gln Lys Trp Val
      275           280           285

Ser Lys Met Ser Lys Gly Leu Glu Leu Lys Arg Asp Ile Leu Arg Thr
      290           295           300

Ala Leu Asp Lys Ala Gly Leu Lys Thr His Asp Ser Met Gly Thr Tyr
      305           310           315           320

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Leu Val Leu Ser Asp Glu Val Tyr Glu His Leu Val Phe Asp Asp Gln
    200                                205                                210

aag cat gtg agt gtc gcg aag ctg ccc ggt atg tgg gat cgc acg gtg   787
Lys His Val Ser Val Ala Lys Leu Pro Gly Met Trp Asp Arg Thr Val
    215                                220                                225

acg gtg tcg tcg gcg gcg aaa acg ttc aat gtg act ggt tgg aag acg   835
Thr Val Ser Ser Ala Ala Lys Thr Phe Asn Val Thr Gly Trp Lys Thr
    230                                235                                240                                245

ggg tgg gcg ttg gca ccg gag ccg ttg ttg gag gcg gtg ttg aag gcg   883
Gly Trp Ala Leu Ala Pro Glu Pro Leu Leu Glu Ala Val Leu Lys Ala
    250                                255                                260

aag cag ttt atg tct tat gtg ggg gct aca cct ttt cag ccg gct gtg   931
Lys Gln Phe Met Ser Tyr Val Gly Ala Thr Pro Phe Gln Pro Ala Val
    265                                270                                275

gcg cat gcg att gaa cat gag cag aag tgg gtg tca aag atg tct aag   979
Ala His Ala Ile Glu His Glu Gln Lys Trp Val Ser Lys Met Ser Lys
    280                                285                                290

ggg ctt gag ctc aag cgg gat att ttg cgt act gcg tta gat aag gcg
1027
Gly Leu Glu Leu Lys Arg Asp Ile Leu Arg Thr Ala Leu Asp Lys Ala
    295                                300                                305

ggg ctg aag act cat gac agt atg ggc acg tat ttc atc gtt gcg gat
1075
Gly Leu Lys Thr His Asp Ser Met Gly Thr Tyr Phe Ile Val Ala Asp
    310                                315                                320                                325

att ggg gat cgt gat ggt gcg gag ttc tgt ttt gag ttg att gag aag
1123
Ile Gly Asp Arg Asp Gly Ala Glu Phe Cys Phe Glu Leu Ile Glu Lys
    330                                335                                340

gtt ggg gtg gcg gcg att ccg gtg cag gcg ttt gtg gat cat ccg aag
1171
Val Gly Val Ala Ala Ile Pro Val Gln Ala Phe Val Asp His Pro Lys
    345                                350                                355

aag tgg tcg tcg aag gtt cgt ttt gcg ttt tgc aaa aaa gaa gag acg
1219
Lys Trp Ser Ser Lys Val Arg Phe Ala Phe Cys Lys Lys Glu Glu Thr
    360                                365                                370

ctc cgc gaa gct gcg gag cgt ctc aag ggg att aag aaa cta
1261
Leu Arg Glu Ala Ala Glu Arg Leu Lys Gly Ile Lys Lys Leu
    375                                380                                385

tagtttgaac aggttggttg ggg
1284

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&lt;210&gt; 112

&lt;211&gt; 387

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum



&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1261)

&lt;223&gt; RXN00116

&lt;400&gt; 111

cgcggcacgc acgctggggg caagcgtcga caagcacaaa ctttttgctt aattgaatcc 60

tttgcgccacc aatcaatggg ggatcaaata tagtagctgc	atg agt aat gac ttc	115
	Met Ser Asn Asp Phe	
	1 5	

gtc gtt tct agg ctt aga ccc ttt ggt gaa acg att ttt gca acc atg	163
Val Val Ser Arg Leu Arg Pro Phe Gly Glu Thr Ile Phe Ala Thr Met	
10 15 20	

acc cag cga gct gtt gag gcg ggt gca atc aat ctt ggt cag ggc ttt	211
Thr Gln Arg Ala Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly Phe	
25 30 35	

cct gat gag gat ggt cct cgt cgg atg tta gag atc gcg tcg gag cag	259
Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu Gln	
40 45 50	

att ctc ggg gga aat aat cag tat tcg gcg ggg cgt ggg gat gct tcg	307
Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala Ser	
55 60 65	

ttg agg gca gct gtg gct cgt gat cat ttg gag agg ttt gat ctg gag	355
Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu Glu	
70 75 80 85	

tac aac cct gat tcg gag gtg ttg atc acg gtg ggg gcc act gag gcg	403
Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu Ala	
90 95 100	

att acg gcg act gtg ttg ggt ttg gtg gag cct ggg gat gaa gtg atc	451
Ile Thr Ala Thr Val Leu Gly Leu Val Glu Pro Gly Asp Glu Val Ile	
105 110 115	

gtt ttg gaa ccg tat tac gat gcg tat gcg gcg gct att gcg ttg gcg	499
Val Leu Glu Pro Tyr Tyr Asp Ala Tyr Ala Ala Ala Ile Ala Leu Ala	
120 125 130	

ggg gcg acg ccg gtg gcg gtt cct ttg cag gag gtg gag aac tcg tgg	547
Gly Ala Thr Arg Val Ala Val Pro Leu Gln Glu Val Glu Asn Ser Trp	
135 140 145	

gat gtg gat gtc gat aag ttg cat gcg gcg gtg act aag aag acg ccg	595
Asp Val Asp Val Asp Lys Leu His Ala Ala Val Thr Lys Lys Thr Arg	
150 155 160 165	

atg att atc gtt aat tcg ccg cat aat ccg acg ggt tcg gtg ttt tct	643
Met Ile Ile Val Asn Ser Pro His Asn Pro Thr Gly Ser Val Phe Ser	
170 175 180	

aag aag gcg ttg aag cag ttg gcg ggt gtt gct cgt gcg tat gac ttg	691
Lys Lys Ala Leu Lys Gln Leu Ala Gly Val Ala Arg Ala Tyr Asp Leu	
185 190 195	

ttg gtg ttg tca gat gag gtg tat gag cat ctt gtt ttt gat gat cag	739
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His Val Lys Val Val Leu Ser Gly Glu Gly Ala Asp Glu Leu Phe Gly  
 340 345 350  
 Gly Tyr Thr Ile Tyr Lys Glu Pro Leu Ser Leu Ala Pro Phe Glu Lys  
 355 360 365  
 Ile Pro Ser Pro Leu Arg Lys Gly Leu Gly Lys Leu Ser Lys Val Leu  
 370 375 380  
 Pro Asp Gly Met Lys Gly Lys Ser Leu Leu Glu Arg Gly Ser Met Thr  
 385 390 395 400  
 Met Glu Glu Arg Tyr Tyr Gly Asn Ala Arg Ser Phe Asn Phe Glu Gln  
 405 410 415  
 Met Gln Arg Val Ile Pro Trp Ala Lys Arg Glu Trp Asp His Arg Glu  
 420 425 430  
 Val Thr Ala Pro Ile Tyr Ala Gln Ser Arg Asn Phe Asp Pro Val Ala  
 435 440 445  
 Arg Met Gln His Leu Asp Leu Phe Thr Trp Met Arg Gly Asp Ile Leu  
 450 455 460  
 Val Lys Ala Asp Lys Ile Asn Met Ala Asn Ser Leu Glu Leu Arg Val  
 465 470 475 480  
 Pro Phe Leu Asp Lys Glu Val Phe Lys Val Ala Glu Thr Ile Pro Tyr  
 485 490 495  
 Asp Leu Lys Ile Ala Asn Gly Thr Thr Lys Tyr Ala Leu Arg Arg Ala  
 500 505 510  
 Leu Glu Gln Ile Val Pro Pro His Val Leu His Arg Lys Lys Leu Gly  
 515 520 525  
 Phe Pro Val Pro Met Arg His Trp Leu Ala Gly Asp Glu Leu Phe Gly  
 530 535 540  
 Trp Ala Gln Asp Thr Ile Lys Glu Ser Gly Thr Glu Asp Ile Phe Asn  
 545 550 555 560  
 Lys Gln Ala Val Leu Asp Met Leu Asn Glu His Arg Asp Gly Val Ser  
 565 570 575  
 Asp His Ser Arg Arg Leu Trp Thr Val Leu Ser Phe Met Val Trp His  
 580 585 590  
 Gly Ile Phe Val Glu Asn Arg Ile Asp Pro Gln Ile Glu Asp Arg Ser  
 595 600 605  
 Tyr Pro Val Glu Leu  
 610

&lt;210&gt; 111

&lt;211&gt; 1284

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

1	5	10	15
Ala Ala Phe Gly Phe Asn Arg Leu Ser Ile Ile Asp Ile Ala His Ser	20	25	30
His Gln Pro Leu Arg Trp Gly Pro Ala Asp Glu Pro Asp Arg Tyr Ala	35	40	45
Met Thr Phe Asn Gly Glu Ile Tyr Asn Tyr Val Glu Leu Arg Lys Glu	50	55	60
Leu Ser Asp Leu Gly Tyr Ala Phe Asn Thr Ser Gly Asp Gly Glu Pro	65	70	75
Ile Val Val Gly Phe His His Trp Gly Glu Ser Val Val Glu His Leu	85	90	95
Arg Gly Met Phe Gly Ile Ala Ile Trp Asp Thr Lys Glu Lys Ser Leu	100	105	110
Phe Leu Ala Arg Asp Gln Phe Gly Ile Lys Pro Leu Phe Tyr Ala Thr	115	120	125
Thr Glu His Gly Thr Val Phe Ser Ser Glu Lys Lys Thr Ile Leu Glu	130	135	140
Met Ala Glu Glu Met Asn Leu Asp Leu Gly Leu Asp Lys Arg Thr Ile	145	150	155
Glu His Tyr Val Asp Leu Gln Tyr Val Pro Glu Pro Asp Thr Leu His	165	170	175
Ala Gln Ile Ser Arg Leu Glu Ser Gly Cys Thr Ala Thr Val Arg Pro	180	185	190
Gly Gly Lys Leu Glu Gln Lys Arg Tyr Phe Lys Pro Gln Phe Pro Val	195	200	205
Gln Lys Val Val Lys Gly Lys Glu Gln Asp Leu Phe Asp Arg Ile Ala	210	215	220
Gln Val Leu Glu Asp Ser Val Glu Lys His Met Arg Ala Asp Val Thr	225	230	235
Val Gly Ser Phe Leu Phe Gly Gly Ile Asp Ser Thr Ala Ile Ala Ala	245	250	255
Leu Ala Lys Arg His Asn Pro Asp Leu Leu Thr Phe Thr Thr Gly Phe	260	265	270
Glu Arg Glu Gly Tyr Ser Glu Val Asp Val Ala Ala Glu Ser Ala Ala	275	280	285
Ala Ile Gly Ala Glu His Ile Val Lys Ile Val Ser Pro Glu Glu Tyr	290	295	300
Ala Asn Ala Ile Pro Lys Ile Met Trp Tyr Leu Asp Asp Pro Val Ala	305	310	315
Asp Pro Ser Leu Val Pro Leu Tyr Phe Val Ala Ala Glu Ala Arg Lys	325	330	335

gat ctg ttc acc tgg atg cgc ggc gac atc ctg gtc aag gct gac aag  
1507

Asp Leu Phe Thr Trp Met Arg Gly Asp Ile Leu Val Lys Ala Asp Lys  
455 460 465

atc aac atg gcg aac tcc ctt gag ctg cga gtt cca ttc ttg gat aag  
1555

Ile Asn Met Ala Asn Ser Leu Glu Leu Arg Val Pro Phe Leu Asp Lys  
470 475 480 485

gaa gtt ttc aag gtt gca gag acc att cct tac gac ctg aag att gcc  
1603

Glu Val Phe Lys Val Ala Glu Thr Ile Pro Tyr Asp Leu Lys Ile Ala  
490 495 500

aac ggt acc acc aag tac gcg ctg cgc agg gca ctc gag cag att gtt  
1651

Asn Gly Thr Thr Lys Tyr Ala Leu Arg Arg Ala Leu Glu Gln Ile Val  
505 510 515

ccg cct cac gtt ttg cac cgc aag aag ctg ggc ttc cct gtt ccc atg  
1699

Pro Pro His Val Leu His Arg Lys Lys Leu Gly Phe Pro Val Pro Met  
520 525 530

cgc cac, tgg ctt gcc ggc gat gag ctg ttc ggt tgg gcg cag gac acc  
1747

Arg His Trp Leu Ala Gly Asp Glu Leu Phe Gly Trp Ala Gln Asp Thr  
535 540 545

atc aag gaa tcc ggt act gaa gat atc ttc aac aag cag gct gtg ctg  
1795

Ile Lys Glu Ser Gly Thr Glu Asp Ile Phe Asn Lys Gln Ala Val Leu  
550 555 560 565

gat atg ctg aac gag cac cgc gat ggc gtg tca gat cat tcc cgt cga  
1843

Asp Met Leu Asn Glu His Arg Asp Gly Val Ser Asp His Ser Arg Arg  
570 575 580

ctg tgg act gtt ctg tca ttt atg gtg tgg cac ggc att ttt gtg gaa  
1891

Leu Trp Thr Val Leu Ser Phe Met Val Trp His Gly Ile Phe Val Glu  
585 590 595

aac cgc att gat cca cag att gag gac cgc tcc tac cca gtc gag ctt  
1939

Asn Arg Ile Asp Pro Gln Ile Glu Asp Arg Ser Tyr Pro Val Glu Leu  
600 605 610

taagtcttaa agcctaaacc ccc  
1962

<210> 110

<211> 613

<212> PRT

<213> Corynebacterium glutamicum

<400> 110

Met Arg His Arg Gly Pro Asp Asp Ala Gly Thr Trp His Asp Ala Asp

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Asn Pro Asp Leu Leu Thr Phe Thr Thr Gly Phe Glu Arg Glu Gly Tyr			
265	270	275	
tcg gag gtc gat gtg gct gcg gag tcc gcc gct gcg att ggc gct gag			979
Ser Glu Val Asp Val Ala Ala Glu Ser Ala Ala Ala Ile Gly Ala Glu			
280	285	290	
cac atc gtg aag att gtc tcg cct gag gaa tac gcc aac gcg att cct			
1027			
His Ile Val Lys Ile Val Ser Pro Glu Glu Tyr Ala Asn Ala Ile Pro			
295	300	305	
aag atc atg tgg tac ttg gat gat cct gta gct gac cca tca ttg gtc			
1075			
Lys Ile Met Trp Tyr Leu Asp Asp Pro Val Ala Asp Pro Ser Leu Val			
310	315	320	325
ccg ctg tac ttc gtg gca gcg gaa gca cgt aag cac gtc aag gtt gtg			
1123			
Pro Leu Tyr Phe Val Ala Ala Glu Ala Arg Lys His Val Lys Val Val			
330	335	340	
ctg tct ggc gag ggc gca gat gag ctg ttc ggt gga tac acc att tac			
1171			
Leu Ser Gly Glu Gly Ala Asp Glu Leu Phe Gly Gly Tyr Thr Ile Tyr			
345	350	355	
aag gag ccg cta tcg ctt gct cca ttt gag aag atc cct tcc cca cta			
1219			
Lys Glu Pro Leu Ser Leu Ala Pro Phe Glu Lys Ile Pro Ser Pro Leu			
360	365	370	
cgt aaa ggc ctg gga aag ctc agc aag gtt ctg cca gac ggc atg aag			
1267			
Arg Lys Gly Leu Gly Lys Leu Ser Lys Val Leu Pro Asp Gly Met Lys			
375	380	385	
ggc aag tcc ctt ctt gag cgt ggc tcc atg acc atg gaa gag cgc tac			
1315			
Gly Lys Ser Leu Leu Glu Arg Gly Ser Met Thr Met Glu Glu Arg Tyr			
390	395	400	405
tac ggc aac gct cgc tcc ttc aat ttc gag cag atg caa cgc gtt att			
1363			
Tyr Gly Asn Ala Arg Ser Phe Asn Phe Glu Gln Met Gln Arg Val Ile			
410	415	420	
cca tgg gca aag cgc gaa tgg gac cac cgc gaa gtc act gcg ccg atc			
1411			
Pro Trp Ala Lys Arg Glu Trp Asp His Arg Glu Val Thr Ala Pro Ile			
425	430	435	
tac gca cag tcc cgc aac ttt gat cca gta gcc cgc atg caa cac ctg			
1459			
Tyr Ala Gln Ser Arg Asn Phe Asp Pro Val Ala Arg Met Gln His Leu			
440	445	450	

Pro	Asp	Asp	Ala	Gly	Thr	Trp	His	Asp	Ala	Asp	Ala	Ala	Phe	Gly	Phe		
				10					15					20			
aac	cgc	ctc	tcc	atc	att	gat	att	gca	cac	tcc	cac	caa	cca	ctg	cgt	211	
Asn	Arg	Leu	Ser	Ile	Ile	Asp	Ile	Ala	His	Ser	His	Gln	Pro	Leu	Arg		
		25						30				35					
tgg	gga	cct	gcg	gat	gaa	ccc	gac	cgc	tac	gca	atg	act	ttc	aac	ggc	259	
Trp	Gly	Pro	Ala	Asp	Glu	Pro	Asp	Arg	Tyr	Ala	Met	Thr	Phe	Asn	Gly		
		40					45					50					
gag	atc	tac	aac	tac	gtt	gag	ctg	cgt	aaa	gag	ctc	tcg	gat	ttg	gga	307	
Glu	Ile	Tyr	Asn	Tyr	Val	Glu	Leu	Arg	Lys	Glu	Leu	Ser	Asp	Leu	Gly		
	55					60					65						
tat	gcc	ttt	aat	act	tct	ggc	gat	ggc	gag	cca	att	gtt	gtc	ggc	ttc	355	
Tyr	Ala	Phe	Asn	Thr	Ser	Gly	Asp	Gly	Glu	Pro	Ile	Val	Val	Gly	Phe		
	70				75					80					85		
cac	cac	tgg	ggc	gag	tcc	gtg	gtc	gag	cat	ctc	cgc	gga	atg	ttc	ggc	403	
His	His	Trp	Gly	Glu	Ser	Val	Val	Glu	His	Leu	Arg	Gly	Met	Phe	Gly		
			90					95						100			
att	gcc	att	tgg	gat	aca	aag	gaa	aag	tcg	ctt	ttc	ctt	gcg	cgt	gat	451	
Ile	Ala	Ile	Trp	Asp	Thr	Lys	Glu	Lys	Ser	Leu	Phe	Leu	Ala	Arg	Asp		
			105					110					115				
cag	ttc	ggc	att	aag	cca	ctg	ttc	tac	gca	acc	acc	gag	cat	ggc	acc	499	
Gln	Phe	Gly	Ile	Lys	Pro	Leu	Phe	Tyr	Ala	Thr	Thr	Glu	His	Gly	Thr		
		120					125					130					
gtg	ttc	tcc	tca	gag	aag	aag	acc	atc	ttg	gag	atg	gcc	gag	gag	atg	547	
Val	Phe	Ser	Ser	Glu	Lys	Lys	Thr	Ile	Leu	Glu	Met	Ala	Glu	Glu	Met		
		135				140					145						
aat	cta	gat	ctg	ggc	ctt	gat	aag	cgc	acc	att	gag	cac	tac	gtg	gac	595	
Asn	Leu	Asp	Leu	Gly	Leu	Asp	Lys	Arg	Thr	Ile	Glu	His	Tyr	Val	Asp		
	150				155				160						165		
ttg	cag	tac	gtg	ccc	gag	cca	gat	acc	ctt	cac	gcg	cag	att	tcc	cgc	643	
Leu	Gln	Tyr	Val	Pro	Glu	Pro	Asp	Thr	Leu	His	Ala	Gln	Ile	Ser	Arg		
			170					175						180			
ttg	gag	tca	ggc	tgc	acc	gca	aca	gtt	cgt	ccg	ggc	ggc	aag	ctg	gaa	691	
Leu	Glu	Ser	Gly	Cys	Thr	Ala	Thr	Val	Arg	Pro	Gly	Gly	Lys	Leu	Glu		
		185					190					195					
cag	aag	cgt	tac	ttc	aag	cct	cag	ttc	cca	gta	cag	aag	gtc	gta	aag	739	
Gln	Lys	Arg	Tyr	Phe	Lys	Pro	Gln	Phe	Pro	Val	Gln	Lys	Val	Val	Lys		
		200					205					210					
ggc	aag	gag	cag	gac	ctc	ttc	gat	cgc	att	gcc	cag	gtg	ttg	gag	gat	787	
Gly	Lys	Glu	Gln	Asp	Leu	Phe	Asp	Arg	Ile	Ala	Gln	Val	Leu	Glu	Asp		
		215				220					225						
agc	gtc	gaa	aag	cat	atg	cgt	gcc	gac	gtg	acc	gta	ggc	tcg	ttc	ctt	835	
Ser	Val	Glu	Lys	His	Met	Arg	Ala	Asp	Val	Thr	Val	Gly	Ser	Phe	Leu		
	230				235				240						245		
ttc	ggc	ggc	att	gac	tca	acc	gca	att	gcg	gcg	ctt	gca	aag	cgc	cac	883	
Phe	Gly	Gly	Ile	Asp	Ser	Thr	Ala	Ile	Ala	Ala	Leu	Ala	Lys	Arg	His		

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 1206  
 Arg Ala Tyr Val  
 360

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 <213> Corynebacterium glutamicum

<400> 130  
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 Thr Arg Val Leu Lys Gln Met Ala Gly Pro Ala Lys Leu Met Ala Val  
 20 25 30  
 Val Lys Ala Asn Ala Tyr Asn His Gly Val Glu Lys Val Ala Pro Val  
 35 40 45  
 Ile Ala Ala His Gly Ala Asp Ala Phe Gly Val Ala Thr Leu Ala Glu  
 50 55 60  
 Ala Met Gln Leu Arg Asp Ile Gly Ile Ser Gln Glu Val Leu Cys Trp  
 65 70 75 80  
 Ile Trp Thr Pro Glu Gln Asp Phe Arg Ala Ala Ile Asp Arg Asn Ile  
 85 90 95  
 Asp Leu Ala Val Ile Ser Pro Ala His Ala Lys Ala Leu Ile Glu Thr  
 100 105 110  
 Asp Ala Glu His Ile Arg Val Ser Ile Lys Ile Asp Ser Gly Leu His  
 115 120 125  
 Arg Ser Gly Val Asp Glu Gln Glu Trp Glu Gly Val Phe Ser Ala Leu  
 130 135 140  
 Ala Ala Ala Pro His Ile Glu Val Thr Gly Met Phe Thr His Leu Ala  
 145 150 155 160  
 Cys Ala Asp Glu Pro Glu Asn Pro Glu Thr Asp Arg Gln Ile Ile Ala  
 165 170 175  
 Phe Arg Arg Ala Leu Ala Leu Ala Arg Lys His Gly Leu Glu Cys Pro  
 180 185 190  
 Val Asn His Val Cys Asn Ser Pro Ala Phe Leu Thr Arg Ser Asp Leu  
 195 200 205  
 His Met Glu Met Val Arg Pro Gly Leu Ala Phe Tyr Gly Leu Glu Pro  
 210 215 220  
 Val Ala Gly Leu Glu His Gly Leu Lys Pro Ala Met Thr Trp Glu Ala  
 225 230 235 240  
 Lys Val Ser Val Val Lys Gln Ile Glu Ala Gly Gln Gly Thr Ser Tyr  
 245 250 255  
 Gly Leu Thr Trp Arg Ala Glu Asp Arg Gly Phe Val Ala Val Val Pro

gag cag gag tgg gag ggc gtg ttc agc gcg ttg gct gct gcc ccg cac	547
Glu Gln Glu Trp Glu Gly Val Phe Ser Ala Leu Ala Ala Ala Pro His	
135 140 145	
att gag gtc acg ggc atg ttc acg cac ttg gcg tgc gcg gat gag cca	595
Ile Glu Val Thr Gly Met Phe Thr His Leu Ala Cys Ala Asp Glu Pro	
150 155 160 165	
gag aat ccg gaa act gat cgc caa att att gct ttt cga cgc gcc ctt	643
Glu Asn Pro Glu Thr Asp Arg Gln Ile Ile Ala Phe Arg Arg Ala Leu	
170 175 180	
gcg ctc gcc cgc aag cac ggg ctt gag tgc ccg gtc aac cac gta tgc	691
Ala Leu Ala Arg Lys His Gly Leu Glu Cys Pro Val Asn His Val Cys	
185 190 195	
aac tca cct gca ttc ttg act cga tct gat tta cac atg gag atg gtc	739
Asn Ser Pro Ala Phe Leu Thr Arg Ser Asp Leu His Met Glu Met Val	
200 205 210	
cga ccg ggt ttg gcc ttt tat ggg ttg gaa ccc gtg gcg gga ctg gag	787
Arg Pro Gly Leu Ala Phe Tyr Gly Leu Glu Pro Val Ala Gly Leu Glu	
215 220 225	
cat ggt ttg aag ccg gcg atg acg tgg gag gcg aag gtg agc gtc gta	835
His Gly Leu Lys Pro Ala Met Thr Trp Glu Ala Lys Val Ser Val Val	
230 235 240 245	
aag caa att gaa gct gga caa ggc act tcc tat ggc ctg acc tgg cgc	883
Lys Gln Ile Glu Ala Gly Gln Gly Thr Ser Tyr Gly Leu Thr Trp Arg	
250 255 260	
gct gag gat cgc ggc ttt gtg gct gtg gtg cct gcg ggc tat gcc gat	931
Ala Glu Asp Arg Gly Phe Val Ala Val Val Pro Ala Gly Tyr Ala Asp	
265 270 275	
ggc atg ccg cgg cat gcc cag ggg aaa ttc tcc gtc acg att gat ggc	979
Gly Met Pro Arg His Ala Gln Gly Lys Phe Ser Val Thr Ile Asp Gly	
280 285 290	
ctg gac tat ccg cag gtt ggg cgc gta tgc atg gat cag ttc gtt att	1027
Leu Asp Tyr Pro Gln Val Gly Arg Val Cys Met Asp Gln Phe Val Ile	
295 300 305	
tct ttg ggc gac aat cca cac ggc gtg gaa gct ggg gcg aag gcc gtg	1075
Ser Leu Gly Asp Asn Pro His Gly Val Glu Ala Gly Ala Lys Ala Val	
310 315 320 325	
ata ttc ggt gag aat ggg cat gac gca act gat ttt gcg gag cgt tta	1123
Ile Phe Gly Glu Asn Gly His Asp Ala Thr Asp Phe Ala Glu Arg Leu	
330 335 340	
gac acc att aac tat gag gta gtg tgc cga cca acc ggc cga act gtc	1171
Asp Thr Ile Asn Tyr Glu Val Val Cys Arg Pro Thr Gly Arg Thr Val	
345 350 355	



180	185	190
Leu Gly Leu Gly Trp Asp Asp Glu Asn Pro Pro Ile Ser Ile Leu Asp		
195	200	205
Pro Arg Val Cys Asp Gly Asp His Thr Asn Leu Ile Ala Ile His Ser		
210	215	220
Leu		
225		
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atcgtatttc tgtccgcggt tgggtggcaca atagttcaac atg aac ttg ctg acc 115		
		Met Asn Leu Leu Thr 5
acc aaa att gac ctg gat gcc atc gcc cat aac acg agg gtg ctt aaa 163		
Thr Lys Ile Asp Leu Asp Ala Ile Ala His Asn Thr Arg Val Leu Lys	10	15 20
caa atg gcg ggt ccg gcg aag ctg atg gcg gtg gtg aag gcg aat gca 211		
Gln Met Ala Gly Pro Ala Lys Leu Met Ala Val Val Lys Ala Asn Ala	25	30 35
tat aac cat ggc gta gag aag gtc gct ccg gtt att gct gct cat ggt 259		
Tyr Asn His Gly Val Glu Lys Val Ala Pro Val Ile Ala Ala His Gly	40	45 50
gcg gat gcg ttt ggt gtg gca act ctt gcg gag gct atg cag ttg cgt 307		
Ala Asp Ala Phe Gly Val Ala Thr Leu Ala Glu Ala Met Gln Leu Arg	55	60 65
gat atc ggc atc agc caa gag gtt ttg tgt tgg att tgg aca ccg gag 355		
Asp Ile Gly Ile Ser Gln Glu Val Leu Cys Trp Ile Trp Thr Pro Glu	70	75 80 85
cag gat ttc cgc gcc gcc att gat cgc aat att gat ttg gct gtt att 403		
Gln Asp Phe Arg Ala Ala Ile Asp Arg Asn Ile Asp Leu Ala Val Ile	90	95 100
tct ccc gcg cat gcc aaa gcc ttg atc gaa act gat gcg gag cat att 451		
Ser Pro Ala His Ala Lys Ala Leu Ile Glu Thr Asp Ala Glu His Ile	105	110 115
cgg gtg tcc atc aag att gat tct ggg ttg cat cgt tcc ggt gtg gat 499		
Arg Val Ser Ile Lys Ile Asp Ser Gly Leu His Arg Ser Gly Val Asp	120	125 130

atc ccg tcg atg atg ttt atc aac tca cca tcc aac ccc aca ggc aag 595  
 Ile Pro Ser Met Met Phe Ile Asn Ser Pro Ser Asn Pro Thr Gly Lys  
 150 155 160 165

gtt ctg ggc atc cca cac ttg cgc aag gtt gtg aag tgg gcg cag gaa 643  
 Val Leu Gly Ile Pro His Leu Arg Lys Val Val Lys Trp Ala Gln Glu  
 170 175 180

aac aac gtg atc ctc gca gct gat gaa tgc tac ttg ggt ctt ggc tgg 691  
 Asn Asn Val Ile Leu Ala Ala Asp Glu Cys Tyr Leu Gly Leu Gly Trp  
 185 190 195

gac gat gaa aac cca ccg atc tca att ttg gat cca cgt gtc tgc gat 739  
 Asp Asp Glu Asn Pro Pro Ile Ser Ile Leu Asp Pro Arg Val Cys Asp  
 200 205 210

ggc gac cac acc aac ttg atc gcc att cac tcg ctg 775  
 Gly Asp His Thr Asn Leu Ile Ala Ile His Ser Leu  
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<210> 128

<211> 225

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 128

Met Thr Ser Arg Thr Pro Leu Val Ser Val Leu Pro Asp Phe Pro Trp  
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Asp Ser Leu Ala Ser Ala Lys Ala Lys Ala Ala Ser His Pro Asp Gly  
 20 25 30

Ile Val Asn Leu Ser Val Gly Thr Pro Val Asp Pro Val Ala Pro Ser  
 35 40 45

Ile Gln Ile Ala Leu Ala Glu Ala Ala Gly Phe Ser Gly Tyr Pro Gln  
 50 55 60

Thr Ile Gly Thr Pro Glu Leu Arg Ala Ala Ile Arg Gly Ala Leu Glu  
 65 70 75 80

Arg Arg Tyr Asn Met Thr Lys Leu Val Asp Ala Ser Leu Leu Pro Val  
 85 90 95

Val Gly Thr Lys Glu Ala Ile Ala Leu Leu Pro Phe Ala Leu Gly Ile  
 100 105 110

Ser Gly Thr Val Val Ile Pro Glu Ile Ala Tyr Pro Thr Tyr Glu Val  
 115 120 125

Ala Val Val Ala Ala Gly Cys Thr Val Leu Arg Ser Asp Ser Leu Phe  
 130 135 140

Lys Leu Gly Pro Gln Ile Pro Ser Met Met Phe Ile Asn Ser Pro Ser  
 145 150 155 160

Asn Pro Thr Gly Lys Val Leu Gly Ile Pro His Leu Arg Lys Val Val  
 165 170 175

Lys Trp Ala Gln Glu Asn Asn Val Ile Leu Ala Ala Asp Glu Cys Tyr

Gly Gln Ala Arg Ile Leu Leu Ala Ile Ala Ile Ala Thr Gly Ala His  
 305 310 315 320

Pro Val Thr Leu Tyr  
 325

<210> 127

<211> 775

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(775)

<223> RXN03003

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caatgatcgc tgcgctgccg cctcaggcat aatctaacgc atg acc tct cgc acc 115  
 Met Thr Ser Arg Thr  
 1 5

ccg ctt gtt tct gtt ctt cct gat ttt ccg tgg gat tcg ctc gct tcc 163  
 Pro Leu Val Ser Val Leu Pro Asp Phe Pro Trp Asp Ser Leu Ala Ser  
 10 15 20

gca aaa gcc aaa gct gcg tct cac ccg gat ggg atc gtg aat ctt tct 211  
 Ala Lys Ala Lys Ala Ala Ser His Pro Asp Gly Ile Val Asn Leu Ser  
 25 30 35

gtt ggc act ccg gtt gat ccg gtc gcg ccc agc att cag atc gcg ttg 259  
 Val Gly Thr Pro Val Asp Pro Val Ala Pro Ser Ile Gln Ile Ala Leu  
 40 45 50

gca gaa gca gcg ggg ttt tcg ggt tac cct caa acc atc ggc acc ccg 307  
 Ala Glu Ala Ala Gly Phe Ser Gly Tyr Pro Gln Thr Ile Gly Thr Pro  
 55 60 65

gaa ctc cgc gca gcc atc agg ggc gcg ctt gag cgg cgc tac aac atg 355  
 Glu Leu Arg Ala Ala Ile Arg Gly Ala Leu Glu Arg Arg Tyr Asn Met  
 70 75 80 85

aca aag ctt gtc gac gcc tcc ctc ctc ccc gtc gtg ggt acc aag gag 403  
 Thr Lys Leu Val Asp Ala Ser Leu Leu Pro Val Val Gly Thr Lys Glu  
 90 95 100

gca att gcc ctt ctt cca ttc gcg ttg ggt att tcc ggc acc gtt gtc 451  
 Ala Ile Ala Leu Leu Pro Phe Ala Leu Gly Ile Ser Gly Thr Val Val  
 105 110 115

atc cca gag att gcg tac cca acc tac gaa gtc gct gtc gtg gcc gca 499  
 Ile Pro Glu Ile Ala Tyr Pro Thr Tyr Glu Val Ala Val Val Ala Ala  
 120 125 130

gga tgc acc gtg ttg cgt tct gat tcg ctg ttt aag ctc ggc ccg cag 547  
 Gly Cys Thr Val Leu Arg Ser Asp Ser Leu Phe Lys Leu Gly Pro Gln  
 135 140 145

&lt;211&gt; 325

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 126

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Met Ser Lys Gln His Ser Thr Pro Leu Asn Asn Asp Glu Glu His Thr
 1              5              10              15

Ser Ala Pro Gln Lys Val Ala Val Ile Thr Thr Gly Gly Thr Ile Ala
      20              25              30

Cys Thr Ser Asp Ala Asn Gly His Leu Leu Pro Thr Val Ser Gly Ala
      35              40              45

Asp Leu Leu Ala Pro Ile Ala Pro Arg Phe Asn Gly Ala Gln Ile Ala
      50              55              60

Phe Glu Ile His Glu Ile Asn Arg Leu Asp Ser Ser Ser Met Thr Phe
      65              70              75              80

Glu Asp Leu Asp Ser Ile Ile Ala Thr Val His Lys Val Leu Glu Asp
      85              90              95

Pro Asp Val Val Gly Val Val Val Thr His Gly Thr Asp Ser Met Glu
      100             105             110

Glu Ser Ala Ile Ala Val Asp Thr Phe Leu Asp Asp Pro Arg Pro Val
      115             120             125

Ile Phe Thr Gly Ala Gln Lys Pro Phe Asp His Pro Glu Ala Asp Gly
      130             135             140

Pro Asn Asn Leu Phe Glu Ala Cys Leu Ile Ala Ser Asp Pro Ser Ala
      145             150             155             160

Arg Gly Ile Gly Ala Leu Ile Val Phe Gly His Ala Val Ile Pro Ala
      165             170             175

Arg Gly Cys Val Lys Trp His Thr Ser Asp Glu Leu Ala Phe Ala Thr
      180             185             190

Asn Gly Pro Glu Glu Pro Glu Arg Pro Asp Ala Leu Pro Val Ala Lys
      195             200             205

Leu Ala Asp Val Ser Val Glu Ile Ile Pro Ala Tyr Pro Gly Ala Thr
      210             215             220

Gly Ala Met Val Glu Ala Ala Ile Ala Ala Gly Ala Gln Gly Leu Val
      225             230             235             240

Val Glu Ala Met Gly Ser Gly Asn Val Gly Ser Arg Met Gly Asp Ala
      245             250             255

Leu Gly Lys Ala Leu Asp Ala Gly Ile Pro Val Val Met Ser Thr Arg
      260             265             270

Val Pro Arg Gly Glu Val Ser Gly Val Tyr Gly Gly Ala Gly Gly Gly
      275             280             285

Ala Thr Leu Ala Ala Lys Gly Ala Val Gly Ser Arg Tyr Phe Arg Ala
      290             295             300

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Gln Lys Pro Phe Asp His Pro	Glu Ala Asp Gly Pro Asn Asn Leu Phe		
135	140 145		
gaa gcc tgc ctc atc gca tcc	gac ccc tcc gct cgc gga att ggt gca	595	
Glu Ala Cys Leu Ile Ala Ser	Asp Pro Ser Ala Arg Gly Ile Gly Ala		
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ctc att gtc ttc ggt cac gcc	gtc atc cct gct cgc ggc tgc gtt aaa	643	
Leu Ile Val Phe Gly His Ala	Val Ile Pro Ala Arg Gly Cys Val Lys		
170	175 180		
tgg cac acc tct gat gag ctg	gcg ttt gca acc aac ggc cct gaa gaa	691	
Trp His Thr Ser Asp Glu Leu	Ala Phe Ala Thr Asn Gly Pro Glu Glu		
185	190 195		
cca gag cgc ccc gat gcg ctg	ccc gta gct aaa ttg gcg gat gtc tct	739	
Pro Glu Arg Pro Asp Ala Leu	Pro Val Ala Lys Leu Ala Asp Val Ser		
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gtc gaa atc atc ccc gca tac	cct ggt gcc acc ggc gca atg gtg gaa	787	
Val Glu Ile Ile Pro Ala Tyr	Pro Gly Ala Thr Gly Ala Met Val Glu		
215	220 225		
gct gcc atc gct gcc ggt gct	caa gga ctt gta gtg gaa gca atg gga	835	
Ala Ala Ile Ala Ala Gly Ala	Gln Gly Leu Val Val Glu Ala Met Gly		
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tca ggc aat gtt ggt tcc cgc	atg ggt gat gcc cta ggt aaa gca ctt	883	
Ser Gly Asn Val Gly Ser Arg	Met Gly Asp Ala Leu Gly Lys Ala Leu		
250	255 260		
gac gct gga att ccc gtg gtg	atg agc act agg gtt cct cgt ggt gaa	931	
Asp Ala Gly Ile Pro Val Val	Met Ser Thr Arg Val Pro Arg Gly Glu		
265	270 275		
gta tcc gga gtg tat ggc ggt	gca ggt gga ggt gcg act ttg gct gcg	979	
Val Ser Gly Val Tyr Gly Gly	Ala Gly Gly Gly Ala Thr Leu Ala Ala		
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1027			
Lys Gly Ala Val Gly Ser Arg	Tyr Phe Arg Ala Gly Gln Ala Arg Ile		
295	300 305		
ttg ctc gcg att gcc att gcg	acg ggc gca cat ccg gtg acg ctt tac		
1075			
Leu Leu Ala Ile Ala Ile Ala	Thr Gly Ala His Pro Val Thr Leu Tyr		
310	315 320 325		
taatttcgcc cttggtcttg cat			
1098			

&lt;210&gt; 126

435	440	445
Ala Asp Val Cys Arg Ala Tyr Val Asp Asn Ser Ile Gly Ile Ile Thr		
450	455	460
Tyr Leu Asn Pro Phe Leu Gly His Asp Ile Gly Asp Gln Ile Gly Lys		
465	470	475
Glu Ala Ala Glu Thr Gly Arg Pro Val Arg Glu Leu Ile Leu Glu Lys		
	485	490
		495
Lys Leu Met Asp Glu Lys Thr Leu Glu Ala Val Leu Ser Lys Glu Asn		
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Leu Met His Pro Met Phe Arg Gly Arg Leu Tyr Leu Glu Asn		
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 Met Ser Lys Gln His  
 1 5  
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 Ser Thr Pro Leu Asn Asn Asp Glu Glu His Thr Ser Ala Pro Gln Lys  
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 Val Ala Val Ile Thr Thr Gly Gly Thr Ile Ala Cys Thr Ser Asp Ala  
 25 30 35  
 aat ggg cat ctg ctt ccc acc gtc agc ggt gca gac ctg ctt gcg cca 259  
 Asn Gly His Leu Leu Pro Thr Val Ser Gly Ala Asp Leu Leu Ala Pro  
 40 45 50  
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 Ile Ala Pro Arg Phe Asn Gly Ala Gln Ile Ala Phe Glu Ile His Glu  
 55 60 65  
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 Ile Asn Arg Leu Asp Ser Ser Ser Met Thr Phe Glu Asp Leu Asp Ser  
 70 75 80 85  
 atc atc gcc acg gtt cat aag gtg ttg gag gat ccg gat gtt gtt ggc 403  
 Ile Ile Ala Thr Val His Lys Val Leu Glu Asp Pro Asp Val Val Gly  
 90 95 100  
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 Val Val Val Thr His Gly Thr Asp Ser Met Glu Glu Ser Ala Ile Ala

Asn Arg Arg Leu His Thr Leu Pro Ala Gln Lys Ala Glu Ala Ile Val  
 115 120 125  
 Trp Ala Cys Asp Gln Ile Leu Ile Glu Glu Arg Cys Met Asp Gln Phe  
 130 135 140  
 Pro Ile Asp Val Phe Gln Gly Gly Ala Gly Thr Ser Leu Asn Met Asn  
 145 150 155 160  
 Thr Asn Glu Val Val Ala Asn Leu Ala Leu Glu Phe Leu Gly His Glu  
 165 170 175  
 Lys Gly Glu Tyr His Ile Leu His Pro Met Asp Asp Val Asn Met Ser  
 180 185 190  
 Gln Ser Thr Asn Asp Ser Tyr Pro Thr Gly Phe Arg Leu Gly Ile Tyr  
 195 200 205  
 Ala Gly Leu Gln Thr Leu Ile Ala Glu Ile Asp Glu Leu Gln Val Ala  
 210 215 220  
 Phe Arg His Lys Gly Asn Glu Phe Val Asp Ile Ile Lys Met Gly Arg  
 225 230 235 240  
 Thr Gln Leu Gln Asp Ala Val Pro Met Ser Leu Gly Glu Glu Phe Arg  
 245 250 255  
 Ala Phe Ala His Asn Leu Ala Glu Glu Gln Thr Val Leu Arg Glu Ala  
 260 265 270  
 Ala Asn Arg Leu Leu Glu Val Asn Leu Gly Ala Thr Ala Ile Gly Thr  
 275 280 285  
 Gly Val Asn Thr Pro Ala Gly Tyr Arg His Gln Val Val Ala Ala Leu  
 290 295 300  
 Ser Glu Val Thr Gly Leu Glu Leu Lys Ser Ala Arg Asp Leu Ile Glu  
 305 310 315 320  
 Ala Thr Ser Asp Thr Gly Ala Tyr Val His Ala His Ser Ala Ile Lys  
 325 330 335  
 Arg Ala Ala Met Lys Leu Ser Lys Ile Cys Asn Asp Leu Arg Leu Leu  
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 Ser Ser Gly Pro Arg Ala Gly Leu Asn Glu Ile Asn Leu Pro Pro Arg  
 355 360 365  
 Gln Ala Gly Ser Ser Ile Met Pro Ala Lys Val Asn Pro Val Ile Pro  
 370 375 380  
 Glu Val Val Asn Gln Val Cys Phe Lys Val Phe Gly Asn Asp Leu Thr  
 385 390 395 400  
 Val Thr Met Ala Ala Glu Ala Gly Gln Leu Gln Leu Asn Val Met Glu  
 405 410 415  
 Pro Val Ile Gly Glu Ser Leu Phe Gln Ser Leu Arg Ile Leu Gly Asn  
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 Ala Ala Lys Thr Leu Arg Glu Lys Cys Val Val Gly Ile Thr Ala Asn

cgt gag aag tgc gtc gta gga atc acc gcc aac gct gat gtt tgc cgt  
1459

Arg Glu Lys Cys Val Val Gly Ile Thr Ala Asn Ala Asp Val Cys Arg  
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gct tac gtt gat aac tcc atc ggg att atc act tac ctg aac cca ttc  
1507

Ala Tyr Val Asp Asn Ser Ile Gly Ile Ile Thr Tyr Leu Asn Pro Phe  
455 460 465

ctg ggc cac gac att gga gat cag atc ggt aag gaa gca gcc gaa act  
1555

Leu Gly His Asp Ile Gly Asp Gln Ile Gly Lys Glu Ala Ala Glu Thr  
470 475 480 485

ggt cga cca gtg cgt gaa ctc atc ctg gaa aag aag ctc atg gat gaa  
1603

Gly Arg Pro Val Arg Glu Leu Ile Leu Glu Lys Lys Leu Met Asp Glu  
490 495 500

aag acg ctc gag gca gtc ctg tcc aag gag aac ctc atg cac cca atg  
1651

Lys Thr Leu Glu Ala Val Leu Ser Lys Glu Asn Leu Met His Pro Met  
505 510 515

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Phe Arg Gly Arg Leu Tyr Leu Glu Asn  
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tac  
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<212> PRT

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Ser Gln Ser Ser Asp Ser Ala Ala Val Ser Glu Arg Val Val Glu Pro  
35 40 45

Lys Thr Thr Val Gln Lys Lys Phe Arg Ile Glu Ser Asp Leu Leu Gly  
50 55 60

Glu Leu Gln Ile Pro Ser His Ala Tyr Tyr Gly Val His Thr Leu Arg  
65 70 75 80

Ala Val Asp Asn Phe Gln Ile Ser Arg Thr Thr Ile Asn His Val Pro  
85 90 95

Asp Phe Ile Arg Gly Met Val Gln Val Lys Lys Ala Ala Ala Leu Ala  
100 105 110



aat gag ttt gtc gac atc atc aag atg ggc cgc acc cag ttg cag gat 835  
 Asn Glu Phe Val Asp Ile Ile Lys Met Gly Arg Thr Gln Leu Gln Asp  
 230 235 240 245

gct gtt ccc atg agc ttg ggc gaa gag ttc cga gca ttc gcg cac aac 883  
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Asn Lys Ser Ser Ala Asp Ser Lys Asn Asp Ala Lys Ala Glu Asp Ile									
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Val Asn Gly Glu Asn Gln Ile Ala Thr Asn Glu Ser Gln Ser Ser Asp									
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agc gct gca gtt tgc gaa cgt gtc gtc gaa cca aaa acc acg gtt cag	259								
Ser Ala Ala Val Ser Glu Arg Val Val Glu Pro Lys Thr Thr Val Gln									
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aaa aag ttc cga atc gaa tgc gat ctg ctt ggt gaa ctt cag atc cca	307								
Lys Lys Phe Arg Ile Glu Ser Asp Leu Leu Gly Glu Leu Gln Ile Pro									
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Ser His Ala Tyr Tyr Gly Val His Thr Leu Arg Ala Val Asp Asn Phe									
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Gln Ile Ser Arg Thr Thr Ile Asn His Val Pro Asp Phe Ile Arg Gly									
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Met Val Gln Val Lys Lys Ala Ala Ala Leu Ala Asn Arg Arg Leu His									
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aca ctt cca gca caa aaa gca gaa gca att gtc tgg gct tgt gat cag	499								
Thr Leu Pro Ala Gln Lys Ala Glu Ala Ile Val Trp Ala Cys Asp Gln									
	120		125		130				
atc ctc att gag gaa cgc tgt atg gat cag ttc ccc atc gat gtg ttc	547								
Ile Leu Ile Glu Glu Arg Cys Met Asp Gln Phe Pro Ile Asp Val Phe									
	135		140		145				
cag ggt ggc gca ggt acc tca ctg aac atg aac acc aac gag gtt gtt	595								
Gln Gly Gly Ala Gly Thr Ser Leu Asn Met Asn Thr Asn Glu Val Val									
	150		155		160			165	
gcc aac ctt gca ctt gag ttc tta ggc cat gaa aag ggc gag tac cac	643								
Ala Asn Leu Ala Leu Glu Phe Leu Gly His Glu Lys Gly Glu Tyr His									
	170		175		180				
atc ctg cac ccc atg gat gat gtg aac atg tcc cag tcc acc aac gat	691								
Ile Leu His Pro Met Asp Asp Val Asn Met Ser Gln Ser Thr Asn Asp									
	185		190		195				
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Ser Tyr Pro Thr Gly Phe Arg Leu Gly Ile Tyr Ala Gly Leu Gln Thr									
	200		205		210				
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Leu Ile Ala Glu Ile Asp Glu Leu Gln Val Ala Phe Arg His Lys Gly									
	215		220		225				

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Ser Gln Leu Leu Ala Tyr Gly Arg Asp Phe Ala Glu Val Met Lys Asp	
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aat gag cgc tta atc cac ggg gat ctt ggc aca gtg gat gcc cat ttg	691
Asn Glu Arg Leu Ile His Gly Asp Leu Gly Thr Val Asp Ala His Leu	
185 190 195	
gat cga gtg tgg cag att atg cag gag tgc gtg gca caa ggc atc gca	739
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Thr Pro Gly Ile Leu Pro Gly Gly Leu Asn Val Gln Arg Arg Ala Pro	
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Gln Val His Ala Leu Ile Ser Asn Gly Asp Thr Cys Glu Leu Gly Ala	
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Asp Leu Asp Ala Val Glu Trp Val Asn Leu Tyr Ala Leu Ala Val Asn	
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Ala Ala Gly Ile Ile Pro Ala Val Met His Tyr Ala Arg Asp Phe Leu	
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Ala Val Gly Ile Ile Ile Lys Glu Asn Ala Ser Ile Ser Gly Ala Glu	
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Ala Glu Ile Ala Leu Glu His Asn Leu Gly Leu Thr Cys Asp Pro Val	
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gtt gat cta ttt agc atc ggt atc gga cca tca tcc tca cat acc gtc 163  
Val Asp Leu Phe Ser Ile Gly Ile Gly Pro Ser Ser Ser His Thr Val  
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Gly Pro Met Arg Ala Ala Leu Thr Tyr Ile Ser Glu Phe Pro Ser Ser  
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His Val Asp Ile Thr Leu His Gly Ser Leu Ala Ala Thr Gly Lys Gly  
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cac tgc act gac cgg gcg gta tta ctg ggt ctg gtg gga tgg gaa cca 307  
His Cys Thr Asp Arg Ala Val Leu Leu Gly Leu Val Gly Trp Glu Pro  
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Thr Ile Val Pro Ile Asp Ala Ala Pro Ser Pro Gly Ala Pro Ile Pro  
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Thr Phe Asp Pro His Pro Leu Pro Glu His Pro Asn Ala Val Thr Phe  
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Met Thr Leu Glu Asp Phe Arg Lys Leu Asp Asp Ile Gly Ser Gly Val  
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&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 140

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Gln Ile Trp Ile Lys Ala Glu Phe Leu Gln Lys Cys Gly Val Phe Lys
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Thr Arg Gly Ala Phe Asn Arg Gln Leu Ala Ala Ser Glu Asn Gly Leu
          50           55           60

Leu Asp Pro Thr Val Gly Ile Val Ala Ala Ser Gly Gly Asn Ala Gly
          65           70           75           80

Leu Ala Asn Ala Phe Ala Ala Ala Ser Leu Ser Val Pro Ala Thr Val
          85           90           95

Leu Val Pro Glu Thr Ala Pro Gln Val Lys Val Asp Arg Leu Lys Gln
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Tyr Gly Ala Thr Val Gln Gln Ile Gly Ser Glu Tyr Ala Glu Ala Phe
          115          120          125

Glu Ala Ala Gln Thr Phe Glu Ser Glu Thr Gly Ala Leu Phe Cys His
          130          135          140

Ala Tyr Asp Gln Pro Asp Ile Ala Ala Gly Ala Gly Val Ile Gly Leu
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Glu Ile Val Glu Asp Leu Pro Asp Val Asp Thr Ile Val Val Ala Val
          165          170          175

Gly Gly Gly Gly Leu Tyr Ala Gly Ile Ala Ala Val Val Ala Ala His
          180          185          190

Asp Ile Lys Val Val Ala Val Glu Pro Ser Lys Ile Pro Thr Leu His
          195          200          205

Asn Ser Leu Ile Ala Gly Gln Pro Val Asp Val Asn Val Ser Gly Ile
          210          215          220

Ala Ala Asp Ser Leu Gly Ala Arg Gln Ile Gly Arg Glu Ala Phe Asp
          225          230          235          240

Ile Ala Thr Ala His Pro Pro Ile Gly Val Leu Val Asp Asp Glu Ala
          245          250          255

Ile Ile Ala Ala Arg Arg His Leu Trp Asp Asn Tyr Arg Ile Pro Ala
          260          265          270

Glu His Gly Ala Ala Ala Ala Leu Ala Ser Leu Thr Ser Gly Ala Tyr
          275          280          285

Lys Pro Ala Ala Asp Glu Lys Val Ala Val Ile Val Cys Gly Ala Asn
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ttt gag tcg gaa act ggt gct ctg ttt tgc cac gcc tac gac cag ccc 547  
 Phe Glu Ser Glu Thr Gly Ala Leu Phe Cys His Ala Tyr Asp Gln Pro  
 135 140 145

gac atc gca gct gga gca ggc gtc att ggg cta gaa att gtc gaa gat 595  
 Asp Ile Ala Ala Gly Ala Gly Val Ile Gly Leu Glu Ile Val Glu Asp  
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ctt ccc gac gtt gac acc atc gtg gtt gct gtc ggt ggc ggt gga ctc 643  
 Leu Pro Asp Val Asp Thr Ile Val Val Ala Val Gly Gly Gly Gly Leu  
 170 175 180

tat gca gga atc gca gcc gtc gta gca gcc cac gac atc aaa gtg gtg 691  
 Tyr Ala Gly Ile Ala Ala Val Val Ala Ala His Asp Ile Lys Val Val  
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gcc gtt gaa ccc tcc aaa att cca acc ctg cac aac tca ctc att gcc 739  
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ggg gct cgc caa att gga cga gaa gcc ttt gac atc gca act gcc cat 835  
 Gly Ala Arg Gln Ile Gly Arg Glu Ala Phe Asp Ile Ala Thr Ala His  
 230 235 240 245

ccc cca ata ggc gtc cta gtg gac gat gaa gca atc atc gca gct cga 883  
 Pro Pro Ile Gly Val Leu Val Asp Asp Glu Ala Ile Ile Ala Ala Arg  
 250 255 260

cgc cac ctc tgg gac aac tac cgc atc cct gcc gag cat ggc gct gcc 931  
 Arg His Leu Trp Asp Asn Tyr Arg Ile Pro Ala Glu His Gly Ala Ala  
 265 270 275

gca gca ctc gcc tct ctt acc agt gga gca tac aaa cct gca gca gat 979  
 Ala Ala Leu Ala Ser Leu Thr Ser Gly Ala Tyr Lys Pro Ala Ala Asp  
 280 285 290

gaa aaa gtg gca gtc att gtg tgc gga gcg aac act gac ctc aca aca  
 1027  
 Glu Lys Val Ala Val Ile Val Cys Gly Ala Asn Thr Asp Leu Thr Thr  
 295 300 305

ctg tgatgtgatt tcaaacgac aca  
 1053  
 Leu  
 310

&lt;210&gt; 140

35 40 45  
 Ile Thr Asn Gly Ala Arg Leu Glu Thr Tyr Val Ile Val Gly Asp Ala  
 50 55 60  
 Gly Thr Gly Asn Ile Cys Ile Asn Gly Ala Ala Ala His Leu Ile Asn  
 65 70 75 80  
 Pro Gly Asp Leu Val Ile Ile Met Ser Tyr Leu Gln Ala Thr Asp Ala  
 85 90 95  
 Glu Ala Lys Ala Tyr Glu Pro Lys Ile Val His Val Asp Ala Asp Asn  
 100 105 110  
 Arg Ile Val Ala Leu Gly Asn Asp Leu Ala Glu Ala Leu Pro Gly Ser  
 115 120 125  
 Gly Leu Leu Thr Ser Arg Ser Ile  
 130 135  
  
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 <211> 1053  
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 <213> Corynebacterium glutamicum  
  
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 <223> RXA01561  
  
 <400> 139  
 gtgccagaa attctgcttg cactcaccca agccgttttag caaattgaac ctcacgttca 60  
  
 taataatggt cattttcatc gagttctaga aaacacaggc atg ctc acc ctc aac 115  
 Met Leu Thr Leu Asn  
 1 5  
  
 gat gtc atc acc gcc caa caa cga acc gcc cct cat gtt cga cga acg 163  
 Asp Val Ile Thr Ala Gln Gln Arg Thr Ala Pro His Val Arg Arg Thr  
 10 15 20  
  
 cca ctt ttc gaa gca gac ccc atc gac ggc aca caa atc tgg atc aaa 211  
 Pro Leu Phe Glu Ala Asp Pro Ile Asp Gly Thr Gln Ile Trp Ile Lys  
 25 30 35  
  
 gca gag ttc ctc caa aag tgc ggc gtg ttc aaa acg cgt gga gca ttc 259  
 Ala Glu Phe Leu Gln Lys Cys Gly Val Phe Lys Thr Arg Gly Ala Phe  
 40 45 50  
  
 aac cgc cag ctc gca gct tcg gaa aac gga cta ctc gac cca acg gtt 307  
 Asn Arg Gln Leu Ala Ala Ser Glu Asn Gly Leu Leu Asp Pro Thr Val  
 55 60 65  
  
 ggc atc gtc gcg gca tca ggc gga aac gca gga ctc gca aat gct ttt 355  
 Gly Ile Val Ala Ala Ser Gly Gly Asn Ala Gly Leu Ala Asn Ala Phe  
 70 75 80 85  
  
 gcc gca gca tcc tta agc gtt ccc gcc acg gta ttg gtg ccc gaa act 403  
 Ala Ala Ala Ser Leu Ser Val Pro Ala Thr Val Leu Val Pro Glu Thr  
 90 95 100

&lt;221&gt; CDS

&lt;222&gt; (101)..(508)

&lt;223&gt; RXS02299

&lt;400&gt; 137

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acgcgggggt tggtgccgga tcgaaatatt cctttccttg tcatctcacg ctatgatttc 60

taaaacttgc aggacaaccc ccataaggac accacaggac atg ctg cgc acc atc 115
                                         Met Leu Arg Thr Ile
                                         1           5

ctc gga agt aag att cac cga gcc act gtc act caa gct gat cta gat 163
Leu Gly Ser Lys Ile His Arg Ala Thr Val Thr Gln Ala Asp Leu Asp
                10                15                20

tat gtt ggc tct gta acc atc gac gcc gac ctg gtt cac gcc gcc gga 211
Tyr Val Gly Ser Val Thr Ile Asp Ala Asp Leu Val His Ala Ala Gly
                25                30                35

ttg atc gaa ggc gaa aaa gtt gcc atc gta gac atc acc aac ggc gct 259
Leu Ile Glu Gly Glu Lys Val Ala Ile Val Asp Ile Thr Asn Gly Ala
                40                45                50

cgt ctg gaa act tat gtc att gtg ggc gac gcc gga acg ggc aat att 307
Arg Leu Glu Thr Tyr Val Ile Val Gly Asp Ala Gly Thr Gly Asn Ile
                55                60                65

tgc atc aat ggt gcc gct gca cac ctt att aat cct ggc gat ctt gtg 355
Cys Ile Asn Gly Ala Ala Ala His Leu Ile Asn Pro Gly Asp Leu Val
                70                75                80                85

atc atc atg agc tac ctt cag gca act gat gcg gaa gcc aag gcg tat 403
Ile Ile Met Ser Tyr Leu Gln Ala Thr Asp Ala Glu Ala Lys Ala Tyr
                90                95                100

gag cca aag att gtg cac gtg gac gcc gac aac cgc atc gtt gcg ctc 451
Glu Pro Lys Ile Val His Val Asp Ala Asp Asn Arg Ile Val Ala Leu
                105                110                115

ggc aac gat ctt gcg gaa gca cta cct gga tcc ggg ctt ttg acg tcg 499
Gly Asn Asp Leu Ala Glu Ala Leu Pro Gly Ser Gly Leu Leu Thr Ser
                120                125                130

aga agc att tagcgtttta gctcgccaat att 531
Arg Ser Ile
                135

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&lt;210&gt; 138

&lt;211&gt; 136

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 138

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Met Leu Arg Thr Ile Leu Gly Ser Lys Ile His Arg Ala Thr Val Thr
  1           5           10           15

Gln Ala Asp Leu Asp Tyr Val Gly Ser Val Thr Ile Asp Ala Asp Leu
  20           25           30

Val His Ala Ala Gly Leu Ile Glu Gly Glu Lys Val Ala Ile Val Asp

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Ser Phe Val Gly Ser Thr Pro Ile Ala Lys Tyr Ile Tyr Glu Thr Ser  
 225 230 235 240  
 Ala Lys Asn Gly Lys Arg Val Gln Ala Leu Gly Gly Ala Lys Asn His  
 245 250 255  
 Met Leu Val Leu Pro Asp Ala Asp Leu Asp Leu Val Ala Asp Gln Ala  
 260 265 270  
 Ile Asn Ala Gly Tyr Gly Ala Ala Gly Glu Arg Cys Met Ala Val Ser  
 275 280 285  
 Val Val Leu Ala Ile Glu Ser Val Ala Asp Glu Leu Ile Glu Lys Ile  
 290 295 300  
 Lys Glu Arg Ile Asp Thr Leu Arg Ile Gly Asn Gly Ala Gly Asp Glu  
 305 310 315 320  
 Gln Gly Glu Pro His Leu Gly Pro Leu Ile Thr Asp Val His Arg Asp  
 325 330 335  
 Lys Val Ala Ser Tyr Val Asp Ile Ala Glu Ala Asp Gly Ala Lys Ile  
 340 345 350  
 Ile Val Asp Gly Arg Asn Cys Ala Val Asp Gly His Glu Glu Gly Phe  
 355 360 365  
 Phe Phe Gly Pro Thr Leu Ile Asp Asp Ile Pro Leu Thr Phe Arg Ala  
 370 375 380  
 Tyr Thr Glu Glu Ile Phe Gly Pro Val Leu Ser Val Val Arg Val Ala  
 385 390 395 400  
 Ser Phe Asp Glu Ala Ile Glu Leu Ile Asn Ser Gly Glu Phe Gly Asn  
 405 410 415  
 Gly Thr Ala Ile Phe Thr Asn Asp Gly Gly Ala Ala Arg Arg Phe Gln  
 420 425 430  
 His Glu Ile Glu Val Gly Met Ile Gly Ile Asn Val Pro Ile Pro Val  
 435 440 445  
 Pro Val Ala Tyr His Ser Phe Gly Gly Trp Lys Asn Ser Leu Phe Gly  
 450 455 460  
 Asp Ala Lys Ala Tyr Gly Thr Gln Gly Phe Asp Phe Phe Thr Arg Glu  
 465 470 475 480  
 Lys Ala Ile Thr Ser Arg Trp Leu Asp Pro Ala Thr His Gly Gly Ile  
 485 490 495  
 Asn Leu Gly Phe Pro Gln Asn Asp  
 500

&lt;210&gt; 137

&lt;211&gt; 531

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

470 475 480 485

cgt tgg ctc gac cca gca acc cac ggt ggc att aac ctc ggt ttc cca  
1603

Arg Trp Leu Asp Pro Ala Thr His Gly Gly Ile Asn Leu Gly Phe Pro  
490 495 500

cag aac gat taattgaagg agagcacagg act  
1635

Gln Asn Asp

Gly Ala Ala Gly Glu Arg Cys Met Ala Val Ser Val Val Leu Ala Ile  
 280 285 290  
 gaa tct gtt gcc gac gag ctc att gag aag atc aag gag cgc atc gac  
 1027  
 Glu Ser Val Ala Asp Glu Leu Ile Glu Lys Ile Lys Glu Arg Ile Asp  
 295 300 305  
 acc ctg cgc atc ggc aac ggt gcc ggc gac gag cag ggc gag ccg cac  
 1075  
 Thr Leu Arg Ile Gly Asn Gly Ala Gly Asp Glu Gln Gly Glu Pro His  
 310 315 320 325  
 ctg ggc cca cta atc acc gac gtc cac cgc gac aag gtc gct tct tat  
 1123  
 Leu Gly Pro Leu Ile Thr Asp Val His Arg Asp Lys Val Ala Ser Tyr  
 330 335 340  
 gtc gac atc gct gag gcc gac ggc gcc aag atc atc gtg gac ggg cgt  
 1171  
 Val Asp Ile Ala Glu Ala Asp Gly Ala Lys Ile Ile Val Asp Gly Arg  
 345 350 355  
 aac tgc gcc gta gac ggg cac gag gag ggc ttc ttc ttc ggc cct acg  
 1219  
 Asn Cys Ala Val Asp Gly His Glu Glu Gly Phe Phe Phe Gly Pro Thr  
 360 365 370  
 ctt atc gac gac atc cca ctc acg ttc cgc gcc tac acc gaa gaa atc  
 1267  
 Leu Ile Asp Asp Ile Pro Leu Thr Phe Arg Ala Tyr Thr Glu Glu Ile  
 375 380 385  
 ttc ggc ccg gtc ctc tct gtc gtt cgt gtc gca tcc ttc gac gag gca  
 1315  
 Phe Gly Pro Val Leu Ser Val Val Arg Val Ala Ser Phe Asp Glu Ala  
 390 395 400 405  
 att gag ctg atc aac tcc ggt gaa ttc ggc aac gga acc gca atc ttc  
 1363  
 Ile Glu Leu Ile Asn Ser Gly Glu Phe Gly Asn Gly Thr Ala Ile Phe  
 410 415 420  
 acc aac gat ggt gga gcg gca cgc cgc ttc cag cat gag atc gaa gtg  
 1411  
 Thr Asn Asp Gly Gly Ala Ala Arg Arg Phe Gln His Glu Ile Glu Val  
 425 430 435  
 ggc atg atc ggc atc aac gta cca atc cca gtg cct gtt gcg tac cac  
 1459  
 Gly Met Ile Gly Ile Asn Val Pro Ile Pro Val Pro Val Ala Tyr His  
 440 445 450  
 tcc ttc ggt ggt tgg aag aac tcc ctc ttc ggt gac gcc aag gca tat  
 1507  
 Ser Phe Gly Gly Trp Lys Asn Ser Leu Phe Gly Asp Ala Lys Ala Tyr  
 455 460 465  
 ggc act caa ggt ttt gat ttc ttc acc agg gaa aag gcg atc acc agc  
 1555  
 Gly Thr Gln Gly Phe Asp Phe Phe Thr Arg Glu Lys Ala Ile Thr Ser

gtt gcg ctg gct agc cag gaa gag atc gat gcc acc atc gct tct gcc	259
Val Ala Leu Ala Ser Gln Glu Glu Ile Asp Ala Thr Ile Ala Ser Ala	
40 45 50	
acc aag gct gct aag acg tgg ggc aac ctg tct atc gct aag cgc caa	307
Thr Lys Ala Ala Lys Thr Trp Gly Asn Leu Ser Ile Ala Lys Arg Gln	
55 60 65	
gct gtg ctt ttc aac ttc cgt gag ctg ctg aat gct cgc aag ggt gag	355
Ala Val Leu Phe Asn Phe Arg Glu Leu Leu Asn Ala Arg Lys Gly Glu	
70 75 80 85	
ctg gcg gag atc atc act gca gag cac ggc aag gtc ttg tcc gat gcc	403
Leu Ala Glu Ile Ile Thr Ala Glu His Gly Lys Val Leu Ser Asp Ala	
90 95 100	
atg ggt gaa atc ctg cgc ggc cag gaa gtc gtg gag ctt gct acc ggt	451
Met Gly Glu Ile Leu Arg Gly Gln Glu Val Val Glu Leu Ala Thr Gly	
105 110 115	
ttc cca cac ctg ctt aaa ggt gcg ttc aac gag aac gtc tcc acc ggc	499
Phe Pro His Leu Leu Lys Gly Ala Phe Asn Glu Asn Val Ser Thr Gly	
120 125 130	
att gat gtg tat tcc ttg aag cag cca ctg ggt gtt gtc ggt atc atc	547
Ile Asp Val Tyr Ser Leu Lys Gln Pro Leu Gly Val Val Gly Ile Ile	
135 140 145	
agc ccg ttc aac ttc cct gcg atg gtg ccg atg tgg ttt ttc cca atc	595
Ser Pro Phe Asn Phe Pro Ala Met Val Pro Met Trp Phe Phe Pro Ile	
150 155 160 165	
gca atc gct gca ggc aac gca gtt att ttg aag cct tca gag aag gat	643
Ala Ile Ala Ala Gly Asn Ala Val Ile Leu Lys Pro Ser Glu Lys Asp	
170 175 180	
cct tcg gca gcg ctg tgg atg gct cag atc tgg aag gaa gct ggt ctt	691
Pro Ser Ala Ala Leu Trp Met Ala Gln Ile Trp Lys Glu Ala Gly Leu	
185 190 195	
cca gac ggc gta ttc aac gtg ctc cag ggc gac aag ctg gct gtt gat	739
Pro Asp Gly Val Phe Asn Val Leu Gln Gly Asp Lys Leu Ala Val Asp	
200 205 210	
ggt ttg ctg aac agc cct gat gtc tct gcg att tcc ttc gtg ggt tcc	787
Gly Leu Leu Asn Ser Pro Asp Val Ser Ala Ile Ser Phe Val Gly Ser	
215 220 225	
acc cca atc gca aag tac atc tac gag act tcc gcg aag aac ggc aag	835
Thr Pro Ile Ala Lys Tyr Ile Tyr Glu Thr Ser Ala Lys Asn Gly Lys	
230 235 240 245	
cgc gtc cag gcg ttg ggc ggc gcg aag aac cac atg ctg gtg ctg cca	883
Arg Val Gln Ala Leu Gly Gly Ala Lys Asn His Met Leu Val Leu Pro	
250 255 260	
gat gct gat ctg gat ctg gtt gcc gat cag gca atc aac gca ggt tac	931
Asp Ala Asp Leu Asp Leu Val Ala Asp Gln Ala Ile Asn Ala Gly Tyr	
265 270 275	
ggc gct gcc ggt gag cgt tgc atg gct gtt tct gtg gtc ttg gct att	979

65	70	75	80
Ile Ser Arg Val Asn Asn Thr Val Leu	Ile Ser Gly Ala Gly Leu His		
85	90	95	
Gln Gly Tyr Asn Lys Ile His Thr Tyr Asp Ala Phe Gly Tyr Arg Glu			
100	105	110	
Ser Asp Thr Val Lys Pro Gly Asp Glu Leu Val Val Phe Glu Val Asp			
115	120	125	
Asp Ile Lys Phe Gly Val Ala Thr Cys Tyr Asp Ile Arg Phe Pro Glu			
130	135	140	
Gln Phe Lys Asp Leu Ala Arg Asn Gly Ala Gln Ile Ile Val Val Pro			
145	150	155	160
Thr Ser Trp Gln Asp Gly Pro Gly Lys Leu Glu Gln Trp Glu Val Leu			
165	170	175	
Pro Arg Ala Arg Ala Leu Asp Ser Thr Cys Trp Ile Val Ala Cys Gly			
180	185	190	
Gln Ala Arg Leu Pro Glu Glu Leu Arg Asp Glu Arg Lys Gly Pro Thr			
195	200	205	
Gly Ile Gly His Ser Met Val Thr Asn Pro His Gly Glu Val Ile Ala			
210	215	220	
Ser Ala Gly Tyr Glu Pro Glu Met Leu Ile Ala Asp Ile Asp Val Ser			
225	230	235	240
Gly Leu Ala Lys Ile Arg Glu Ala Leu Pro Val Leu			
245	250		

<210> 135  
 <211> 1635  
 <212> DNA  
 <213> *Corynebacterium glutamicum*  
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 <222> (101)..(1612)  
 <223> RXS00870  
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 caacaattca cttcgagag catttaagga atttacacac atg tct gaa cca caa 115  
 Met Ser Glu Pro Gln 5  
 1  
 acc atc tcg cac tgg att gac ggc gcg att tcc cca tcc act tcc ggc 163  
 Thr Ile Ser His Trp Ile Asp Gly Ala Ile Ser Pro Ser Thr Ser Gly 20  
 10 15  
 aag acc gct cct gtc tac aat cct gca act ggc cag gtc acc gcc aat 211  
 Lys Thr Ala Pro Val Tyr Asn Pro Ala Thr Gly Gln Val Thr Ala Asn 35  
 25 30

att cac aca tat gac gcg ttc ggt tat agg gaa tcc gac act gtg aaa 451  
 Ile His Thr Tyr Asp Ala Phe Gly Tyr Arg Glu Ser Asp Thr Val Lys  
                   105                                  110                                  115

ccg ggc gat gag ctg gtt gta ttc gag gtc gac gat att aaa ttt ggt 499  
 Pro Gly Asp Glu Leu Val Val Phe Glu Val Asp Asp Ile Lys Phe Gly  
                   120                                  125                                  130

gtg gcg aca tgc tac gat att cga ttc cca gaa cag ttc aaa gac ctc 547  
 Val Ala Thr Cys Tyr Asp Ile Arg Phe Pro Glu Gln Phe Lys Asp Leu  
                   135                                  140                                  145

gcc cgc aac ggt gca cag ata att gtg gtt ccc acg tcg tgg caa gac 595  
 Ala Arg Asn Gly Ala Gln Ile Ile Val Val Pro Thr Ser Trp Gln Asp  
                   150                                  155                                  160                                  165

ggt cct gga aaa tta gaa caa tgg gaa gtc ctc cct cgc gcg cgt gca 643  
 Gly Pro Gly Lys Leu Glu Gln Trp Glu Val Leu Pro Arg Ala Arg Ala  
                                   170                                  175                                  180

ctg gat tcc acc tgc tgg atc gta gcg tgt ggg caa gcg cga ctt cca 691  
 Leu Asp Ser Thr Cys Trp Ile Val Ala Cys Gly Gln Ala Arg Leu Pro  
                                   185                                  190                                  195

gaa gaa tta cgc gat gaa cga aaa ggc cct acg ggg att ggt cat tcc 739  
 Glu Glu Leu Arg Asp Glu Arg Lys Gly Pro Thr Gly Ile Gly His Ser  
                   200                                  205                                  210

atg gtg aca aac cca cac ggt gaa gta att gct agc gcg ggt tat gag 787  
 Met Val Thr Asn Pro His Gly Glu Val Ile Ala Ser Ala Gly Tyr Glu  
                   215                                  220                                  225

cca gaa atg ttg atc gcg gat att gat gtc agc ggt ttg gcc aaa att 835  
 Pro Glu Met Leu Ile Ala Asp Ile Asp Val Ser Gly Leu Ala Lys Ile  
                   230                                  235                                  240                                  245

cgg gag gca ttg cct gtt ctt taaccactgt ctaaggaatc act 879  
 Arg Glu Ala Leu Pro Val Leu  
                                   250

&lt;210&gt; 134

&lt;211&gt; 252

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 134

Met Asp Asn Phe Ala Leu Leu Arg Asp Ala Ala Glu Lys Ala Ala Glu  
   1                                  5                                  10                                  15

Gln Gly Ala Arg Val Leu Val Phe Pro Glu Ala Thr Ser Gln Ser Phe  
                   20                                  25                                  30

Gly Thr Gly Arg Leu Asp Thr Gln Ala Glu Glu Leu Asp Gly Glu Phe  
                   35                                  40                                  45

Ser Thr Ala Val Arg Lys Leu Ala Asp Glu Leu Asp Val Val Ile Val  
                   50                                  55                                  60

Ala Gly Met Phe Thr Pro Ala Asp Thr Val Gln Arg Gly Glu Lys Thr

	245		250		255
Ile Leu Ser Thr Asp Lys Pro Ala Trp Ile Asp Gly Asn Gly Phe Val	260	265	270		
Leu Gly Asn Pro Glu Ala Arg Ile Ser Ala Leu Ser Glu His His Ala	275	280	285		
Thr Ile Phe Trp Pro Asp Lys Val Leu Leu Pro Val Ile Gly Glu Gln	290	295	300		
Leu Asn Ile Val Pro Asn His Ala Cys Asn Val Ile Asn Leu Val Asp	305	310	315	320	
Glu Val Tyr Val Arg Glu Ala Asp Gly Thr Phe Arg Thr Trp Lys Val	325	330	335		
Val Ala Arg Gly Arg Asn Asn	340				

<210> 133  
 <211> 879  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(856)  
 <223> RXA02536

<400> 133  
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gcgtattgcc ttgcttcaga tctcgacgaa ttccgataag atg gac aac ttc gcc 115  
 Met Asp Asn Phe Ala  
 1 5

ctg ctg cgt gat gct gct gaa aaa gct gcg gaa cag ggg gct cgg gtg 163  
 Leu Leu Arg Asp Ala Ala Glu Lys Ala Ala Glu Gln Gly Ala Arg Val  
 10 15 20

ttg gtg ttt ccg gag gcg act tcg caa agc ttt ggt acg gga agg ctt 211  
 Leu Val Phe Pro Glu Ala Thr Ser Gln Ser Phe Gly Thr Gly Arg Leu  
 25 30 35

gat act cag gcg gag gag ctc gat ggc gaa ttc tcc acc gcg gta cga 259  
 Asp Thr Gln Ala Glu Glu Leu Asp Gly Glu Phe Ser Thr Ala Val Arg  
 40 45 50

aaa tta gcc gat gag ctg gac gtt gtc atc gtt gcg ggc atg ttc acc 307  
 Lys Leu Ala Asp Glu Leu Asp Val Val Ile Val Ala Gly Met Phe Thr  
 55 60 65

cct gct gac acc gtg cag cgc ggt gaa aaa acg atc tcg cgc gtc aac 355  
 Pro Ala Asp Thr Val Gln Arg Gly Glu Lys Thr Ile Ser Arg Val Asn  
 70 75 80 85

aac acc gtg ctg att agt ggc gct gga ttg cat cag gga tac aac aaa 403  
 Asn Thr Val Leu Ile Ser Gly Ala Gly Leu His Gln Gly Tyr Asn Lys  
 90 95 100

Glu Ala Asp Gly Thr Phe Arg Thr Trp Lys Val Val Ala Arg Gly Arg  
 330 335 340

aac aat tagggaaacc tcttgacctt cac

1152

Asn Asn

<210> 132

<211> 343

<212> PRT

<213> Corynebacterium glutamicum

<400> 132

Met Met Ile Asp Thr Pro Ala Val Leu Ile Asp Arg Glu Arg Leu Thr  
 1 5 10 15

Ala Asn Ile Ser Arg Met Ala Ala His Ala Gly Ala His Glu Ile Ala  
 20 25 30

Leu Arg Pro His Val Lys Thr His Lys Ile Ile Glu Ile Ala Gln Met  
 35 40 45

Gln Val Asp Ala Gly Ala Arg Gly Ile Thr Cys Ala Thr Ile Gly Glu  
 50 55 60

Ala Glu Ile Phe Ala Gly Ala Gly Phe Thr Asp Ile Phe Ile Ala Tyr  
 65 70 75 80

Pro Leu Tyr Leu Thr Asp His Ala Val Gln Arg Leu Asn Ala Ile Pro  
 85 90 95

Gly Glu Ile Ser Ile Gly Val Asp Ser Val Glu Met Ala Gln Ala Thr  
 100 105 110

Ala Gly Leu Arg Glu Asp Ile Lys Ala Leu Ile Glu Val Asp Ser Gly  
 115 120 125

His Arg Arg Ser Gly Val Thr Ala Thr Ala Ser Glu Leu Ser Gln Ile  
 130 135 140

Arg Glu Ala Leu Gly Ser Arg Tyr Ala Gly Val Phe Thr Phe Pro Gly  
 145 150 155 160

His Ser Tyr Gly Pro Gly Asn Gly Glu Gln Ala Ala Ala Asp Glu Leu  
 165 170 175

Gln Ala Leu Asn Asn Ser Val Gln Arg Leu Ala Gly Gly Leu Thr Ser  
 180 185 190

Gly Gly Ser Ser Pro Ser Ala Gln Phe Thr Asp Ala Ile Asp Glu Met  
 195 200 205

Arg Pro Gly Val Tyr Val Phe Asn Asp Ser Gln Gln Ile Thr Ser Gly  
 210 215 220

Ala Cys Thr Glu Lys Gln Val Ala Met Thr Val Leu Ser Thr Val Val  
 225 230 235 240

Ser Arg Asn Val Ser Asp Arg Arg Ile Ile Leu Asp Ala Gly Ser Lys



ggc gtg gat tgc gta gag atg gca cag gcg acg gcg ggt ttg cgg gaa	451
Gly Val Asp Ser Val Glu Met Ala Gln Ala Thr Ala Gly Leu Arg Glu	
105 110 115	
gat atc aag gct ctg att gaa gtg gat tgc gga cat cgt aga agt gga	499
Asp Ile Lys Ala Leu Ile Glu Val Asp Ser Gly His Arg Arg Ser Gly	
120 125 130	
gtc acg gcg act gct tca gaa ttg agt cag atc cgc gag gcg ctg ggc	547
Val Thr Ala Thr Ala Ser Glu Leu Ser Gln Ile Arg Glu Ala Leu Gly	
135 140 145	
agc agg tat gca gga gtg ttt act ttt cct ggg cat tct tat ggc ccg	595
Ser Arg Tyr Ala Gly Val Phe Thr Phe Pro Gly His Ser Tyr Gly Pro	
150 155 160 165	
gga aat ggt gag cag gca gca gct gat gag ctt cag gct cta aac aac	643
Gly Asn Gly Glu Gln Ala Ala Ala Asp Glu Leu Gln Ala Leu Asn Asn	
170 175 180	
agc gtc cag cga ctt gct ggc ggc ctg act tct ggc ggt tcc tcg ccg	691
Ser Val Gln Arg Leu Ala Gly Gly Leu Thr Ser Gly Gly Ser Ser Pro	
185 190 195	
tct gcg cag ttt aca gac gca atc gat gag atg cga cca ggc gtg tat	739
Ser Ala Gln Phe Thr Asp Ala Ile Asp Glu Met Arg Pro Gly Val Tyr	
200 205 210	
gtg ttt aac gat tcc cag cag atc acc tcg gga gca tgc act gag aag	787
Val Phe Asn Asp Ser Gln Gln Ile Thr Ser Gly Ala Cys Thr Glu Lys	
215 220 225	
cag gtg gca atg acg gtg ctg tct act gtg gtc agc cga aat gtg tca	835
Gln Val Ala Met Thr Val Leu Ser Thr Val Val Ser Arg Asn Val Ser	
230 235 240 245	
gat cgt cgg atc att ttg gat gcg gga tcc aaa atc ctc agc act gat	883
Asp Arg Arg Ile Ile Leu Asp Ala Gly Ser Lys Ile Leu Ser Thr Asp	
250 255 260	
aaa cca gca tgg att gat ggc aat ggt ttt gtt ctg ggg aat cct gaa	931
Lys Pro Ala Trp Ile Asp Gly Asn Gly Phe Val Leu Gly Asn Pro Glu	
265 270 275	
gcc cga atc tct gct ttg tcg gag cat cac gca acc att ttc tgg cca	979
Ala Arg Ile Ser Ala Leu Ser Glu His His Ala Thr Ile Phe Trp Pro	
280 285 290	
gat aaa gtg cta ctt cca gta atc ggg gag cag ctc aac atc gtg ccc	
1027	
Asp Lys Val Leu Leu Pro Val Ile Gly Glu Gln Leu Asn Ile Val Pro	
295 300 305	
aac cat gcc tgc aac gtg att aat ttg gtg gat gag gtc tac gtt cgg	
1075	
Asn His Ala Cys Asn Val Ile Asn Leu Val Asp Glu Val Tyr Val Arg	
310 315 320 325	
gaa gcc gat ggc act ttc cgt acc tgg aag gta gtt gcc cgc ggc aga	
1123	

260 265 270  
 Ala Gly Tyr Ala Asp Gly Met Pro Arg His Ala Gln Gly Lys Phe Ser  
 275 280 285  
 Val Thr Ile Asp Gly Leu Asp Tyr Pro Gln Val Gly Arg Val Cys Met  
 290 295 300  
 Asp Gln Phe Val Ile Ser Leu Gly Asp Asn Pro His Gly Val Glu Ala  
 305 310 315 320  
 Gly Ala Lys Ala Val Ile Phe Gly Glu Asn Gly His Asp Ala Thr Asp  
 325 330 335  
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 <213> Corynebacterium glutamicum

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 Met Met Ile Asp Thr  
 1 5  
 cct gct gtt ctc att gac cgc gag cgc tta act gcc aac att tcc agg 163  
 Pro Ala Val Leu Ile Asp Arg Glu Arg Leu Thr Ala Asn Ile Ser Arg  
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 atg gca gct cac gcc ggt gcc cat gag att gcc ctg cgt ccg cat gtg 211  
 Met Ala Ala His Ala Gly Ala His Glu Ile Ala Leu Arg Pro His Val  
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 aaa acg cac aaa atc att gaa att gcg cag atg cag gtc gac gcc ggt 259  
 Lys Thr His Lys Ile Ile Glu Ile Ala Gln Met Gln Val Asp Ala Gly  
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 Ala Arg Gly Ile Thr Cys Ala Thr Ile Gly Glu Ala Glu Ile Phe Ala  
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 Gly Ala Gly Phe Thr Asp Ile Phe Ile Ala Tyr Pro Leu Tyr Leu Thr  
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 Asp His Ala Val Gln Arg Leu Asn Ala Ile Pro Gly Glu Ile Ser Ile  
 90 95 100

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 Ala Leu Arg Glu Gly Tyr Leu Pro Ala Val Ile Thr Val Ser Gly Lys  
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 Asp Arg Pro Gly Val Thr Ala Ala Phe Phe Arg Val Leu Ser Ala Asn  
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 Asn Leu Ala Ala Phe Val Gly Ile Ala Pro Glu Arg Val Glu Thr Val  
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 Thr Thr Gly Leu Thr Asp Thr Leu Lys Val His Gly Gln Ser Val Val  
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 Val Glu Leu Gln Glu Thr Val Gln Ser Ser Arg Pro Arg Ser Ser His  
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&lt;210&gt; 156

&lt;211&gt; 130

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 156

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Ala Gly Gln Gln Val Ala Leu Arg Glu Gly Tyr Leu Pro Ala Val Ile  
                   20                                  25                                  30

Thr Val Ser Gly Lys Asp Arg Pro Gly Val Thr Ala Ala Phe Phe Arg  
                   35                                  40                                  45

Val Leu Ser Ala Asn Gln Val Gln Val Leu Asp Val Glu Gln Ser Met  
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Phe Arg Gly Phe Leu Asn Leu Ala Ala Phe Val Gly Ile Ala Pro Glu  
   65                                  70                                  75                                  80

Arg Val Glu Thr Val Thr Thr Gly Leu Thr Asp Thr Leu Lys Val His  
                   85                                  90                                  95

Gly Gln Ser Val Val Val Glu Leu Gln Glu Thr Val Gln Ser Ser Arg  
                   100                                  105                                  110

Pro Arg Ser Ser His Val Val Val Val Leu Gly Asp Pro Val Asp Ala  
   115                                  120                                  125

Leu Asp  
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<211> 433

<212> PRT

<213> Corynebacterium glutamicum

<400> 154

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Thr Val Ser Gly Lys Asp Arg Pro Gly Val Thr Ala Ala Phe Phe Arg  
35 40 45

Val Leu Ser Ala Asn Gln Val Gln Val Leu Asp Val Glu Gln Ser Met  
50 55 60

Phe Arg Gly Phe Leu Asn Leu Ala Ala Phe Val Gly Ile Ala Pro Glu  
65 70 75 80

Arg Val Glu Thr Val Thr Thr Gly Leu Thr Asp Thr Leu Lys Val His  
85 90 95

Gly Gln Ser Val Val Val Glu Leu Gln Glu Thr Val Gln Ser Ser Arg  
100 105 110

Pro Arg Ser Ser His Val Val Val Val Leu Gly Asp Pro Val Asp Ala  
115 120 125

Leu Asp Ile Ser Arg Ile Gly Gln Thr Leu Ala Asp Tyr Asp Ala Asn  
130 135 140

Ile Asp Thr Ile Arg Gly Ile Ser Asp Tyr Pro Val Thr Gly Leu Glu  
145 150 155 160

Leu Lys Val Thr Val Pro Asp Val Ser Pro Gly Gly Gly Glu Ala Met  
165 170 175

Arg Lys Ala Leu Ala Ala Leu Thr Ser Glu Leu Asn Val Asp Ile Ala  
180 185 190

Ile Glu Arg Ser Gly Leu Leu Arg Arg Ser Lys Arg Leu Val Cys Phe  
195 200 205

Asp Cys Asp Ser Thr Leu Ile Thr Gly Glu Val Ile Glu Met Leu Ala  
210 215 220

Ala His Ala Gly Lys Glu Ala Glu Val Ala Ala Val Thr Glu Arg Ala  
225 230 235 240

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gaa gct gaa gtt gcg gca gtt act gag cgt gcg atg cgc ggt gag ctc Glu Ala Glu Val Ala Ala Val Thr Glu Arg Ala Met Arg Gly Glu Leu 230 235 240 245			835
gat ttc gag gag tct ctg cgt gag cgt gtg aag gcg ttg gct ggt ttg Asp Phe Glu Glu Ser Leu Arg Glu Arg Val Lys Ala Leu Ala Gly Leu 250 255 260			883
gat gcg tcg gtg atc gat gag gtc gct gcc gct att gag ctg acc cct Asp Ala Ser Val Ile Asp Glu Val Ala Ala Ala Ile Glu Leu Thr Pro 265 270 275			931
ggt gcg cgc acc acg atc cgt acg ctg aac cgc atg ggt tac cag acc Gly Ala Arg Thr Thr Ile Arg Thr Leu Asn Arg Met Gly Tyr Gln Thr 280 285 290			979
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gag ttg gag ttg gat tat gtc cgc gcc aac act ttg gaa atc gtt gat 1075 Glu Leu Glu Leu Asp Tyr Val Arg Ala Asn Thr Leu Glu Ile Val Asp 310 315 320 325			
ggc aag ctg acc ggc aac gtc acc gga aag atc gtt gac cgc gct gcg 1123 Gly Lys Leu Thr Gly Asn Val Thr Gly Lys Ile Val Asp Arg Ala Ala 330 335 340			
aag gct gag ttc ctc cgt gag ttc gct gcg gat tct ggc ctg aag atg 1171 Lys Ala Glu Phe Leu Arg Glu Phe Ala Ala Asp Ser Gly Leu Lys Met 345 350 355			
tac cag act gtc gct gtc ggt gat ggc gct aat gac atc gat atg ctc 1219 Tyr Gln Thr Val Ala Val Gly Asp Gly Ala Asn Asp Ile Asp Met Leu 360 365 370			
tcc gct gcg ggt ctg ggt gtt gct ttc aac gcg aag cct gcg ctg aag 1267 Ser Ala Ala Gly Leu Gly Val Ala Phe Asn Ala Lys Pro Ala Leu Lys 375 380 385			
gag att gcg gat act tcc gtg aac cac cca ttc ctc gac gag gtt ttg 1315 Glu Ile Ala Asp Thr Ser Val Asn His Pro Phe Leu Asp Glu Val Leu 390 395 400 405			
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cag aat gaa tcc caa gaa atc gct gag ctg gaa gcc ggc cag cag gtt 163
Gln Asn Glu Ser Gln Glu Ile Ala Glu Leu Glu Ala Gly Gln Gln Val
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Ala Leu Arg Glu Gly Tyr Leu Pro Ala Val Ile Thr Val Ser Gly Lys
                               25 30 35

gac cgc cca ggt gtg act gcc gcg ttc ttt agg gtc ttg tcc gct aat 259
Asp Arg Pro Gly Val Thr Ala Ala Phe Phe Arg Val Leu Ser Ala Asn
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Asn Leu Ala Ala Phe Val Gly Ile Ala Pro Glu Arg Val Glu Thr Val
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Thr Thr Gly Leu Thr Asp Thr Leu Lys Val His Gly Gln Ser Val Val
                               90 95 100

gtg gag ctg cag gaa act gtg cag tcg tcc cgt cct cgt tct tcc cat 451
Val Glu Leu Gln Glu Thr Val Gln Ser Ser Arg Pro Arg Ser Ser His
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Val Val Val Val Leu Gly Asp Pro Val Asp Ala Leu Asp Ile Ser Arg
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Ile Gly Gln Thr Leu Ala Asp Tyr Asp Ala Asn Ile Asp Thr Ile Arg
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ggt att tcg gat tac cct gtg acc ggc ctg gag ctg aag gtg act gtg 595
Gly Ile Ser Asp Tyr Pro Val Thr Gly Leu Glu Leu Lys Val Thr Val
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ccg gat gtc agc cct ggt ggt ggt gaa gcg atg cgt aag gcg ctt gct 643
Pro Asp Val Ser Pro Gly Gly Gly Glu Ala Met Arg Lys Ala Leu Ala
                               170 175 180

gct ctt acc tct gag ctg aat gtg gat att gcg att gag cgt tct ggt 691
Ala Leu Thr Ser Glu Leu Asn Val Asp Ile Ala Ile Glu Arg Ser Gly
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Leu Leu Arg Arg Ser Lys Arg Leu Val Cys Phe Asp Cys Asp Ser Thr

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 Lys Leu Ala Pro Trp Leu Asp Glu Pro Glu Ile Val Thr Ala Glu Thr  
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 Pro Glu Gly Ser Glu Gly Ser Leu Val Ala Ile Asp Ala Thr Ser Gly  
 165 170 175  
 Ala Gly Gly Leu Pro Val Asp Ile Lys Asn Ser Asp Val Tyr Tyr Phe  
 180 185 190  
 Ser Pro Gln Lys Cys Phe Ala Ser Asp Gly Gly Leu Trp Leu Ala Ala  
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 210 215 220  
 Arg Phe Ile Pro Glu Phe Leu Asn Leu Gln Thr Ala Val Asp Asn Ser  
 225 230 235 240  
 Leu Lys Asn Gln Thr Tyr Asn Thr Pro Ala Val Ala Thr Leu Leu Met  
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 275 280 285  
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 Tyr Arg Lys Leu Gly Arg Asn Gln Leu Arg Ile Gly Met Phe Pro Ala  
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&lt;210&gt; 153

&lt;211&gt; 1422

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;



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 Ala Val Lys Asn Val Val Gly Ser Ile Arg Glu Gly Leu Ser Asp Leu  
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 Phe Ser Leu Pro Glu Gly Tyr Glu Ile Ile Leu Ser Leu Gly Gly Ala  
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 Thr Ala Phe Trp Asp Ala Ala Thr Phe Gly Leu Ile Glu Lys Lys Ser  
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Ala	Ser	Val	Ile	Gly	Thr	Ser	His	Arg	Gln	Pro	Ala	Val	Lys	Asn	Val		
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gtg	ggg	tca	atc	cgc	gag	gga	ctc	tcc	gac	ctc	ttc	tcc	ctt	cca	gaa	307	
Val	Gly	Ser	Ile	Arg	Glu	Gly	Leu	Ser	Asp	Leu	Phe	Ser	Leu	Pro	Glu		
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Gly	Tyr	Glu	Ile	Ile	Leu	Ser	Leu	Gly	Gly	Ala	Thr	Ala	Phe	Trp	Asp		
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Ala	Ala	Thr	Phe	Gly	Leu	Ile	Glu	Lys	Lys	Ser	Gly	His	Leu	Ser	Phe		
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Gly	Glu	Phe	Ser	Ser	Lys	Phe	Ala	Lys	Ala	Ser	Lys	Leu	Ala	Pro	Trp		
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Leu	Asp	Glu	Pro	Glu	Ile	Val	Thr	Ala	Glu	Thr	Gly	Asp	Ser	Pro	Ala		
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Pro	Gln	Ala	Phe	Glu	Gly	Ala	Asp	Val	Ile	Ala	Trp	Ala	His	Asn	Glu		
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gta	gac	atc	aag	aac	tcc	gat	ggt	tac	tac	ttc	tcc	cca	cag	aag	tgc	691	
Val	Asp	Ile	Lys	Asn	Ser	Asp	Val	Tyr	Tyr	Phe	Ser	Pro	Gln	Lys	Cys		
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Phe	Ala	Ser	Asp	Gly	Gly	Leu	Trp	Leu	Ala	Ala	Met	Ser	Pro	Ala	Ala		
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ctc	gag	cgc	atc	gag	aag	atc	aac	gct	tcc	gat	cgc	ttc	atc	cct	gag	787	
Leu	Glu	Arg	Ile	Glu	Lys	Ile	Asn	Ala	Ser	Asp	Arg	Phe	Ile	Pro	Glu		
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Phe	Leu	Asn	Leu	Gln	Thr	Ala	Val	Asp	Asn	Ser	Leu	Lys	Asn	Gln	Thr		
230					235					240				245			
tac	aac	acc	cca	gct	ggt	gct	acc	ttg	ctg	atg	ctg	gac	aac	cag	gtc	883	
Tyr	Asn	Thr	Pro	Ala	Val	Ala	Thr	Leu	Leu	Met	Leu	Asp	Asn	Gln	Val		
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Lys	Trp	Met	Asn	Ser	Asn	Gly	Gly	Leu	Asp	Gly	Met	Val	Ala	Arg	Thr		

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 Ala Gln Met  
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460

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Phe Gly Ile Ser His Gly Tyr Gly Ala Phe Thr Gly Glu Ser Arg Leu  
 35 40 45

Phe Arg Met Ala Tyr His Glu Gly Ser Thr Tyr Val Pro Leu Leu Lys  
 50 55 60

Arg Ala Arg Ala Leu Trp Ser Ser Leu Ser Glu Ile Ser Gly Arg Glu  
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Leu Phe His Asn Phe Gly Val Leu Ser Thr Gly Lys Glu Asp Glu Ala  
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 Met Thr Asp Phe Pro  
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acc ctg ccc tct gag ttc atc cct ggc gac ggc cgt ttc ggc tgc gga 163  
 Thr Leu Pro Ser Glu Phe Ile Pro Gly Asp Gly Arg Phe Gly Cys Gly  
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cct tcc aag gtt cga cca gaa cag att cag gct att gtc gac gga tcc 211

Phe	Gly	Ile	Ser	His	Gly	Tyr	Gly	Ala	Phe	Thr	Gly	Glu	Ser	Arg	Leu
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Phe	Arg	Met	Ala	Tyr	His	Glu	Gly	Ser	Thr	Tyr	Val	Pro	Leu	Leu	Lys
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Arg	Ala	Arg	Ala	Leu	Trp	Ser	Ser	Leu	Ser	Glu	Ile	Ser	Gly	Arg	Glu
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Leu	Phe	His	Asn	Phe	Gly	Val	Leu	Ser	Thr	Gly	Lys	Glu	Asp	Glu	Ala
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Pro	Phe	Gln	Arg	Leu	Val	Glu	Ser	Val	Glu	Arg	Tyr	Glu	Leu	Pro	His
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&lt;211&gt; 488

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(478)

&lt;223&gt; RXN02263

&lt;400&gt; 147

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Ile	Gly	Leu	Gly	Ser	Thr	Gly	Ser	Met	Ala	Leu	Trp	His	Leu	Ser	Asn	
			10					15						20		

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Ile	Pro	Gly	Val	Glu	Ala	Ile	Gly	Phe	Glu	Gln	Phe	Gly	Ile	Ser	His	
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ggc	tac	ggc	gca	ttc	aca	ggg	gag	tcc	cga	ctg	ttt	cgc	atg	gcc	tac	259
Gly	Tyr	Gly	Ala	Phe	Thr	Gly	Glu	Ser	Arg	Leu	Phe	Arg	Met	Ala	Tyr	
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cac	gaa	ggc	agc	acc	tac	gtt	ccg	ttg	ctc	aaa	cgc	gca	cga	gca	cta	307
His	Glu	Gly	Ser	Thr	Tyr	Val	Pro	Leu	Leu	Lys	Arg	Ala	Arg	Ala	Leu	
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Trp	Ser	Ser	Leu	Ser	Glu	Ile	Ser	Gly	Arg	Glu	Leu	Phe	His	Asn	Phe	
	70				75				80					85		

ggt	gtc	tta	agc	acc	ggc	aag	gaa	gac	gaa	gca	ccc	ttc	caa	cgc	ctg	403
Gly	Val	Leu	Ser	Thr	Gly	Lys	Glu	Asp	Glu	Ala	Pro	Phe	Gln	Arg	Leu	
				90				95					100			

gtg	gaa	tca	gtg	gaa	cgt	tat	gag	ctg	cca	cat	gaa	cga	ctt	acc	gcc	451
Val	Glu	Ser	Val	Glu	Arg	Tyr	Glu	Leu	Pro	His	Glu	Arg	Leu	Thr	Ala	
			105				110						115			

gcg	cag	atg	cgc	agc	gtt	acc	cag	gtc	tagacttccg	488
Ala	Gln	Met	Arg	Ser	Val	Thr	Gln	Val		
	120					125				

&lt;210&gt; 148

&lt;211&gt; 126

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 148

Met	Lys	Ile	Ala	Val	Ile	Gly	Leu	Gly	Ser	Thr	Gly	Ser	Met	Ala	Leu
1				5					10				15		

Trp	His	Leu	Ser	Asn	Ile	Pro	Gly	Val	Glu	Ala	Ile	Gly	Phe	Glu	Gln
			20				25					30			

20	25	30	
gaa acc aca atc gtg gac cgc gtt atc gtc acc acc ggc agc tgg aca			144
Glu Thr Thr Ile Val Asp Arg Val Ile Val Thr Thr Gly Ser Trp Thr			
35	40	45	
agc gag ctc gtg ccc tcc atc gcg cca ctg ctt gaa gtg cga cgc cta			192
Ser Glu Leu Val Pro Ser Ile Ala Pro Leu Leu Glu Val Arg Arg Leu			
50	55	60	
gtg ctc acc tgg ttc ctg ccc aac aat cca gtg gac ttc caa ccg gaa			240
Val Leu Thr Trp Phe Leu Pro Asn Asn Pro Val Asp Phe Gln Pro Glu			
65	70	75	80
aac ctg cca tgc ttc atc cgt gac cgt gat ggc ttc cac gta ttt gga			288
Asn Leu Pro Cys Phe Ile Arg Asp Arg Asp Gly Phe His Val Phe Gly			
85	90	95	
gca cca tgc gtc gat ggg tac agc atc aaa att gcc gga ttg gat gag			336
Ala Pro Cys Val Asp Gly Tyr Ser Ile Lys Ile Ala Gly Leu Asp Glu			
100	105	110	
tgg ggc gtt cca tta agc ctc gat cca ccg atg tgc cct cgg			378
Trp Gly Val Pro Leu Ser Leu Asp Pro Pro Met Cys Pro Arg			
115	120	125	
tgatgtcctg atccccggttc cgg			401
<210> 146			
<211> 126			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 146			
Arg Asn Ser Gln Gly Lys Trp Cys Pro Ser Thr Arg Ser Pro Lys Asn			
1	5	10	15
Thr Ser Ile Glu Asp Asn Gly Asp His Val Val Ile Gln Ala Gly Glu			
20	25	30	
Glu Thr Thr Ile Val Asp Arg Val Ile Val Thr Thr Gly Ser Trp Thr			
35	40	45	
Ser Glu Leu Val Pro Ser Ile Ala Pro Leu Leu Glu Val Arg Arg Leu			
50	55	60	
Val Leu Thr Trp Phe Leu Pro Asn Asn Pro Val Asp Phe Gln Pro Glu			
65	70	75	80
Asn Leu Pro Cys Phe Ile Arg Asp Arg Asp Gly Phe His Val Phe Gly			
85	90	95	
Ala Pro Cys Val Asp Gly Tyr Ser Ile Lys Ile Ala Gly Leu Asp Glu			
100	105	110	
Trp Gly Val Pro Leu Ser Leu Asp Pro Pro Met Cys Pro Arg			
115	120	125	

&lt;210&gt; 147

Val Pro Tyr Ser Asp Val Val Ser Ser Thr Val His Lys Thr Leu Gly  
 225 230 235 240  
 Gly Pro Arg Ser Gly Ile Ile Leu Ala Lys Gln Glu Tyr Ala Lys Lys  
 245 250 255  
 Leu Asn Ser Ser Val Phe Pro Gly Gln Gln Gly Gly Pro Leu Met His  
 260 265 270  
 Ala Val Ala Ala Lys Ala Thr Ser Leu Lys Ile Ala Gly Thr Glu Gln  
 275 280 285  
 Phe Arg Asp Arg Gln Ala Arg Thr Leu Glu Gly Ala Arg Ile Leu Ala  
 290 295 300  
 Glu Arg Leu Thr Ala Ser Asp Ala Lys Ala Ala Gly Val Asp Val Leu  
 305 310 315 320  
 Thr Gly Gly Thr Asp Val His Leu Val Leu Ala Asp Leu Arg Asn Ser  
 325 330 335  
 Gln Met Asp Gly Gln Gln Ala Glu Asp Leu Leu His Glu Val Gly Ile  
 340 345 350  
 Thr Val Asn Arg Asn Ala Val Pro Phe Asp Pro Arg Pro Pro Met Val  
 355 360 365  
 Thr Ser Gly Leu Arg Ile Gly Thr Pro Ala Leu Ala Thr Arg Gly Phe  
 370 375 380  
 Asp Ile Pro Ala Phe Thr Glu Val Ala Asp Ile Ile Gly Thr Ala Leu  
 385 390 395 400  
 Ala Asn Gly Lys Ser Ala Asp Ile Glu Ser Leu Arg Gly Arg Val Ala  
 405 410 415  
 Lys Leu Ala Ala Asp Tyr Pro Leu Tyr Glu Gly Leu Glu Asp Trp Thr  
 420 425 430  
 Ile Val

&lt;210&gt; 145

&lt;211&gt; 401

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(378)

&lt;223&gt; RXA01821

&lt;400&gt; 145

cga aac agc caa ggc aaa tgg tgc cca agt acg cga tca cca aaa aat 48  
 Arg Asn Ser Gln Gly Lys Trp Cys Pro Ser Thr Arg Ser Pro Lys Asn  
 1 5 10 15

acc agc atc gaa gac aac ggc gat cac gta gtc atc caa gca ggc gaa 96  
 Thr Ser Ile Glu Asp Asn Gly Asp His Val Val Ile Gln Ala Gly Glu

gca gac att gag tct ctg cgt ggc cgt gta gca aag ctt gct gca gat  
1363

Ala Asp Ile Glu Ser Leu Arg Gly Arg Val Ala Lys Leu Ala Ala Asp  
410 415 420

tac cca ctg tat gag ggc ttg gaa gac tgg acc atc gtc taagtttttc  
1412

Tyr Pro Leu Tyr Glu Gly Leu Glu Asp Trp Thr Ile Val  
425 430

tttgagtttt cat  
1425

<210> 144

<211> 434

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 144

Met Thr Asp Ala His Gln Ala Asp Asp Val Arg Tyr Gln Pro Leu Asn  
1 5 10 15

Glu Leu Asp Pro Glu Val Ala Ala Ala Ile Ala Gly Glu Leu Ala Arg  
20 25 30

Gln Arg Asp Thr Leu Glu Met Ile Ala Ser Glu Asn Phe Val Pro Arg  
35 40 45

Ser Val Leu Gln Ala Gln Gly Ser Val Leu Thr Asn Lys Tyr Ala Glu  
50 55 60

Gly Tyr Pro Gly Arg Arg Tyr Tyr Gly Gly Cys Glu Gln Val Asp Ile  
65 70 75 80

Ile Glu Asp Leu Ala Arg Asp Arg Ala Lys Ala Leu Phe Gly Ala Glu  
85 90 95

Phe Ala Asn Val Gln Pro His Ser Gly Ala Gln Ala Asn Ala Ala Val  
100 105 110

Leu Met Thr Leu Ala Glu Pro Gly Asp Lys Ile Met Gly Leu Ser Leu  
115 120 125

Ala His Gly Gly His Leu Thr His Gly Met Lys Leu Asn Phe Ser Gly  
130 135 140

Lys Leu Tyr Glu Val Val Ala Tyr Gly Val Asp Pro Glu Thr Met Arg  
145 150 155 160

Val Asp Met Asp Gln Val Arg Glu Ile Ala Leu Lys Glu Gln Pro Lys  
165 170 175

Val Ile Ile Ala Gly Trp Ser Ala Tyr Pro Arg His Leu Asp Phe Glu  
180 185 190

Ala Phe Gln Ser Ile Ala Ala Glu Val Gly Ala Lys Leu Trp Val Asp  
195 200 205

Met Ala His Phe Ala Gly Leu Val Ala Ala Gly Leu His Pro Ser Pro  
210 215 220



185	190	195	
gct gcg gaa gtt ggc gcg aag ctg tgg gtc gat atg gct cac ttc gct Ala Ala Glu Val Gly Ala Lys Leu Trp Val Asp Met Ala His Phe Ala 200 205 210			739
ggt ctt gtt gct gct ggt ttg cac cca agc cca gtt cct tac tct gat Gly Leu Val Ala Ala Gly Leu His Pro Ser Pro Val Pro Tyr Ser Asp 215 220 225			787
ggt gtt tct tcc act gtc cac aag act ttg ggt gga cct cgt tcc ggc Val Val Ser Ser Thr Val His Lys Thr Leu Gly Gly Pro Arg Ser Gly 230 235 240 245			835
atc att ctg gct aag cag gag tac gcg aag aag ctg aac tct tcc gta Ile Ile Leu Ala Lys Gln Glu Tyr Ala Lys Lys Leu Asn Ser Ser Val 250 255 260			883
ttc cca ggt cag cag ggt ggt cct ttg atg cac gca gtt gct gcg aag Phe Pro Gly Gln Gln Gly Gly Pro Leu Met His Ala Val Ala Ala Lys 265 270 275			931
gct act tct ttg aag att gct ggc act gag cag ttc cgt gac cgt cag Ala Thr Ser Leu Lys Ile Ala Gly Thr Glu Gln Phe Arg Asp Arg Gln 280 285 290			979
gct cgc acg ttg gag ggt gct cgc att ctt gct gag cgt ctg act gct 1027 Ala Arg Thr Leu Glu Gly Ala Arg Ile Leu Ala Glu Arg Leu Thr Ala 295 300 305			
tct gat gcg aag gcc gct ggc gtg gat gtc ttg acc ggt ggc act gat 1075 Ser Asp Ala Lys Ala Ala Gly Val Asp Val Leu Thr Gly Gly Thr Asp 310 315 320 325			
gtg cac ttg gtt ttg gct gat ctg cgt aac tcc cag atg gat ggc cag 1123 Val His Leu Val Leu Ala Asp Leu Arg Asn Ser Gln Met Asp Gly Gln 330 335 340			
cag gcg gaa gat ctg ctg cac gag gtt ggt atc act gtg aac cgt aac 1171 Gln Ala Glu Asp Leu Leu His Glu Val Gly Ile Thr Val Asn Arg Asn 345 350 355			
gcg gtt cct ttc gat cct cgt cca cca atg gtt act tct ggt ctg cgt 1219 Ala Val Pro Phe Asp Pro Arg Pro Pro Met Val Thr Ser Gly Leu Arg 360 365 370			
att ggt act cct gcg ctg gct acc cgt ggt ttc gat att cct gca ttc 1267 Ile Gly Thr Pro Ala Leu Ala Thr Arg Gly Phe Asp Ile Pro Ala Phe 375 380 385			
act gag gtt gca gac atc att ggt act gct ttg gct aat ggt aag tcc 1315 Thr Glu Val Ala Asp Ile Ile Gly Thr Ala Leu Ala Asn Gly Lys Ser 390 395 400 405			

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1402)

&lt;223&gt; RXA00580

&lt;400&gt; 143

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ttttatatat ggggtatcggc ggtctatgct tgtgggcgta cctgtcccg c gagtgaggtc 60
ttacgcgcggg gattcgtctt gtgaaagggtt agctgacctg atg acc gat gcc cac 115
                                         Met Thr Asp Ala His
                                         1           5

caa gcg gac gat gtc cgt tac cag cca ctg aac gag ctt gat cct gag 163
Gln Ala Asp Asp Val Arg Tyr Gln Pro Leu Asn Glu Leu Asp Pro Glu
                        10           15           20

gtg gct gct gcc atc gct ggg gaa ctt gcc cgt caa cgc gat aca tta 211
Val Ala Ala Ala Ile Ala Gly Glu Leu Ala Arg Gln Arg Asp Thr Leu
                        25           30           35

gag atg atc gcg tct gag aac ttc gtt ccc cgt tct gtt ttg cag gcg 259
Glu Met Ile Ala Ser Glu Asn Phe Val Pro Arg Ser Val Leu Gln Ala
                        40           45           50

cag ggt tct gtt ctt acc aat aag tat gcc gag ggt tac cct ggc cgc 307
Gln Gly Ser Val Leu Thr Asn Lys Tyr Ala Glu Gly Tyr Pro Gly Arg
                        55           60           65

cgt tac tac ggt ggt tgc gaa caa gtt gac atc att gag gat ctt gca 355
Arg Tyr Tyr Gly Gly Cys Glu Gln Val Asp Ile Ile Glu Asp Leu Ala
                        70           75           80           85

cgt gat cgt gcg aag gct ctc ttc ggt gca gag ttc gcc aat gtt cag 403
Arg Asp Arg Ala Lys Ala Leu Phe Gly Ala Glu Phe Ala Asn Val Gln
                        90           95           100

cct cac tct ggc gca cag gct aat gct gct gtg ctg atg act ttg gct 451
Pro His Ser Gly Ala Gln Ala Asn Ala Ala Val Leu Met Thr Leu Ala
                        105           110           115

gag cca ggc gac aag atc atg ggt ctg tct ttg gct cat ggt ggt cac 499
Glu Pro Gly Asp Lys Ile Met Gly Leu Ser Leu Ala His Gly Gly His
                        120           125           130

ttg acc cac gga atg aag ttg aac ttc tcc gga aag ctg tac gag gtt 547
Leu Thr His Gly Met Lys Leu Asn Phe Ser Gly Lys Leu Tyr Glu Val
                        135           140           145

gtt gcg tac ggt gtt gat cct gag acc atg cgt gtt gat atg gat cag 595
Val Ala Tyr Gly Val Asp Pro Glu Thr Met Arg Val Asp Met Asp Gln
                        150           155           160           165

gtt cgt gag att gct ctg aag gag cag cca aag gta att atc gct ggc 643
Val Arg Glu Ile Ala Leu Lys Glu Gln Pro Lys Val Ile Ile Ala Gly
                        170           175           180

tgg tct gca tac cct cgc cac ctt gat ttc gag gct ttc cag tct att 691
Trp Ser Ala Tyr Pro Arg His Leu Asp Phe Glu Ala Phe Gln Ser Ile

```

Pro Phe Gln Lys Ser Ser Gln Leu Leu Ala Tyr Gly Arg Asp Phe Ala  
 165 170 175  
 Glu Val Met Lys Asp Asn Glu Arg Leu Ile His Gly Asp Leu Gly Thr  
 180 185 190  
 Val Asp Ala His Leu Asp Arg Val Trp Gln Ile Met Gln Glu Cys Val  
 195 200 205  
 Ala Gln Gly Ile Ala Thr Pro Gly Ile Leu Pro Gly Gly Leu Asn Val  
 210 215 220  
 Gln Arg Arg Ala Pro Gln Val His Ala Leu Ile Ser Asn Gly Asp Thr  
 225 230 235 240  
 Cys Glu Leu Gly Ala Asp Leu Asp Ala Val Glu Trp Val Asn Leu Tyr  
 245 250 255  
 Ala Leu Ala Val Asn Glu Glu Asn Ala Ala Gly Gly Arg Val Val Thr  
 260 265 270  
 Ala Pro Thr Asn Gly Ala Ala Gly Ile Ile Pro Ala Val Met His Tyr  
 275 280 285  
 Ala Arg Asp Phe Leu Thr Gly Phe Gly Ala Glu Gln Ala Arg Thr Phe  
 290 295 300  
 Leu Tyr Thr Ala Gly Ala Val Gly Ile Ile Ile Lys Glu Asn Ala Ser  
 305 310 315 320  
 Ile Ser Gly Ala Glu Val Gly Cys Gln Gly Glu Val Gly Ser Ala Ser  
 325 330 335  
 Ala Met Ala Ala Ala Gly Leu Cys Ala Val Leu Gly Gly Ser Pro Gln  
 340 345 350  
 Gln Val Glu Asn Ala Ala Glu Ile Ala Leu Glu His Asn Leu Gly Leu  
 355 360 365  
 Thr Cys Asp Pro Val Gly Gly Leu Val Gln Ile Pro Cys Ile Glu Arg  
 370 375 380  
 Asn Ala Ile Ala Ala Met Lys Ser Ile Asn Ala Ala Arg Leu Ala Arg  
 385 390 395 400  
 Ile Gly Asp Gly Asn Asn Arg Val Ser Leu Asp Asp Val Val Val Thr  
 405 410 415  
 Met Ala Ala Thr Gly Arg Asp Met Leu Thr Lys Tyr Lys Glu Thr Ser  
 420 425 430  
 Leu Gly Gly Leu Ala Thr Thr Leu Gly Phe Pro Val Ser Met Thr Glu  
 435 440 445

Cys

&lt;210&gt; 143

&lt;211&gt; 1425

375                      380                      385  
 atg aag tcc atc aat gcg gca agg ctt gcc cgg att ggt gat ggc aac  
 1315  
 Met Lys Ser Ile Asn Ala Ala Arg Leu Ala Arg Ile Gly Asp Gly Asn  
 390                      395                      400                      405  
 aat cgc gtg agt ttg gat gat gtg gtg gtc acg atg gct gcc acc ggc  
 1363  
 Asn Arg Val Ser Leu Asp Asp Val Val Val Thr Met Ala Ala Thr Gly  
 410                      415                      420  
 cgg gac atg ctg acc aaa tat aag gaa acg tcc ctt ggt ggt ttg gca  
 1411  
 Arg Asp Met Leu Thr Lys Tyr Lys Glu Thr Ser Leu Gly Gly Leu Ala  
 425                      430                      435  
 acc acc ttg ggc ttc ccg gtg tcg atg acg gag tgt tagcggtagc  
 1457  
 Thr Thr Leu Gly Phe Pro Val Ser Met Thr Glu Cys  
 440                      445  
 gctttaacac ggc  
 1470

<210> 142  
 <211> 449  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 142  
 Met Ala Ile Ser Val Val Asp Leu Phe Ser Ile Gly Ile Gly Pro Ser  
 1                      5                      10                      15  
 Ser Ser His Thr Val Gly Pro Met Arg Ala Ala Leu Thr Tyr Ile Ser  
 20                      25                      30  
 Glu Phe Pro Ser Ser His Val Asp Ile Thr Leu His Gly Ser Leu Ala  
 35                      40                      45  
 Ala Thr Gly Lys Gly His Cys Thr Asp Arg Ala Val Leu Leu Gly Leu  
 50                      55                      60  
 Val Gly Trp Glu Pro Thr Ile Val Pro Ile Asp Ala Ala Pro Ser Pro  
 65                      70                      75                      80  
 Gly Ala Pro Ile Pro Ala Lys Gly Ser Val Asn Gly Pro Lys Gly Thr  
 85                      90                      95  
 Val Ser Tyr Ser Leu Thr Phe Asp Pro His Pro Leu Pro Glu His Pro  
 100                      105                      110  
 Asn Ala Val Thr Phe Lys Gly Ser Thr Thr Arg Thr Tyr Leu Ser Val  
 115                      120                      125  
 Gly Gly Gly Phe Ile Met Thr Leu Glu Asp Phe Arg Lys Leu Asp Asp  
 130                      135                      140  
 Ile Gly Ser Gly Val Ser Thr Ile His Pro Glu Ala Glu Val Pro Cys  
 145                      150                      155                      160

```

aaa act gtc ggt atc gtc ggt ttt ggc cac att ggt cag ttg ttt gct 163
Lys Thr Val Gly Ile Val Gly Phe Gly His Ile Gly Gln Leu Phe Ala
      10                      15                      20

cag cgt ctt gct gcg ttt gag acc acc att gtt gct tac gat cct tac 211
Gln Arg Leu Ala Ala Phe Glu Thr Thr Ile Val Ala Tyr Asp Pro Tyr
      25                      30                      35

gct aac cct gct cgt gcg gct cag ctg aac gtt gag ttg gtt gag ttg 259
Ala Asn Pro Ala Arg Ala Ala Gln Leu Asn Val Glu Leu Val Glu Leu
      40                      45                      50

gat gag ctg atg agc cgt tct gac ttt gtc acc att cac ctt cct aag 307
Asp Glu Leu Met Ser Arg Ser Asp Phe Val Thr Ile His Leu Pro Lys
      55                      60                      65

acc aag gaa act gct ggc atg ttt gat gcg cac ctc ctt gct aag tcc 355
Thr Lys Glu Thr Ala Gly Met Phe Asp Ala His Leu Leu Ala Lys Ser
      70                      75                      80                      85

aag aag ggc cag atc atc atc aac gct gct cgt ggt ggc ctt gtt gat 403
Lys Lys Gly Gln Ile Ile Ile Asn Ala Ala Arg Gly Gly Leu Val Asp
      90                      95                      100

gag cag gct ttg gct gat gcg att gag tcc ggt cac att cgt ggc gct 451
Glu Gln Ala Leu Ala Asp Ala Ile Glu Ser Gly His Ile Arg Gly Ala
      105                      110                      115

ggt ttc gat gtg tac tcc acc gag cct tgc act gat tct cct ttg ttc 499
Gly Phe Asp Val Tyr Ser Thr Glu Pro Cys Thr Asp Ser Pro Leu Phe
      120                      125                      130

aag ttg cct cag gtt gtt gtg act cct cac ttg ggt gct tct act gaa 547
Lys Leu Pro Gln Val Val Val Thr Pro His Leu Gly Ala Ser Thr Glu
      135                      140                      145

gag gct caa gat cgt gcg ggt act gac att gct gat tct gtg ctc aag 595
Glu Ala Gln Asp Arg Ala Gly Thr Asp Ile Ala Asp Ser Val Leu Lys
      150                      155                      160                      165

gcg ctg gct 604
Ala Leu Ala

```

&lt;210&gt; 168

&lt;211&gt; 168

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 168

```

Val Glu Ile Phe Gly Lys Thr Val Gly Ile Val Gly Phe Gly His Ile
  1                      5                      10                      15

Gly Gln Leu Phe Ala Gln Arg Leu Ala Ala Phe Glu Thr Thr Ile Val
      20                      25                      30

Ala Tyr Asp Pro Tyr Ala Asn Pro Ala Arg Ala Ala Gln Leu Asn Val
      35                      40                      45

```

<211> 201  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 166

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Met Asp Leu Ala Arg Lys Leu Gly Leu Leu Ala Gly Lys Leu Val Asp
  1              5              10              15

Ala Ala Pro Val Ser Ile Glu Val Glu Ala Arg Gly Glu Leu Ser Ser
      20              25              30

Glu Gln Val Asn Ala Leu Gly Leu Ser Ala Val Arg Gly Leu Phe Ser
      35              40              45

Gly Ile Ile Glu Glu Ser Val Thr Phe Val Asn Ala Pro Arg Ile Ala
      50              55              60

Glu Glu Arg Gly Leu Asp Ile Ser Val Lys Thr Asn Ser Glu Ser Val
      65              70              75              80

Thr His Arg Ser Val Leu Gln Val Lys Val Ile Thr Gly Ser Gly Ala
      85              90              95

Ser Ala Thr Val Val Gly Ala Leu Thr Gly Leu Glu Arg Val Glu Lys
      100             105             110

Ile Thr Arg Ile Asn Gly Arg Gly Leu Asp Leu Arg Ala Glu Gly Leu
      115             120             125

Asn Leu Phe Leu Gln Tyr Thr Asp Ala Pro Gly Ala Leu Gly Thr Val
      130             135             140

Gly Thr Lys Leu Gly Ala Ala Gly Ile Asn Ile Glu Ala Ala Ala Leu
      145             150             155             160

Thr Gln Ala Glu Lys Gly Asp Gly Ala Val Leu Ile Leu Arg Val Glu
      165             170             175

Ser Ala Val Ser Glu Glu Leu Glu Ala Glu Ile Asn Ala Glu Leu Gly
      180             185             190

Ala Thr Ser Phe Gln Val Asp Leu Asp
      195             200
  
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<210> 167  
 <211> 604  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(604)  
 <223> RXS03112

<400> 167

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gtgagcagcg aatttctttg ctgctgtcta ctgctcgcca gatcctgctg ctgatgcgac 60

gctgcgtgag ggcgagtgga agcggctcttc tttcaacggt gtg gaa att ttc gga 115
              Val Glu Ile Phe Gly
              1              5
  
```

&lt;223&gt; RXS01130

&lt;400&gt; 165

```

agttcgtggc ggatgctgtg aacgtttccg gtggtcgcgt gggcgaagag gttctgtgtg 60
gatg gat ctg gct cgc aag ctt ggt ctt ctt gct ggc aag ctt gtc gac 109
Met Asp Leu Ala Arg Lys Leu Gly Leu Leu Ala Gly Lys Leu Val Asp
  1           5           10           15

gcc gcc cca gtc tcc att gag gtt gag gct cga ggc gag ctt tct tcc 157
Ala Ala Pro Val Ser Ile Glu Val Glu Ala Arg Gly Glu Leu Ser Ser
          20           25           30

gag cag gtc aat gca ctt ggt ttg tcc gct gtt cgt ggt ttg ttc tcc 205
Glu Gln Val Asn Ala Leu Gly Leu Ser Ala Val Arg Gly Leu Phe Ser
          35           40           45

gga att atc gaa gag tcc gtt act ttc gtc aac gct cct cgc att gct 253
Gly Ile Ile Glu Glu Ser Val Thr Phe Val Asn Ala Pro Arg Ile Ala
          50           55           60

gaa gag cgt ggc ctg gac atc tcc gtg aag acc aac tct gag tct gtt 301
Glu Glu Arg Gly Leu Asp Ile Ser Val Lys Thr Asn Ser Glu Ser Val
          65           70           75           80

act cac cgt tcc gtc ctg cag gtc aag gtc att act ggc agc ggc gcg 349
Thr His Arg Ser Val Leu Gln Val Lys Val Ile Thr Gly Ser Gly Ala
          85           90           95

agc gca act gtt gtt ggt gcc ctg act ggt ctt gag cgc gtt gag aag 397
Ser Ala Thr Val Val Gly Ala Leu Thr Gly Leu Glu Arg Val Glu Lys
          100          105          110

atc acc cgc atc aat ggc cgt ggc ctg gat ctg cgc gca gag ggt ctg 445
Ile Thr Arg Ile Asn Gly Arg Gly Leu Asp Leu Arg Ala Glu Gly Leu
          115          120          125

aac ctc ttc ctg cag tac act gac gct cct ggt gca ctg ggt acc gtt 493
Asn Leu Phe Leu Gln Tyr Thr Asp Ala Pro Gly Ala Leu Gly Thr Val
          130          135          140

ggt acc aag ctg ggt gct gct ggc atc aac atc gag gct gct gcg ttg 541
Gly Thr Lys Leu Gly Ala Ala Gly Ile Asn Ile Glu Ala Ala Ala Leu
          145          150          155          160

act cag gct gag aag ggt gac ggc gct gtc ctg atc ctg cgt gtt gag 589
Thr Gln Ala Glu Lys Gly Asp Gly Ala Val Leu Ile Leu Arg Val Glu
          165          170          175

tcc gct gtc tct gaa gag ctg gaa gct gaa atc aac gct gag ttg ggt 637
Ser Ala Val Ser Glu Glu Leu Glu Ala Glu Ile Asn Ala Glu Leu Gly
          180          185          190

gct act tcc ttc cag gtt gat ctt gac taattagaga tccatttgct 684
Ala Thr Ser Phe Gln Val Asp Leu Asp
          195          200

tga 687

```

&lt;210&gt; 166

ggc gaa ctc gca gca caa cga gcg gtc gga aac acc tcg ccg ctg tac 451  
 Gly Glu Leu Ala Ala Gln Arg Ala Val Gly Asn Thr Ser Pro Leu Tyr  
                   105                                  110                                  115  
  
 agc gaa gac ttt cgg atc gcc tcg cat gaa cca atc aaa gag cgg tgc 499  
 Ser Glu Asp Phe Arg Ile Ala Ser His Glu Pro Ile Lys Glu Arg Cys  
                   120                                  125                                  130  
  
 acg tat aga aag cta acc ttt tta agt gcg cgg ttt taggggtgaga 545  
 Thr Tyr Arg Lys Leu Thr Phe Leu Ser Ala Arg Phe  
                   135                                  140                                  145  
  
 atctaacgct gag 558

<210> 164  
 <211> 145  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 164  
 Leu Ile Leu Pro Val Gln Glu Gly Ile Ser Tyr Phe Pro Thr Pro Leu  
   1                                  5                                  10                                  15  
  
 His Leu Asn His Ile Gly Gly Ser Arg Leu Ser Ala His Val Glu Asp  
                   20                                  25                                  30  
  
 Glu Asp Leu Arg Leu Asp Arg Asp Ala Val Ser Glu Phe Gly Arg Lys  
                   35                                  40                                  45  
  
 Thr His Glu Leu Phe Pro Gly Val Asn Pro Glu Pro Asn Arg Phe Ser  
                   50                                  55                                  60  
  
 Val His Tyr Asp Thr Tyr Thr Ala Asp Lys Ser Pro Ile Ile Asp Ala  
   65                                  70                                  75                                  80  
  
 Val Asp Asn Val Ile Val Leu Thr Gly Gly Ser Gly His Ala Phe Lys  
                   85                                  90                                  95  
  
 Leu Ser Pro Ala Tyr Gly Glu Leu Ala Ala Gln Arg Ala Val Gly Asn  
                   100                                  105                                  110  
  
 Thr Ser Pro Leu Tyr Ser Glu Asp Phe Arg Ile Ala Ser His Glu Pro  
                   115                                  120                                  125  
  
 Ile Lys Glu Arg Cys Thr Tyr Arg Lys Leu Thr Phe Leu Ser Ala Arg  
                   130                                  135                                  140  
  
 Phe  
 145

<210> 165  
 <211> 687  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (62)..(664)



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Ser Lys Leu Arg Lys Glu Ala Glu Thr Arg Gly Trp Asp Val Arg Asp 305 310 315 320		
Phe Arg Ser Ile Arg Lys Ala Thr Arg Glu Tyr Gly Ile Pro Ala Leu 325 330 335		
Val Thr Ala Ala Phe Ser Val Ala Gly Trp Ser Leu Arg Arg Arg Trp 340 345 350		
Arg Lys Gln 355		
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agggtgccttt ctggcagggtg aatcaggact ctaagcaagc ttg att ctt cca gtt 115		
	Leu Ile Leu Pro Val	
	1 5	
cag gag ggc att tcc tat ttt ccc acg ccg tta cac ctg aat cac atc 163		
Gln Glu Gly Ile Ser Tyr Phe Pro Thr Pro Leu His Leu Asn His Ile		
	10 15 20	
ggt gga tcc agg tta agc gca cat gta gaa gat gaa gat ctc cgc ctc 211		
Gly Gly Ser Arg Leu Ser Ala His Val Glu Asp Glu Asp Leu Arg Leu		
	25 30 35	
gac cgg gac gca gtc tct gaa ttt ggt cgg aaa acc cac gaa ctc ttc 259		
Asp Arg Asp Ala Val Ser Glu Phe Gly Arg Lys Thr His Glu Leu Phe		
	40 45 50	
ccc ggg gtc aac cca gag ccc aac cgt ttc agc gtc cac tat gac acc 307		
Pro Gly Val Asn Pro Glu Pro Asn Arg Phe Ser Val His Tyr Asp Thr		
	55 60 65	
tac act gca gac aaa tct cca att atc gac gcg gtt gac aat gtc att 355		
Tyr Thr Ala Asp Lys Ser Pro Ile Ile Asp Ala Val Asp Asn Val Ile		
	70 75 80 85	
gtg ctc acc gga gga tcc gga cac gcc ttc aag ctc tct cca gct tat 403		
Val Leu Thr Gly Gly Ser Gly His Ala Phe Lys Leu Ser Pro Ala Tyr		
	90 95 100	

345 350 355

taacgcacag gagccgtttt aag  
1188

<210> 162  
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<212> PRT  
<213> Corynebacterium glutamicum

<400> 162  
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Thr Pro Glu Asp Phe Leu Ala Ser Trp Ser Ala Ser Arg Gly Asn Leu  
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Arg Arg Phe Phe Glu Asp His Ala Ala Ala Pro Ile Asn Asp Ala Ala  
35 40 45  
Gln Arg Gln Ala Gly Glu Ala Ala Ala Thr Gln Ala Val Ala Ala Ile  
50 55 60  
Tyr Gly Met Glu Leu Asn Glu Phe Asn Ala Gly Val Asp Ala Val Ala  
65 70 75 80  
Gly Ala Ile Glu Ser Ala Gly Ala Ile His Val Ser Ile Pro Asp Pro  
85 90 95  
Asp Val Pro Gln Asp Val Gly Ala Ala Ala Phe Phe Asp Val Asp Asn  
100 105 110  
Thr Leu Ile Gln Gly Ser Ser Leu Ile Val Phe Ala Gln Gly Leu Phe  
115 120 125  
Arg Lys Lys Phe Phe Thr Ile Lys Glu Ile Leu Pro Val Val Trp Lys  
130 135 140  
Gln Val Lys Phe Lys Leu Thr Gly Ser Glu Asn Ala Asp Asp Val Ser  
145 150 155 160  
Arg Gly Arg Glu Gln Ala Leu Glu Phe Ile Lys Gly Arg Pro Val Gln  
165 170 175  
Glu Leu Val Asp Leu Cys Glu Glu Ile Val Asp Gln Arg Met Ala Asp  
180 185 190  
Lys Met Trp Pro Gly Thr Lys Gln Leu Ala Asp Met His Ile Ala Ala  
195 200 205  
Gly His Gln Val Trp Leu Val Ser Ala Thr Pro Val Gln Leu Ala Gln  
210 215 220  
Ile Leu Ala Gln Arg Leu Gly Phe Thr Gly Ala Ile Gly Thr Val Ala  
225 230 235 240  
Glu Ala Lys Asp Gly Val Phe Thr Gly Arg Leu Val Gly Asp Ile Leu  
245 250 255  
His Gly Pro Gly Lys Arg His Ala Val Ala Ala Leu Ala Ser Ile Glu

Ser	Ser	Leu	Ile	Val	Phe	Ala	Gln	Gly	Leu	Phe	Arg	Lys	Lys	Phe	Phe		
		120					125					130					
acc	atc	aaa	gaa	atc	ctc	ccc	gtg	gtg	tgg	aaa	caa	gtg	aaa	ttc	aaa	547	
Thr	Ile	Lys	Glu	Ile	Leu	Pro	Val	Val	Trp	Lys	Gln	Val	Lys	Phe	Lys		
		135				140					145						
ctc	acc	ggc	tcc	gaa	aac	gcc	gac	gac	gtc	tcc	cgc	ggc	cgc	gaa	caa	595	
Leu	Thr	Gly	Ser	Glu	Asn	Ala	Asp	Asp	Val	Ser	Arg	Gly	Arg	Glu	Gln		
		150			155					160					165		
gcc	ctc	gaa	ttc	atc	aaa	ggc	cgc	ccc	gtc	caa	gaa	cta	gtt	gac	ctc	643	
Ala	Leu	Glu	Phe	Ile	Lys	Gly	Arg	Pro	Val	Gln	Glu	Leu	Val	Asp	Leu		
				170					175					180			
tgc	gaa	gaa	atc	gtc	gac	caa	cgc	atg	gcc	gac	aaa	atg	tgg	ccc	ggc	691	
Cys	Glu	Glu	Ile	Val	Asp	Gln	Arg	Met	Ala	Asp	Lys	Met	Trp	Pro	Gly		
			185					190					195				
acc	aaa	caa	ctc	gcc	gac	atg	cac	atc	gcc	gcc	ggc	cac	caa	gtc	tgg	739	
Thr	Lys	Gln	Leu	Ala	Asp	Met	His	Ile	Ala	Ala	Gly	His	Gln	Val	Trp		
		200					205					210					
ctc	gtc	tcc	gca	acc	ccc	gtc	caa	ctc	gcc	caa	atc	ctg	gca	caa	cgc	787	
Leu	Val	Ser	Ala	Thr	Pro	Val	Gln	Leu	Ala	Gln	Ile	Leu	Ala	Gln	Arg		
		215				220					225						
ctc	ggc	ttc	acc	gga	gcg	atc	ggc	aca	gtc	gca	gaa	gca	aaa	gat	gga	835	
Leu	Gly	Phe	Thr	Gly	Ala	Ile	Gly	Thr	Val	Ala	Glu	Ala	Lys	Asp	Gly		
					235				240						245		
gta	ttc	acc	ggc	cga	ctc	gtc	ggc	gac	atc	ctc	cac	gga	ccc	ggc	aaa	883	
Val	Phe	Thr	Gly	Arg	Leu	Val	Gly	Asp	Ile	Leu	His	Gly	Pro	Gly	Lys		
				250				255						260			
aga	cac	gca	gtc	gca	gca	ctc	gca	tcc	atc	gaa	caa	ctc	gac	ctc	acc	931	
Arg	His	Ala	Val	Ala	Ala	Leu	Ala	Ser	Ile	Glu	Gln	Leu	Asp	Leu	Thr		
			265					270					275				
cga	tgc	acc	ggc	tac	tcc	gac	tcc	atc	aac	gac	ctc	ccc	atg	ctc	tcc	979	
Arg	Cys	Thr	Ala	Tyr	Ser	Asp	Ser	Ile	Asn	Asp	Leu	Pro	Met	Leu	Ser		
		280				285						290					
atg	gtc	ggc	acc	gcc	gtc	gca	gta	aac	ccc	gac	tcc	aaa	ctc	cgc	aaa		
Met	Val	Gly	Thr	Ala	Val	Ala	Val	Asn	Pro	Asp	Ser	Lys	Leu	Arg	Lys		
						300					305						
gaa	gcc	gaa	acc	cga	ggc	tgg	gac	gtc	cgc	gat	ttc	cga	agc	atc	cgc		
1075																	
Glu	Ala	Glu	Thr	Arg	Gly	Trp	Asp	Val	Arg	Asp	Phe	Arg	Ser	Ile	Arg		
					315				320						325		
310																	
aaa	gcc	acc	cgc	gaa	tac	gga	atc	ccc	gcc	ctg	gtc	acc	gcc	gca	ttc		
1123																	
Lys	Ala	Thr	Arg	Glu	Tyr	Gly	Ile	Pro	Ala	Leu	Val	Thr	Ala	Ala	Phe		
				330					335					340			
agt	gtc	gcc	ggc	tgg	agt	cta	cgc	cgc	cga	tgg	aga	aaa	caa				
1165																	
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 <213> Corynebacterium glutamicum

<400> 160

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 Leu Ala Ala His Ala Gly Lys Glu Ala Lys Val Ala Ala Val Thr Glu  
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 Arg Ala Met Arg Gly  
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<210> 161  
 <211> 1188  
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<220>  
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 <222> (101)..(1165)  
 <223> RXA02501

<400> 161

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 Met Ser Ser Glu Gly  
 1 5  
 aga aac cac aac tgg gac tac gcc gcc atc ggc acc cca gag gat ttc 163  
 Arg Asn His Asn Trp Asp Tyr Ala Ala Ile Gly Thr Pro Glu Asp Phe  
 10 15 20  
 ctc gcc agc tgg agc gca tcc cgc gga aat cta cga cgc ttt ttc gaa 211  
 Leu Ala Ser Trp Ser Ala Ser Arg Gly Asn Leu Arg Arg Phe Phe Glu  
 25 30 35  
 gac cac gca gcc gcc ccc ata aac gat gcc gcc cag cgc caa gca ggt 259  
 Asp His Ala Ala Pro Ile Asn Asp Ala Ala Gln Arg Gln Ala Gly  
 40 45 50  
 gaa gcc gca gca acc caa gcc gtc gca gcg atc tac ggc atg gag ctc 307  
 Glu Ala Ala Ala Thr Gln Ala Val Ala Ala Ile Tyr Gly Met Glu Leu  
 55 60 65  
 aac gaa ttc aac gca ggt gtc gac gcc gtc gcc ggc gcc atc gaa tct 355  
 Asn Glu Phe Asn Ala Gly Val Asp Ala Val Ala Gly Ala Ile Glu Ser  
 70 75 80 85  
 gcc ggc gcc atc cac gtc agc atc ccc gat ccc gat gtc ccc caa gat 403  
 Ala Gly Ala Ile His Val Ser Ile Pro Asp Pro Asp Val Pro Gln Asp  
 90 95 100  
 gtc gga gcc gca gca ttt ttc gac gtc gac aac acc ctc atc caa ggc 451  
 Val Gly Ala Ala Ala Phe Phe Asp Val Asp Asn Thr Leu Ile Gln Gly  
 105 110 115  
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<213> Corynebacterium glutamicum

<400> 158

Met Gly Tyr Gln Thr Ala Val Val Ser Gly Gly Phe Ile Gln Val Leu  
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Glu Gly Leu Ala Glu Glu Leu Glu Leu Asp Tyr Val Arg Ala Asn Thr  
20 25 30

Leu Glu Ile Val Asp Gly Lys Leu Thr Gly Asn Val Thr Gly Lys Ile  
35 40 45

Val Asp Arg Ala Ala Lys Ala Glu Phe Leu Arg Glu Phe Ala Ala Asp  
50 55 60

Ser Gly Leu Lys Met Tyr Gln Thr Val Ala Val Gly Asp Gly Ala Asn  
65 70 75 80

Asp Ile Asp Met Leu Ser Ala Ala Gly Leu Gly Val Ala Phe Asn Ala  
85 90 95

Lys Pro Ala Leu Lys Glu Ile Ala Asp Thr Ser Val Asn His Pro Phe  
100 105 110

Leu Asp Glu Val Leu His Ile Met Gly Ile Ser Arg Asp Glu Ile Asp  
115 120 125

Leu Ala Asp Gln Glu Asp Gly Thr Phe His Arg Val Pro Leu Thr Asn  
130 135 140

Ala

145

<210> 159

<211> 205

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (72) .. (182)

<223> FRXA02759

<400> 159

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aagcgtctgg tgtg ctt cga ttg tat ccc acg ttg atc act ggt gag gtc 110  
Val Leu Arg Leu Tyr Pro Thr Leu Ile Thr Gly Glu Val  
1 5 10

att gag atg ctg gcg gct cac gcg ggc aag gaa gct aaa gtt gcg gca 158  
Ile Glu Met Leu Ala Ala His Ala Gly Lys Glu Ala Lys Val Ala Ala  
15 20 25

gtt act gag cgt gcg atg cgc ggg tgagctcgat ttcgaggagt ctc 205  
Val Thr Glu Arg Ala Met Arg Gly  
30 35

<210> 160

<210> 157  
 <211> 558  
 <212> DNA  
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<220>  
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 <223> FRXA02758

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acccttggtg cgcgcaccac gatccgtacg gttgaaccgc atg ggt tac cag acc 115
                                         Met Gly Tyr Gln Thr
                                         1           5

gct gtt gtt tcc ggt ggt ttc atc cag gtg ttg gaa ggt ttg gct gag 163
Ala Val Val Ser Gly Gly Phe Ile Gln Val Leu Glu Gly Leu Ala Glu
          10          15          20

gag ttg gag ttg gat tat gtc cgc gcc aac act ttg gaa atc gtt gat 211
Glu Leu Glu Leu Asp Tyr Val Arg Ala Asn Thr Leu Glu Ile Val Asp
          25          30          35

ggc aag ctg acc ggc aac gtc acc gga aag atc gtt gac cgc gct gcg 259
Gly Lys Leu Thr Gly Asn Val Thr Gly Lys Ile Val Asp Arg Ala Ala
          40          45          50

aag gct gag ttc ctc cgt gag ttc gct gcg gat tct ggc ctg aag atg 307
Lys Ala Glu Phe Leu Arg Glu Phe Ala Ala Asp Ser Gly Leu Lys Met
          55          60          65

tac cag act gtc gct gtc ggt gat ggc gct aat gac atc gat atg ctc 355
Tyr Gln Thr Val Ala Val Gly Asp Gly Ala Asn Asp Ile Asp Met Leu
          70          75          80          85

tcc gct gcg ggt ctg ggt gtt gct ttc aac gcg aag cct gcg ctg aag 403
Ser Ala Ala Gly Leu Gly Val Ala Phe Asn Ala Lys Pro Ala Leu Lys
          90          95          100

gag att gcg gat act tcc gtg aac cac cca ttc ctc gac gag gtt ttg 451
Glu Ile Ala Asp Thr Ser Val Asn His Pro Phe Leu Asp Glu Val Leu
          105          110          115

cac atc atg ggc att tcc cgc gac gag atc gat ctg gcg gat cag gaa 499
His Ile Met Gly Ile Ser Arg Asp Glu Ile Asp Leu Ala Asp Gln Glu
          120          125          130

gac ggc act ttc cac cgc gtt cca ttg acc aat gcc taaagattcg 545
Asp Gly Thr Phe His Arg Val Pro Leu Thr Asn Ala
          135          140          145

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<210> 158  
 <211> 145  
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Gly Ala Ala Ala Val Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln  
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 Ile Gly Ile Gln Ser Ala Gln Ile Lys Ala Ile Glu Asn Asp His His  
 180 185 190  
 Trp His Glu Gly Asn Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly  
 195 200 205  
 Leu Gly Ala Ala Arg Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu  
 210 215 220  
 Glu Ile Asp Glu Arg Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro  
 225 230 235 240  
 Leu Gly Pro Tyr Arg Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr  
 245 250 255  
 Leu Asp Tyr Gln Ala Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser  
 260 265 270  
 Tyr Val Leu Leu Thr Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp  
 275 280 285  
 Arg Gly Gly Leu Asn Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu  
 290 295 300  
 Val Ala Gly Val Asp Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu  
 305 310 315 320  
 His Leu Ser Arg Asn Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val  
 325 330 335  
 Ser Pro Val Gly His Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp  
 340 345 350  
 Arg Ile Val Arg Asn Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn  
 355 360 365  
 Pro Ser Thr Tyr Ile Glu Phe Tyr Ile  
 370 375

<210> 179  
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 <212> DNA  
 <213> Corynebacterium glutamicum

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 <223> FRXA00403

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 Met Pro Thr Leu Ala  
 1 5

acc gat att ttg tac ccc tac cac cag caa gaa cac ctc tcc aga aac  
1075

Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu His Leu Ser Arg Asn  
310 315 320 325

ctg gga aat cta ctg gca atg gca aaa atc gta tcc cct gtc ggc cac  
1123

Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val Ser Pro Val Gly His  
330 335 340

gat gct ttc ctc acc gaa agc cgc caa atg gat cgc atc gtg agg aac  
1171

Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp Arg Ile Val Arg Asn  
345 350 355

ttc ttc agc ctc atc tcc cca gac gaa gac aac cct tcg acc tac atc  
1219

Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn Pro Ser Thr Tyr Ile  
360 365 370

gag ttc tac atc taataggtat ttacgacaaa tag  
1254

Glu Phe Tyr Ile  
375

<210> 178

<211> 377

<212> PRT

<213> Corynebacterium glutamicum

<400> 178

Met Pro Thr Leu Ala Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly  
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Asp Val Ser Thr Glu Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala  
20 25 30

Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn  
35 40 45

Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp  
50 55 60

Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile  
65 70 75 80

Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr  
85 90 95

Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe  
100 105 110

Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu  
115 120 125

Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met  
130 135 140

Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val  
145 150 155 160



Leu	Gly	Pro	Gly	Lys	Ala	Ile	Asn	Thr	Asp	Ile	Tyr	Cys	Val	Ile	Cys		
70					75					80					85		
acc aac gtc atc ggt ggt tgc aac ggt tcc acc gga cct ggc tcc atg																403	
Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr Gly Pro Gly Ser Met				90					95						100		
cat cca gat gga aat ttc tgg ggt aat cgc ttc ccc gcc acg tcc att																451	
His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe Pro Ala Thr Ser Ile			105					110						115			
cgt gat cag gta aac gcc gaa aaa caa ttc ctc gac gca ctc ggc atc																499	
Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu Asp Ala Leu Gly Ile			120				125						130				
acc acg gtc gcc gca gta ctt ggt ggt tcc atg ggt ggt gcc cgc acc																547	
Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met Gly Gly Ala Arg Thr			135				140						145				
cta gag tgg gcc gca atg tac cca gaa act gtt ggc gca gct gct gtt																595	
Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val Gly Ala Ala Ala Val						155				160						165	
ctt gca gtt tct gca cgc gcc agc gcc tgg caa atc ggc att caa tcc																643	
Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln Ile Gly Ile Gln Ser				170					175						180		
gcc caa att aag gcg att gaa aac gac cac cac tgg cac gaa ggc aac																691	
Ala Gln Ile Lys Ala Ile Glu Asn Asp His His Trp His Glu Gly Asn				185				190						195			
tac tac gaa tcc ggc tgc aac cca gcc acc gga ctc ggc gcc gcc cga																739	
Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly Leu Gly Ala Ala Arg			200				205						210				
cgc atc gcc cac ctc acc tac cgt ggc gaa cta gaa atc gac gaa cgc																787	
Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu Glu Ile Asp Glu Arg						220							225				
ttc ggc acc aaa gcc caa aag aac gaa aac cca ctc ggt ccc tac cgc																835	
Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro Leu Gly Pro Tyr Arg						235				240					245		
aag ccc gac cag cgc ttc gcc gtg gaa tcc tac ttg gac tac caa gca																883	
Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr Leu Asp Tyr Gln Ala				250				255							260		
gac aag cta gta cag cgt ttc gac gcc ggc tcc tac gtc ttg ctc acc																931	
Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser Tyr Val Leu Leu Thr				265				270						275			
gac gcc ctc aac cgc cac gac att ggt cgc gac cgc gga ggc ctc aac																979	
Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp Arg Gly Gly Leu Asn				280				285					290				
aag gca ctc gaa tcc atc aaa gtt cca gtc ctt gtc gca ggc gta gat																1027	
Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu Val Ala Gly Val Asp																295	
						300							305				



Pro Ala Thr Tyr Pro Gln Leu Asp Asp Ala Gln Leu Ser Lys Trp Arg  
 35 40 45  
 Glu Val Leu Ala Asn Glu Gly Tyr Ala Ala Leu Ala Ala Glu Val Ile  
 50 55 60  
 Ser Leu Phe Val Asp Asp Ile Pro Val Glu Asp Ile Lys Ala Ile Thr  
 65 70 75 80  
 Ala Arg Ala Tyr Thr Tyr Pro Lys Phe Asn Ser Glu Asp Ile Val Pro  
 85 90 95  
 Val Thr Glu Leu Glu Asp Asn Ile Tyr Leu Gly His Leu Ser Glu Gly  
 100 105 110  
 Pro Thr Ala Ala Phe Lys Asp Met Ala Met Gln Leu Leu Gly Glu Leu  
 115 120 125  
 Phe Glu Tyr Glu Leu Arg Arg Arg Asn Glu Thr Ile Asn Ile Leu Gly  
 130 135 140  
 Ala Thr Ser Gly Asp Thr Gly Ser Ser Ala Glu Tyr Ala Met Arg Gly  
 145 150 155 160  
 Arg Glu Gly Ile Arg Val Phe Met Leu Thr Pro Ala Gly Arg Met Thr  
 165 170 175  
 Pro Phe Gln Gln Ala Gln Met Phe Gly Leu Asp Asp Pro Asn Ile Phe  
 180 185 190  
 Asn Ile Ala Leu Asp Gly Val Phe Asp Asp Cys Gln Asp Val Val Lys  
 195 200 205  
 Ala Val Ser Ala Asp Ala Glu Phe Lys Lys Asp Asn Arg Ile Gly Ala  
 210 215 220  
 Val Asn Ser Ile Asn Trp Ala Arg Leu Met Ala Gln Val Val Tyr Tyr  
 225 230 235 240  
 Val Ser Ser Trp Ile Arg Thr Thr Thr Ser Asn Asp Gln Lys Val Ser  
 245 250 255  
 Phe Ser Val Pro Thr Gly Asn Phe Gly Asp Ile Cys Ala Gly His Ile  
 260 265 270  
 Ala Arg Gln Met Gly Leu Pro Ile Asp Arg Leu Ile Val Ala Thr Asn  
 275 280 285  
 Glu Asn Asp Val Leu Asp Glu Phe Phe Arg Thr Gly Asp Tyr Arg Val  
 290 295 300  
 Arg Ser Ser Ala Asp Thr His Glu Thr Ser Ser Pro Ser Met Asp Ile  
 305 310 315 320  
 Ser Arg Ala Ser Asn Phe Glu Arg Phe Ile Phe Asp Leu Leu Gly Arg  
 325 330 335  
 Asp Ala Thr Arg Val Asn Asp Leu Phe Gly Thr Gln Val Arg Gln Gly  
 340 345 350  
 Gly Phe Ser Leu Ala Asp Asp Ala Asn Phe Glu Lys Ala Ala Ala Glu

aac gat cta ttt ggt acc cag gtt cgc caa ggc gga ttc tca ctg gct  
1171

Asn Asp Leu Phe Gly Thr Gln Val Arg Gln Gly Gly Phe Ser Leu Ala  
345 350 355

gat gac gcc aac ttt gag aag gct gca gca gaa tac ggt ttc gcc tcc  
1219

Asp Asp Ala Asn Phe Glu Lys Ala Ala Ala Glu Tyr Gly Phe Ala Ser  
360 365 370

gga cga tcc acc cat gct gac cgt gtg gca acc atc gct gac gtg cat  
1267

Gly Arg Ser Thr His Ala Asp Arg Val Ala Thr Ile Ala Asp Val His  
375 380 385

tcc cgc ctc gac gta cta atc gat ccc cac acc gcc gac ggc gtt cac  
1315

Ser Arg Leu Asp Val Leu Ile Asp Pro His Thr Ala Asp Gly Val His  
390 395 400 405

gtg gca cgc cag tgg agg gac gag gtc aac acc cca atc atc gtc cta  
1363

Val Ala Arg Gln Trp Arg Asp Glu Val Asn Thr Pro Ile Ile Val Leu  
410 415 420

gaa act gca ctc cca gtg aaa ttt gcc gac acc atc gtc gaa gca att  
1411

Glu Thr Ala Leu Pro Val Lys Phe Ala Asp Thr Ile Val Glu Ala Ile  
425 430 435

ggt gaa gca cct caa act cca gag cgt ttc gcc gcg atc atg gat gct  
1459

Gly Glu Ala Pro Gln Thr Pro Glu Arg Phe Ala Ala Ile Met Asp Ala  
440 445 450

cca ttc aag gtt tcc gac cta cca aac gac acc gat gca gtt aag cag  
1507

Pro Phe Lys Val Ser Asp Leu Pro Asn Asp Thr Asp Ala Val Lys Gln  
455 460 465

tac ata gtc gat gcg att gca aac act tcc gtg aag taacttgctt  
1553

Tyr Ile Val Asp Ala Ile Ala Asn Thr Ser Val Lys  
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<210> 176

<211> 481

<212> PRT

<213> Corynebacterium glutamicum

<400> 176

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 Lys Asp Met Ala Met Gln Leu Leu Gly Glu Leu Phe Glu Tyr Glu Leu  
 120 125 130

cgc cgc cgc aac gaa acc atc aac atc ctg ggc gct acc tct ggc gat 547  
 Arg Arg Arg Asn Glu Thr Ile Asn Ile Leu Gly Ala Thr Ser Gly Asp  
 135 140 145

acc ggc tcc tct gcg gaa tac gcc atg cgc ggc cgc gag gga atc cgc 595  
 Thr Gly Ser Ser Ala Glu Tyr Ala Met Arg Gly Arg Glu Gly Ile Arg  
 150 155 160 165

gta ttc atg ctg acc cca gct ggc cgc atg acc cca ttc cag caa gca 643  
 Val Phe Met Leu Thr Pro Ala Gly Arg Met Thr Pro Phe Gln Gln Ala  
 170 175 180

cag atg ttt ggc ctt gac gat cca aac atc ttc aac atc gcc ctc gac 691  
 Gln Met Phe Gly Leu Asp Asp Pro Asn Ile Phe Asn Ile Ala Leu Asp  
 185 190 195

ggc gtt ttc gac gat tgc caa gac gta gtc aag gct gtc tcc gcc gac 739  
 Gly Val Phe Asp Asp Cys Gln Asp Val Val Lys Ala Val Ser Ala Asp  
 200 205 210

gca gaa ttc aaa aaa gac aac cgc atc ggt gcc gtg aac tcc atc aac 787  
 Ala Glu Phe Lys Lys Asp Asn Arg Ile Gly Ala Val Asn Ser Ile Asn  
 215 220 225

tgg gca cgc ctt atg gca cag gtt gtg tac tac gtt tcc tca tgg atc 835  
 Trp Ala Arg Leu Met Ala Gln Val Val Tyr Tyr Val Ser Ser Trp Ile  
 230 235 240 245

cgc acc aca acc agc aat gac caa aag gtc agc ttc tcc gta cca acc 883  
 Arg Thr Thr Thr Ser Asn Asp Gln Lys Val Ser Phe Ser Val Pro Thr  
 250 255 260

ggc aac ttc ggt gac att tgc gca ggc cac atc gcc cgc caa atg gga 931  
 Gly Asn Phe Gly Asp Ile Cys Ala Gly His Ile Ala Arg Gln Met Gly  
 265 270 275

ctt ccc atc gat cgc ctc atc gtg gcc acc aac gaa aac gat gtg ctc 979  
 Leu Pro Ile Asp Arg Leu Ile Val Ala Thr Asn Glu Asn Asp Val Leu  
 280 285 290

gac gag ttc ttc cgt acc ggc gac tac cga gtc cgc agc tcc gca gac  
 1027  
 Asp Glu Phe Phe Arg Thr Gly Asp Tyr Arg Val Arg Ser Ser Ala Asp  
 295 300 305

acc cac gag acc tcc tca cct tcg atg gat atc tcc cgc gcc tcc aac  
 1075  
 Thr His Glu Thr Ser Ser Pro Ser Met Asp Ile Ser Arg Ala Ser Asn  
 310 315 320 325

ttc gag cgt ttc atc ttc gac ctg ctc ggc cgc gac gcc acc cgc gtc  
 1123  
 Phe Glu Arg Phe Ile Phe Asp Leu Leu Gly Arg Asp Ala Thr Arg Val  
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<213> Corynebacterium glutamicum
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<223> RXA00330
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Val Asp Tyr Ile Ser																	5
1																	
acg cgt gat gcc agc cgt acc cct gcc cgc ttc agt gat att ttg ctg																	163
Thr Arg Asp Ala Ser Arg Thr Pro Ala Arg Phe Ser Asp Ile Leu Leu																	20
10 15																	
ggc ggt cta gca cca gac ggc gga ctg tac ctg cct gca acc tac cct																	211
Gly Gly Leu Ala Pro Asp Gly Gly Leu Tyr Leu Pro Ala Thr Tyr Pro																	35
25 30																	
caa cta gat gat gcc cag ctg agt aaa tgg cgt gag gta tta gcc aac																	259
Gln Leu Asp Asp Ala Gln Leu Ser Lys Trp Arg Glu Val Leu Ala Asn																	50
40 45																	
gaa gga tac gca gct ttg gct gct gaa gtt atc tcc ctg ttt gtt gat																	307
Glu Gly Tyr Ala Ala Leu Ala Ala Glu Val Ile Ser Leu Phe Val Asp																	60
55 65																	
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Asp Ile Pro Val Glu Asp Ile Lys Ala Ile Thr Ala Arg Ala Tyr Thr																	85
70 75 80																	
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Tyr Pro Lys Phe Asn Ser Glu Asp Ile Val Pro Val Thr Glu Leu Glu																	100
90 95 100																	
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Asp Asn Ile Tyr Leu Gly His Leu Ser Glu Gly Pro Thr Ala Ala Phe																	115
105 110																	

280 285 290  
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 <213> Corynebacterium glutamicum  
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 35 40 45  
 Glu Val Glu Val Phe Gly Glu Gly Gln Gly Glu Val Pro Leu Asp Gly  
 50 55 60  
 Ser His Leu Val Val Lys Ala Ile Arg Ala Gly Leu Lys Ala Ala Asp  
 65 70 75 80  
 Ala Glu Val Pro Gly Leu Arg Val Val Cys His Asn Asn Ile Pro Gln  
 85 90 95  
 Ser Arg Gly Leu Gly Ser Ser Ala Ala Ala Val Ala Gly Val Ala  
 100 105 110  
 Ala Ala Asn Gly Leu Ala Asp Phe Pro Leu Thr Gln Glu Gln Ile Val  
 115 120 125  
 Gln Leu Ser Ser Ala Phe Glu Gly His Pro Asp Asn Ala Ala Ala Ser  
 130 135 140  
 Val Leu Gly Gly Ala Val Val Ser Trp Thr Asn Leu Ser Ile Asp Gly  
 145 150 155 160  
 Lys Ser Gln Pro Gln Tyr Ala Ala Val Pro Leu Glu Val Gln Asp Asn  
 165 170 175  
 Ile Arg Ala Thr Ala Leu Val Pro Asn Phe His Ala Ser Thr Glu Ala  
 180 185 190  
 Val Arg Arg Val Leu Pro Thr Glu Val Thr His Ile Asp Ala Arg Phe  
 195 200 205  
 Asn Val Ser Arg Val Ala Val Met Ile Val Ala Leu Gln Gln Arg Pro  
 210 215 220  
 Asp Leu Leu Trp Glu Gly Thr Arg Asp Arg Leu His Gln Pro Tyr Arg  
 225 230 235 240

Thr	Val	Glu	Val	Glu	Ile	Ile	Pro	Ser	Gly	Leu	Glu	Val	Glu	Val	Phe		
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ggc	gaa	ggc	caa	ggc	gaa	gtc	cct	ctt	gat	ggc	tcc	cac	ctg	gtg	gtt	307	
Gly	Glu	Gly	Gln	Gly	Glu	Val	Pro	Leu	Asp	Gly	Ser	His	Leu	Val	Val		
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aaa	gct	att	cgt	gct	ggc	ctg	aag	gca	gct	gac	gct	gaa	gtt	cct	gga	355	
Lys	Ala	Ile	Arg	Ala	Gly	Leu	Lys	Ala	Ala	Asp	Ala	Glu	Val	Pro	Gly		
	70				75					80					85		
ttg	cga	gtg	gtg	tgc	cac	aac	aac	att	ccg	cag	tct	cgt	ggg	ctt	ggc	403	
Leu	Arg	Val	Val	Cys	His	Asn	Asn	Ile	Pro	Gln	Ser	Arg	Gly	Leu	Gly		
				90					95					100			
tcc	tct	gct	gca	gcg	gcg	gtt	gct	ggg	gtt	gct	gca	gct	aat	ggg	ttg	451	
Ser	Ser	Ala	Ala	Ala	Ala	Val	Ala	Gly	Val	Ala	Ala	Ala	Asn	Gly	Leu		
			105					110						115			
gcg	gat	ttc	ccg	ctg	act	caa	gag	cag	att	gtt	cag	ttg	tcc	tct	gcc	499	
Ala	Asp	Phe	Pro	Leu	Thr	Gln	Glu	Gln	Ile	Val	Gln	Leu	Ser	Ser	Ala		
		120					125					130					
ttt	gaa	ggc	cac	cca	gat	aat	gct	gcg	gct	tct	gtg	ctg	ggg	gga	gca	547	
Phe	Glu	Gly	His	Pro	Asp	Asn	Ala	Ala	Ala	Ser	Val	Leu	Gly	Gly	Ala		
	135					140					145						
gtg	gtg	tcg	tgg	aca	aat	ctg	tct	atc	gac	ggc	aag	agc	cag	cca	cag	595	
Val	Val	Ser	Trp	Thr	Asn	Leu	Ser	Ile	Asp	Gly	Lys	Ser	Gln	Pro	Gln		
	150				155					160					165		
tat	gct	gct	gta	cca	ctt	gag	gtg	cag	gac	aat	att	cgt	gcg	act	gcg	643	
Tyr	Ala	Ala	Val	Pro	Leu	Glu	Val	Gln	Asp	Asn	Ile	Arg	Ala	Thr	Ala		
				170					175						180		
ctg	gtt	cct	aat	ttc	cac	gca	tcc	acc	gaa	gct	gtg	cgc	cga	gtc	ctt	691	
Leu	Val	Pro	Asn	Phe	His	Ala	Ser	Thr	Glu	Ala	Val	Arg	Arg	Val	Leu		
			185					190						195			
ccc	act	gaa	gtc	act	cac	atc	gat	gcg	cga	ttt	aac	gtg	tcc	cgc	gtt	739	
Pro	Thr	Glu	Val	Thr	His	Ile	Asp	Ala	Arg	Phe	Asn	Val	Ser	Arg	Val		
		200					205					210					
gca	gtg	atg	atc	gtt	gcg	ttg	cag	cag	cgt	cct	gat	ttg	ctg	tgg	gag	787	
Ala	Val	Met	Ile	Val	Ala	Leu	Gln	Gln	Arg	Pro	Asp	Leu	Leu	Trp	Glu		
	215					220					225						
ggg	act	cgt	gac	cgt	ctg	cac	cag	cct	tat	cgt	gca	gaa	gtg	ttg	cct	835	
Gly	Thr	Arg	Asp	Arg	Leu	His	Gln	Pro	Tyr	Arg	Ala	Glu	Val	Leu	Pro		
	230				235					240					245		
att	acc	tct	gag	tgg	gta	aac	cgc	ctg	cgc	aac	cgt	ggc	tac	gcg	gca	883	
Ile	Thr	Ser	Glu	Trp	Val	Asn	Arg	Leu	Arg	Asn	Arg	Gly	Tyr	Ala	Ala		
				250					255					260			
tac	ctt	tcc	ggg	gcc	ggc	cca	acc	gcc	atg	gtg	ctg	tcc	act	gag	cca	931	
Tyr	Leu	Ser	Gly	Ala	Gly	Pro	Thr	Ala	Met	Val	Leu	Ser	Thr	Glu	Pro		
			265					270						275			
att	cca	gac	aag	gtt	ttg	gaa	gat	gct	cgt	gag	tct	ggc	att	aag	gtg	979	
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 <212> PRT  
 <213> Corynebacterium glutamicum

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 35 40 45  
 Gly Gly Pro Leu Glu Val Arg Gly Ile Ala Val Ser Asp Ile Ser Lys  
 50 55 60  
 Pro Arg Glu Gly Val Ala Pro Glu Leu Leu Thr Glu Asp Ala Phe Ala  
 65 70 75 80  
 Leu Ile Glu Arg Glu Asp Val Asp Ile Val Val Glu Val Ile Gly Gly  
 85 90 95  
 Ile Glu Tyr Pro Arg Glu Val Val Leu Ala Ala Leu Lys Ala Gly Lys  
 100 105 110  
 Ser Val Val Thr Ala Asn Lys Ala Leu Val Ala Ala His Ser Ala Glu  
 115 120 125  
 Leu Ala Asp  
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<210> 173  
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 <213> Corynebacterium glutamicum

<220>  
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 <223> RXA00970

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 Met Ala Ile Glu Leu  
 1 5  
 aac gtc ggt cgt aag gtt acc gtc acg gta cct gga tct tct gca aac 163  
 Asn Val Gly Arg Lys Val Thr Val Thr Val Pro Gly Ser Ser Ala Asn  
 10 15 20  
 ctc gga cct ggc ttt gac act tta ggt ttg gca ctg tcg gta tac gac 211  
 Leu Gly Pro Gly Phe Asp Thr Leu Gly Leu Ala Leu Ser Val Tyr Asp  
 25 30 35  
 act gtc gaa gtg gaa att att cca tct ggc ttg gaa gtg gaa gtt ttt 259

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385          390          395          400
Glu Arg Asp Asp Asp Ala Arg Leu Ile Val Val Thr His Ser Ala Leu
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Glu Ser Asp Leu Ser Arg Thr Val Glu Leu Leu Lys Ala Lys Pro Val
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Val Lys Ala Ile Asn Ser Val Ile Arg Leu Glu Arg Asp
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<210> 171
<211> 493
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(493)
<223> FRXA00974

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          Met Thr Ser Ala Ser
          1          5

gcc cca agc ttt aac ccc ggc aag ggt ccc ggc tca gca gtc gga att 163
Ala Pro Ser Phe Asn Pro Gly Lys Gly Pro Gly Ser Ala Val Gly Ile
          10          15          20

gcc ctt tta gga ttc gga aca gtc ggc act gag gtg atg cgt ctg atg 211
Ala Leu Leu Gly Phe Gly Thr Val Gly Thr Glu Val Met Arg Leu Met
          25          30          35

acc gag tac ggt gat gaa ctt gcg cac cgc att ggt ggc cca ctg gag 259
Thr Glu Tyr Gly Asp Glu Leu Ala His Arg Ile Gly Gly Pro Leu Glu
          40          45          50

gtt cgt ggc att gct gtt tct gat atc tca aag cca cgt gaa ggc gtt 307
Val Arg Gly Ile Ala Val Ser Asp Ile Ser Lys Pro Arg Glu Gly Val
          55          60          65

gca cct gag ctg ctc act gag gac gct ttt gca ctc atc gag cgc gag 355
Ala Pro Glu Leu Leu Thr Glu Asp Ala Phe Ala Leu Ile Glu Arg Glu
          70          75          80          85

gat gtt gac atc gtc gtt gag gtt atc ggc ggc att gag tac cca cgt 403
Asp Val Asp Ile Val Val Glu Val Ile Gly Gly Ile Glu Tyr Pro Arg
          90          95          100

gag gta gtt ctc gca gct ctg aag gcc ggc aag tct gtt gtt acc gcc 451
Glu Val Val Leu Ala Ala Leu Lys Ala Gly Lys Ser Val Val Thr Ala
          105          110          115

aat aag gct ctt gtt gca gct cac tct gct gag ctt gct gat 493
Asn Lys Ala Leu Val Ala Ala His Ser Ala Glu Leu Ala Asp
          120          125          130

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Pro Arg Glu Gly Val Ala Pro Glu Leu Leu Thr Glu Asp Ala Phe Ala  
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 Leu Ile Glu Arg Glu Asp Val Asp Ile Val Val Glu Val Ile Gly Gly  
 85 90 95  
 Ile Glu Tyr Pro Arg Glu Val Val Leu Ala Ala Leu Lys Ala Gly Lys  
 100 105 110  
 Ser Val Val Thr Ala Asn Lys Ala Leu Val Ala Ala His Ser Ala Glu  
 115 120 125  
 Leu Ala Asp Ala Ala Glu Ala Ala Asn Val Asp Leu Tyr Phe Glu Ala  
 130 135 140  
 Ala Val Ala Cys Ala Ile Pro Val Val Gly Pro Leu Arg Arg Ser Leu  
 145 150 155 160  
 Ala Gly Asp Gln Ile Gln Ser Val Met Gly Ile Val Asn Gly Thr Thr  
 165 170 175  
 Asn Phe Ile Leu Asp Ala Met Asp Ser Thr Gly Ala Asp Tyr Ala Asp  
 180 185 190  
 Ser Leu Ala Glu Ala Thr Arg Leu Gly Tyr Ala Glu Ala Asp Pro Thr  
 195 200 205  
 Ala Asn Val Glu Gly His Asp Ala Ala Ser Lys Ala Ala Ile Leu Ala  
 210 215 220  
 Cys Ile Ala Phe His Thr Arg Val Thr Ala Asp Asp Val Tyr Cys Glu  
 225 230 235 240  
 Gly Ile Arg Asn Ile Asn Ala Ala Asp Ile Glu Ala Ala Gln Gln Ala  
 245 250 255  
 Gly His Thr Ile Lys Leu Leu Ala Ile Cys Glu Lys Phe Thr Asn Lys  
 260 265 270  
 Glu Gly Lys Ser Ala Ile Ser Ala Arg Val His Pro Thr Leu Leu Pro  
 275 280 285  
 Val Ser His Pro Leu Ala Ser Val Asn Lys Ser Phe Asn Ala Ile Phe  
 290 295 300  
 Val Glu Ala Glu Ala Ala Gly Arg Leu Met Phe Tyr Gly Asn Gly Ala  
 305 310 315 320  
 Gly Gly Ala Pro Thr Ala Ser Ala Val Leu Gly Asp Val Val Gly Ala  
 325 330 335  
 Ala Arg Asn Lys Val His Gly Gly Arg Ala Pro Gly Glu Ser Thr Tyr  
 340 345 350  
 Ala Asn Leu Pro Ile Ala Asp Phe Gly Glu Thr Thr Thr Arg Tyr His  
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 370 375 380  
 Ser Leu Phe Ser Glu Gln Gly Ile Ser Leu Arg Thr Ile Arg Gln Glu

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<212> PRT  
<213> *Corynebacterium glutamicum*

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Val Met Arg Leu Met Thr Glu Tyr Gly Asp Glu Leu Ala His Arg Ile
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Gly Gly Pro Leu Glu Val Arg Gly Ile Ala Val Ser Asp Ile Ser Lys
  50                      55                      60

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Asp Val Asp Ile Val Val Glu Val Ile Gly Gly Ile Glu Tyr Pro Arg	
90 95 100	
gag gta gtt ctc gca gct ctg aag gcc ggc aag tct gtt gtt acc gcc	451
Glu Val Val Leu Ala Ala Leu Lys Ala Gly Lys Ser Val Val Thr Ala	
105 110 115	
aat aag gct ctt gtt gca gct cac tct gct gag ctt gct gat gca gcg	499
Asn Lys Ala Leu Val Ala Ala His Ser Ala Glu Leu Ala Asp Ala Ala	
120 125 130	
gaa gcc gca aac gtt gac ctg tac ttc gag gct gct gtt gca tgc gca	547
Glu Ala Ala Asn Val Asp Leu Tyr Phe Glu Ala Ala Val Ala Cys Ala	
135 140 145	
att cca gtg gtt ggc cca ctg cgt cgc tcc ctg gct ggc gat cag atc	595
Ile Pro Val Val Gly Pro Leu Arg Arg Ser Leu Ala Gly Asp Gln Ile	
150 155 160 165	
cag tct gtg atg ggc atc gtt aac ggc acc acc aac ttc atc ttg gac	643
Gln Ser Val Met Gly Ile Val Asn Gly Thr Thr Asn Phe Ile Leu Asp	
170 175 180	
gcc atg gat tcc acc ggc gct gac tat gca gat tct ttg gct gag gca	691
Ala Met Asp Ser Thr Gly Ala Asp Tyr Ala Asp Ser Leu Ala Glu Ala	
185 190 195	
act cgt ttg ggt tac gcc gaa gct gat cca act gca aac gtc gaa ggc	739
Thr Arg Leu Gly Tyr Ala Glu Ala Asp Pro Thr Ala Asn Val Glu Gly	
200 205 210	
cat gac gcc gca tcc aag gct gca att ttg gca tgc atc gct ttc cac	787
His Asp Ala Ala Ser Lys Ala Ala Ile Leu Ala Cys Ile Ala Phe His	
215 220 225	
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Thr Arg Val Thr Ala Asp Asp Val Tyr Cys Glu Gly Ile Arg Asn Ile	
230 235 240 245	
aac gct gcc gac att gag gca gca cag cag gca ggc cac acc atc aag	883
Asn Ala Ala Asp Ile Glu Ala Ala Gln Gln Ala Gly His Thr Ile Lys	
250 255 260	
ttg ttg gcc atc tgt gag aag ttc acc aac aag gaa gga aag tcg gct	931
Leu Leu Ala Ile Cys Glu Lys Phe Thr Asn Lys Glu Gly Lys Ser Ala	
265 270 275	
att tct gct cgc gtg cac ccg act cta tta cct gtg tcc cac cca ctg	979
Ile Ser Ala Arg Val His Pro Thr Leu Leu Pro Val Ser His Pro Leu	
280 285 290	
gcg tcg gta aac aag tcc ttt aat gca atc ttt gtt gaa gca gaa gca	
1027	
Ala Ser Val Asn Lys Ser Phe Asn Ala Ile Phe Val Glu Ala Glu Ala	
295 300 305	
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1075	
Ala Gly Arg Leu Met Phe Tyr Gly Asn Gly Ala Gly Gly Ala Pro Thr	

Glu Leu Val Glu Leu Asp Glu Leu Met Ser Arg Ser Asp Phe Val Thr  
 50 55 60  
 Ile His Leu Pro Lys Thr Lys Glu Thr Ala Gly Met Phe Asp Ala His  
 65 70 75 80  
 Leu Leu Ala Lys Ser Lys Lys Gly Gln Ile Ile Ile Asn Ala Ala Arg  
 85 90 95  
 Gly Gly Leu Val Asp Glu Gln Ala Leu Ala Asp Ala Ile Glu Ser Gly  
 100 105 110  
 His Ile Arg Gly Ala Gly Phe Asp Val Tyr Ser Thr Glu Pro Cys Thr  
 115 120 125  
 Asp Ser Pro Leu Phe Lys Leu Pro Gln Val Val Val Thr Pro His Leu  
 130 135 140  
 Gly Ala Ser Thr Glu Glu Ala Gln Asp Arg Ala Gly Thr Asp Ile Ala  
 145 150 155 160  
 Asp Ser Val Leu Lys Ala Leu Ala  
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<210> 169  
 <211> 1458  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1435)  
 <223> RXN00969

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 Met Thr Ser Ala Ser  
 1 5  
 gcc cca agc ttt aac ccc ggc aag ggt ccc ggc tca gca gtc gga att 163  
 Ala Pro Ser Phe Asn Pro Gly Lys Gly Pro Gly Ser Ala Val Gly Ile  
 10 15 20  
 gcc ctt tta gga ttc gga aca gtc ggc act gag gtg atg cgt ctg atg 211  
 Ala Leu Leu Gly Phe Gly Thr Val Gly Thr Glu Val Met Arg Leu Met  
 25 30 35  
 acc gag tac ggt gat gaa ctt gcg cac cgc att ggt ggc cca ctg gag 259  
 Thr Glu Tyr Gly Asp Glu Leu Ala His Arg Ile Gly Gly Pro Leu Glu  
 40 45 50  
 gtt cgt ggc att gct gtt tct gat atc tca aag cca cgt gaa ggc gtt 307  
 Val Arg Gly Ile Ala Val Ser Asp Ile Ser Lys Pro Arg Glu Gly Val  
 55 60 65  
 gca cct gag ctg ctc act gag gac gct ttt gca ctc atc gag cgc gag 355  
 Ala Pro Glu Leu Leu Thr Glu Asp Ala Phe Ala Leu Ile Glu Arg Glu  
 70 75 80 85

gac aag cta gta cag cgt ttc gac gcc ggc tcc tac gtc ttg ctc acc 931  
 Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser Tyr Val Leu Leu Thr  
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gac gcc ctc aac cgc cac gac att ggt cgc gac cgc gga ggc ctc aac 979  
 Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp Arg Gly Gly Leu Asn  
                   280                                   285                                   290

aag gca ctc gaa tcc atc aaa gtt cca gtc ctt gtc gca ggc gta gat  
 1027  
 Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu Val Ala Gly Val Asp  
                   295                                   300                                   305

acc gat att ttg tac ccc tac cac cag caa gaa cac ctc tcc aga aac  
 1075  
 Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu His Leu Ser Arg Asn  
                   310                                   315                                   320                                   325

ctg gga aat cta ctg gca atg gca aaa atc gta tcc cct gtc ggc cac  
 1123  
 Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val Ser Pro Val Gly His  
                   330                                   335                                   340

gat gct ttc ctc acc gaa agc cgc caa atg gat cgc atc gtg agg aac  
 1171  
 Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp Arg Ile Val Arg Asn  
                   345                                   350                                   355

ttc ttc agc ctc atc tcc cca gac gaa gac aac cct tcg acc tac atc  
 1219  
 Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn Pro Ser Thr Tyr Ile  
                   360                                   365                                   370

gag ttc tac atc taataggtat ttacgacaaa tag  
 1254  
 Glu Phe Tyr Ile  
                   375

<210> 188

<211> 377

<212> PRT

<213> Corynebacterium glutamicum

<400> 188

Met Pro Thr Leu Ala Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly  
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Asp Val Ser Thr Glu Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala  
                   20                                   25                                   30

Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn  
                   35                                   40                                   45

Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp  
                   50                                   55                                   60

Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile  
                   65                                   70                                   75                                   80

Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr

gcc gga gca atc att aca aac gct gaa atc gcc tat cac cgc tgg ggt Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala Tyr His Arg Trp Gly 25 30 35	211
gaa tac cgc gta gat aaa gaa gga cgc agc aat gtc gtt ctc atc gaa Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn Val Val Leu Ile Glu 40 45 50	259
cac gcc ctc act gga gat tcc aac gca gcc gat tgg tgg gct gac ttg His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp Trp Trp Ala Asp Leu 55 60 65	307
ctc ggt ccc ggc aaa gcc atc aac act gat att tac tgc gtg atc tgt Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile Tyr Cys Val Ile Cys 70 75 80 85	355
acc aac gtc atc ggt ggt tgc aac ggt tcc acc gga cct ggc tcc atg Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr Gly Pro Gly Ser Met 90 95 100	403
cat cca gat gga aat ttc tgg ggt aat cgc ttc ccc gcc acg tcc att His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe Pro Ala Thr Ser Ile 105 110 115	451
cgt gat cag gta aac gcc gaa aaa caa ttc ctc gac gca ctc ggc atc Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu Asp Ala Leu Gly Ile 120 125 130	499
acc acg gtc gcc gca gta ctt ggt ggt tcc atg ggt ggt gcc cgc acc Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met Gly Gly Ala Arg Thr 135 140 145	547
cta gag tgg gcc gca atg tac cca gaa act gtt ggc gca gct gct gtt Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val Gly Ala Ala Ala Val 150 155 160 165	595
ctt gca gtt tct gca cgc gcc agc gcc tgg caa atc ggc att caa tcc Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln Ile Gly Ile Gln Ser 170 175 180	643
gcc caa att aag gcg att gaa aac gac cac cac tgg cac gaa ggc aac Ala Gln Ile Lys Ala Ile Glu Asn Asp His His Trp His Glu Gly Asn 185 190 195	691
tac tac gaa tcc ggc tgc aac cca gcc acc gga ctc ggc gcc gcc cga Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly Leu Gly Ala Ala Arg 200 205 210	739
cgc atc gcc cac ctc acc tac cgt ggc gaa cta gaa atc gac gaa cgc Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu Glu Ile Asp Glu Arg 215 220 225	787
ttc ggc acc aaa gcc caa aag aac gaa aac cca ctc ggt ccc tac cgc Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro Leu Gly Pro Tyr Arg 230 235 240 245	835
aag ccc gac cag cgc ttc gcc gtg gaa tcc tac ttg gac tac caa gca Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr Leu Asp Tyr Gln Ala 250 255 260	883



Ala Gln Gln Thr Tyr Glu Trp Ile Val Arg Phe Pro Asp Gln Val His  
 145 150 155 160

Arg Ala Ala Pro Ile Ala Gly Thr Ala Lys Asn Thr Pro His Asp Phe  
 165 170 175

Ile Phe Thr Gln Thr Leu Asn Glu Thr Val Glu Ala Asp Pro Gly Phe  
 180 185 190

Asn Gly Gly Glu Tyr Ser Ser His Glu Glu Val Ala Asp Gly Leu Arg  
 195 200 205

Arg Gln Ser His Leu Trp Ala Ala Met Gly Phe Ser Thr Glu Phe Trp  
 210 215 220

Lys Gln Glu Ala Trp Arg Arg Leu Gly Leu Glu Ser Lys Glu Ser Val  
 225 230 235 240

Leu Ala Asp Phe Leu Asp Pro Leu Phe Met Ser Met Asp Pro Asn Thr  
 245 250 255

Leu Leu Asn Asn Ala Trp Lys Trp Gln His Gly Asp Val Ser Arg His  
 260 265 270

Thr Gly Gly Asp Leu Ala Ala Ala Leu Gly Arg Val Lys Ala Lys Thr  
 275 280 285

Phe Val Met Pro Ile Ser Glu Asp Met Phe Phe Pro Val Arg Asp Cys  
 290 295 300

Ala Ala Glu Gln Ala Leu Ile Pro Gly Ser Glu Leu Arg Val Ile Glu  
 305 310 315 320

Asp Ile Ala Gly His Leu Gly Leu Phe Asn Val Ser Glu Asn Tyr Ile  
 325 330 335

Pro Gln Ile Asp Lys Asn Leu Lys Glu Leu Phe Glu Ser  
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 <213> Corynebacterium glutamicum

<220>  
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 <223> RXN00403

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 Met Pro Thr Leu Ala  
 1 5

cct tca ggt caa ctt gaa atc caa gcg atc ggt gat gtc tcc acc gaa 163  
 Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly Asp Val Ser Thr Glu  
 10 15 20

tgg aag tgg cag cat ggc gat gtc tct cgc cac acc ggc ggc gac ttg 931  
 Trp Lys Trp Gln His Gly Asp Val Ser Arg His Thr Gly Gly Asp Leu  
                   265                                  270                                  275

gca gcg gct ctt ggc cga gtg aag gct aag acc ttc gtt atg ccc atc 979  
 Ala Ala Ala Leu Gly Arg Val Lys Ala Lys Thr Phe Val Met Pro Ile  
                   280                                  285                                  290

agc gag gac atg ttc ttt cct gtt cgt gac tgt gcc gca gaa caa gca  
 1027  
 Ser Glu Asp Met Phe Phe Pro Val Arg Asp Cys Ala Ala Glu Gln Ala  
                   295                                  300                                  305

ctc atc cca ggc agc gag ctt cga gtg atc gaa gac atc gcc ggt cac  
 1075  
 Leu Ile Pro Gly Ser Glu Leu Arg Val Ile Glu Asp Ile Ala Gly His  
 310                                  315                                  320                                  325

ctt ggg ctt ttt aac gtc tct gag aat tac atc cca cag atc gac aaa  
 1123  
 Leu Gly Leu Phe Asn Val Ser Glu Asn Tyr Ile Pro Gln Ile Asp Lys  
                                   330                                  335                                  340

aat ctg aaa gag ctg ttc gag agc taaacactga tgtcaaagag cct  
 1170  
 Asn Leu Lys Glu Leu Phe Glu Ser  
                   345

<210> 186

<211> 349

<212> PRT

<213> Corynebacterium glutamicum

<400> 186

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Thr Ala Ser Ile Gly Arg Leu Glu Leu Glu Gly Gly Val Ile Glu  
                   20                                  25                                  30

Asp Cys Trp Leu Ala Tyr Ala Thr Ala Gly Thr Leu Asn Glu Asp Lys  
                   35                                  40                                  45

Ser Asn Ala Ile Leu Ile Pro Thr Trp Tyr Ser Gly Thr His Gln Thr  
                   50                                  55                                  60

Trp Phe Gln Gln Tyr Ile Gly Thr Asp His Ala Leu Asp Pro Ser Lys  
   65                                  70                                  75                                  80

Tyr Phe Ile Ile Ser Ile Asn Gln Ile Gly Asn Gly Leu Ser Val Ser  
                                   85                                  90                                  95

Pro Ala Asn Thr Ala Asp Asp Ser Ile Ser Met Ser Lys Phe Pro Asn  
                   100                                  105                                  110

Val Arg Ile Gly Asp Asp Val Val Ala Gln Asp Arg Leu Leu Arg Gln  
                   115                                  120                                  125

Glu Phe Gly Ile Thr Glu Leu Phe Ala Val Val Gly Gly Ser Met Gly  
   130                                  135                                  140

cgg ctc gaa ctc gaa gaa ggg ggt gtg att gag gat tgc tgg ttg gct	211
Arg Leu Glu Leu Glu Glu Gly Gly Val Ile Glu Asp Cys Trp Leu Ala	
25 30 35	
tac gct aca gct gga acg ctc aac gag gac aag tcc aac gcc atc ctc	259
Tyr Ala Thr Ala Gly Thr Leu Asn Glu Asp Lys Ser Asn Ala Ile Leu	
40 45 50	
att ccg acg tgg tac tcc gga acc cat cag acc tgg ttc cag cag tac	307
Ile Pro Thr Trp Tyr Ser Gly Thr His Gln Thr Trp Phe Gln Gln Tyr	
55 60 65	
atc ggc act gat cat gcg ctg gat cca tca aag tat ttc atc atc tcc	355
Ile Gly Thr Asp His Ala Leu Asp Pro Ser Lys Tyr Phe Ile Ile Ser	
70 75 80 85	
atc aac caa atc ggt aat ggt ttg tcg gtc tcc cct gcc aac acg gct	403
Ile Asn Gln Ile Gly Asn Gly Leu Ser Val Ser Pro Ala Asn Thr Ala	
90 95 100	
gat gac agc atc tcg atg tcc aag ttc ccg aat gtt cgc att ggt gat	451
Asp Asp Ser Ile Ser Met Ser Lys Phe Pro Asn Val Arg Ile Gly Asp	
105 110 115	
gat gtc gtt gcc cag gac cgg ctc ttg cgc caa gag ttt ggt att acc	499
Asp Val Val Ala Gln Asp Arg Leu Leu Arg Gln Glu Phe Gly Ile Thr	
120 125 130	
gag ctc ttt gcc gtc gtt ggt ggt tcg atg ggt gcg cag caa acc tat	547
Glu Leu Phe Ala Val Val Gly Gly Ser Met Gly Ala Gln Gln Thr Tyr	
135 140 145	
gag tgg att gtt cgc ttc cct gac caa gtt cat cga gca gct ccg atc	595
Glu Trp Ile Val Arg Phe Pro Asp Gln Val His Arg Ala Ala Pro Ile	
150 155 160 165	
gcg ggc act gcg aag aac act cct cat gat ttc atc ttc acc cag act	643
Ala Gly Thr Ala Lys Asn Thr Pro His Asp Phe Ile Phe Thr Gln Thr	
170 175 180	
ctt aat gag acc gtt gag gcc gat cca ggg ttc aat ggc ggc gaa tac	691
Leu Asn Glu Thr Val Glu Ala Asp Pro Gly Phe Asn Gly Gly Glu Tyr	
185 190 195	
tcc tcc cat gaa gag gta gct gat gga ctt cgc cgt caa tcg cat ctt	739
Ser Ser His Glu Glu Val Ala Asp Gly Leu Arg Arg Gln Ser His Leu	
200 205 210	
tgg gct gcc atg gga ttt tcc aca gag ttc tgg aag cag gag gca tgg	787
Trp Ala Ala Met Gly Phe Ser Thr Glu Phe Trp Lys Gln Glu Ala Trp	
215 220 225	
cgt cgc ctg gga ctt gaa agt aag gag tca gtg ctc gcg gac ttc ctg	835
Arg Arg Leu Gly Leu Glu Ser Lys Glu Ser Val Leu Ala Asp Phe Leu	
230 235 240 245	
gat ccg ctg ttc atg tcc atg gat cct aat acc ttg ctc aac aac gct	883
Asp Pro Leu Phe Met Ser Met Asp Pro Asn Thr Leu Leu Asn Asn Ala	
250 255 260	

Ala Arg Tyr Leu Gln Ala Gln Gly Glu Ala Arg Ala Ile Gln Lys Val  
245 250 255

Asn Ala Ala Ile Lys Ser Ala Lys Leu Thr Pro Glu Val Leu Ala Tyr  
260 265 270

Gln Tyr Leu Glu Lys Leu Pro Lys Ile Ala Glu Gly Asn Ala Ser Lys  
275 280 285

Met Trp Val Ile Pro Ser Gln Phe Ser Asp Ser Leu Glu Gly Phe Ala  
290 295 300

Lys Gln Phe Gly Ala Lys Asp Ala Glu Gly Val Phe Arg Tyr Glu Pro  
305 310 315 320

Asn Thr Val Asp Glu Glu Thr Arg Asp Ile Ala Asn Ala Asp Asn Val  
325 330 335

Glu Asp Trp Phe Ser Thr Glu Ser Asp Pro Glu Ile Ala Ala Val  
340 345 350

Ala Ala Ala Asn Ala Val Ala Asn Lys Pro Val Asp Pro Glu Pro Gly  
355 360 365

Glu Ile Leu Ser Lys Lys Thr Ala Arg Arg Val Glu Pro Glu Ala Val  
370 375 380

Leu Glu Ala Leu Gln Asn Gly Thr Thr Thr Gln Pro Glu Val Glu Ala  
385 390 395 400

Ala Pro Pro Thr Ala Asn Phe Ala Gln Glu Phe Pro Ala Pro Gln Ala  
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420 425 430

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<211> 1170  
<212> DNA  
<213> *Corynebacterium glutamicum*

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<222> (101)..(1147)  
<223> RXA00115

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cgtatattgt gacctacacc ccatactggt aggagttttc atg ctc gac aat agt 115  
Met Leu Asp Asn Ser  
1 5  
ttt tac acc gca gag gtt cag ggc cca tac gaa acc gct tcc att ggc 163  
Phe Tyr Thr Ala Glu Val Gln Gly Pro Tyr Glu Thr Ala Ser Ile Gly  
10 15 20

410 415 420  
 tcc gac caa cac cga gag aat cct tac gga aac taatcaggca taagaaaagg  
 1416  
 Ser Asp Gln His Arg Glu Asn Pro Tyr Gly Asn  
 425 430  
  
 cgg  
 1419  
  
 <210> 184  
 <211> 432  
 <212> PRT  
 <213> Corynebacterium glutamicum  
  
 <400> 184  
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 Ile Glu Arg Leu Gly Ser Tyr Thr Arg Thr Val Ser Gly Gly Leu Thr  
 35 40 45  
 Leu Leu Val Pro Phe Val Asp Arg Val Arg Ala Arg Ile Asp Thr Arg  
 50 55 60  
 Glu Arg Val Val Ser Phe Pro Pro Gln Ala Val Ile Thr Gln Asp Asn  
 65 70 75 80  
 Leu Thr Val Ala Ile Asp Ile Val Val Thr Phe Gln Ile Asn Glu Pro  
 85 90 95  
 Glu Arg Ala Ile Tyr Gly Val Asp Asn Tyr Ile Val Gly Val Glu Gln  
 100 105 110  
 Ile Ser Val Ala Thr Leu Arg Asp Val Val Gly Gly Met Thr Leu Glu  
 115 120 125  
 Glu Thr Leu Thr Ser Arg Asp Val Ile Asn Arg Arg Leu Arg Gly Glu  
 130 135 140  
 Leu Asp Ala Ala Thr Thr Lys Trp Gly Leu Arg Ile Ser Arg Val Glu  
 145 150 155 160  
 Leu Lys Ala Ile Asp Pro Pro Pro Ser Ile Gln Gln Ser Met Glu Lys  
 165 170 175  
 Gln Met Lys Ala Asp Arg Glu Lys Arg Ala Thr Ile Leu Thr Ala Glu  
 180 185 190  
 Gly Gln Arg Glu Ala Asp Ile Lys Thr Ala Glu Gly Glu Lys Gln Ala  
 195 200 205  
 Lys Ile Leu Gln Ala Glu Gly Glu Lys His Ala Ser Ile Leu Asn Ala  
 210 215 220  
 Glu Ala Glu Arg Gln Ala Met Ile Leu Arg Ala Glu Gly Glu Arg Ala  
 225 230 235 240

Asp Ile Lys Thr Ala Glu Gly Glu Lys Gln Ala Lys Ile Leu Gln Ala  
 200 205 210  
 gag ggt gaa aag cac gca tcc atc ctg aac gca gaa gca gaa cgc caa 787  
 Glu Gly Glu Lys His Ala Ser Ile Leu Asn Ala Glu Ala Glu Arg Gln  
 215 220 225  
 gcg atg atc ctg cgc gcc gaa ggt gaa cgc gca gca cgc tac ctc cag 835  
 Ala Met Ile Leu Arg Ala Glu Gly Glu Arg Ala Ala Arg Tyr Leu Gln  
 230 235 240 245  
 gcg cag ggt gaa gcc cga gca atc caa aag gtc aac gca gca atc aag 883  
 Ala Gln Gly Glu Ala Arg Ala Ile Gln Lys Val Asn Ala Ala Ile Lys  
 250 255 260  
 tct gcc aag ttg acc cca gag gtt ctt gct tat caa tac ctc gaa aag 931  
 Ser Ala Lys Leu Thr Pro Glu Val Leu Ala Tyr Gln Tyr Leu Glu Lys  
 265 270 275  
 ctt cct aag atc gca gag ggc aac gcc tcc aag atg tgg gtc atc cca 979  
 Leu Pro Lys Ile Ala Glu Gly Asn Ala Ser Lys Met Trp Val Ile Pro  
 280 285 290  
 agc cag ttc tcc gat tct ctg gaa ggt ttt gcg aag cag ttc ggc gca  
 1027  
 Ser Gln Phe Ser Asp Ser Leu Glu Gly Phe Ala Lys Gln Phe Gly Ala  
 295 300 305  
 aag gat gca gaa ggt gtc ttc cgc tac gaa cca aac acc gtg gat gaa  
 1075  
 Lys Asp Ala Glu Gly Val Phe Arg Tyr Glu Pro Asn Thr Val Asp Glu  
 310 315 320 325  
 gaa acc cgc gac atc gca aac gcc gac aac gtg gaa gac tgg ttc tcc  
 1123  
 Glu Thr Arg Asp Ile Ala Asn Ala Asp Asn Val Glu Asp Trp Phe Ser  
 330 335 340  
 acc gaa tca gac cct gaa atc gca gca gca gtc gcc gca gca aac gcc  
 1171  
 Thr Glu Ser Asp Pro Glu Ile Ala Ala Val Ala Ala Ala Asn Ala  
 345 350 355  
 gtg gcc aac aag cca gtc gat cca gaa ccc ggt gag atc ctt tcc aag  
 1219  
 Val Ala Asn Lys Pro Val Asp Pro Glu Pro Gly Glu Ile Leu Ser Lys  
 360 365 370  
 aag acc gca cga cgc gtt gaa cct gaa gca gta ttg gag gct ttg caa  
 1267  
 Lys Thr Ala Arg Arg Val Glu Pro Glu Ala Val Leu Glu Ala Leu Gln  
 375 380 385  
 aac gga acc act aca caa cct gag gtt gag gca gca cct cct acc gca  
 1315  
 Asn Gly Thr Thr Thr Gln Pro Glu Val Glu Ala Ala Pro Pro Thr Ala  
 390 395 400 405  
 aac ttc gcc caa gaa ttc cct gca cca cag gca aac cct gaa gat tac  
 1363  
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&lt;221&gt; CDS

&lt;222&gt; (101)..(1396)

&lt;223&gt; RXC00152

&lt;400&gt; 183

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caaatagtagtac tggccattcc caactaaaac tggagtaacg atg aca gga cta atc 115
Met Thr Gly Leu Ile
1 5

ctc gcc ata gtt ttc ctg gtc ttt gtc gcc gtc gtg gtg atc aag tcc 163
Leu Ala Ile Val Phe Leu Val Phe Val Ala Val Val Val Ile Lys Ser
10 15 20

ata gcc ctg att ccc cag ggt gaa gcc gcc gtc att gaa cgc ctt ggt 211
Ile Ala Leu Ile Pro Gln Gly Glu Ala Ala Val Ile Glu Arg Leu Gly
25 30 35

agc tac acc cgc acc gtt tca ggt ggc ctg acc ctg ctg gtt cca ttc 259
Ser Tyr Thr Arg Thr Val Ser Gly Gly Leu Thr Leu Leu Val Pro Phe
40 45 50

gtg gac cga gta cgc gca agg atc gac acc cgt gag cgc gtg gtc tca 307
Val Asp Arg Val Arg Ala Arg Ile Asp Thr Arg Glu Arg Val Val Ser
55 60 65

ttc cca ccg cag gct gtt att acc caa gac aac ctg acc gtg gcc atc 355
Phe Pro Pro Gln Ala Val Ile Thr Gln Asp Asn Leu Thr Val Ala Ile
70 75 80 85

gat atc gtg gtg acc ttc caa atc aac gaa cca gag cgc gcc atc tac 403
Asp Ile Val Val Thr Phe Gln Ile Asn Glu Glu Pro Glu Arg Ala Ile Tyr
90 95 100

ggc gtg gac aac tac atc gtc ggt gtg gag cag att tct gta gca aca 451
Gly Val Asp Asn Tyr Ile Val Gly Val Glu Gln Ile Ser Val Ala Thr
105 110 115

ctt cga gac gtt gtc ggt ggc atg acc ctg gaa gaa acc ctc act tca 499
Leu Arg Asp Val Val Gly Gly Met Thr Leu Glu Glu Thr Leu Thr Ser
120 125 130

cgt gac gtg atc aac cgc cgc ctc cgt ggc gag ctc gat gca gca acc 547
Arg Asp Val Ile Asn Arg Arg Leu Arg Gly Glu Leu Asp Ala Ala Thr
135 140 145

acc aaa tgg ggc ctg cgc atc agc cgt gtg gaa cta aag gca att gat 595
Thr Lys Trp Gly Leu Arg Ile Ser Arg Val Glu Leu Lys Ala Ile Asp
150 155 160 165

ccg cca cca tcc atc cag caa tcg atg gaa aag cag atg aag gca gac 643
Pro Pro Pro Ser Ile Gln Gln Ser Met Glu Lys Gln Met Lys Ala Asp
170 175 180

cgt gaa aag cgc gcc acc att ttg acc gca gaa ggt cag cgc gaa gcc 691
Arg Glu Lys Arg Ala Thr Ile Leu Thr Ala Glu Gly Gln Arg Glu Ala
185 190 195

gac atc aaa act gcc gaa ggt gaa aag caa gcc aag atc ctc caa gct 739

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 Ser Leu Arg  
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 <212> PRT  
 <213> Corynebacterium glutamicum

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 20 25 30  
 Pro Thr Asp Thr Leu Tyr Gly Leu Gly Cys Asp Ala Phe Asn Asn Glu  
 35 40 45  
 Ala Val Ala Asn Leu Leu Ala Thr Lys His Arg Gly Pro Asp Met Pro  
 50 55 60  
 Val Pro Val Leu Val Gly Ser Trp Asp Thr Ile Gln Gly Leu Val His  
 65 70 75 80  
 Ser Tyr Ser Ala Gln Ala Lys Ala Leu Val Glu Ala Phe Trp Pro Gly  
 85 90 95  
 Gly Leu Ser Ile Ile Val Pro Gln Ala Pro Ser Leu Pro Trp Asn Leu  
 100 105 110  
 Gly Asp Thr Arg Gly Thr Val Met Leu Arg Met Pro Leu His Pro Val  
 115 120 125  
 Ala Ile Glu Leu Leu Arg Gln Thr Gly Pro Met Ala Val Ser Ser Ala  
 130 135 140  
 Asn Ile Ser Gly His Thr Pro Pro Thr Thr Val Leu Glu Ala Arg Gln  
 145 150 155 160  
 Gln Leu Asn Gln Asn Val Ala Val Tyr Leu Asp Gly Gly Glu Cys Ala  
 165 170 175  
 Leu Ala Thr Pro Ser Thr Ile Val Asp Ile Ser Gly Pro Ala Pro Lys  
 180 185 190  
 Ile Leu Arg Glu Gly Ala Ile Ser Ala Glu Arg Val Gly Glu Val Leu  
 195 200 205  
 Gly Val Ser Ala Glu Ser Leu Arg  
 210 215

<210> 183  
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&lt;221&gt; CDS

&lt;222&gt; (101)..(748)

&lt;223&gt; RXC01207

&lt;400&gt; 181

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                                         Val Ser Arg Ile Tyr
                                         1           5

gac tgt gcc gac caa gac tcc cgt gca gca ggc cta aag gcg gct gtc 163
Asp Cys Ala Asp Gln Asp Ser Arg Ala Ala Gly Leu Lys Ala Ala Val
                10                15                20

gat gca gtc aaa gcc ggt cag ctc gtt gtc ctt ccc acg gat acc ctt 211
Asp Ala Val Lys Ala Gly Gln Leu Val Val Leu Pro Thr Asp Thr Leu
                25                30                35

tat gga ctc ggc tgc gac gct ttc aac aac gag gca gta gcc aac ctt 259
Tyr Gly Leu Gly Cys Asp Ala Phe Asn Asn Glu Ala Val Ala Asn Leu
                40                45                50

ctg gcc acc aaa cac cgt ggc ccc gat atg ccc gtt cca gtg ctc gtc 307
Leu Ala Thr Lys His Arg Gly Pro Asp Met Pro Val Pro Val Leu Val
                55                60                65

ggc agc tgg gac acc att caa gga ctt gtg cac tcc tat tct gcg cag 355
Gly Ser Trp Asp Thr Ile Gln Gly Leu Val His Ser Tyr Ser Ala Gln
                70                75                80                85

gca aaa gcg ctt gtg gag gcg ttc tgg cct ggt gga ctg tcc atc atc 403
Ala Lys Ala Leu Val Glu Ala Phe Trp Pro Gly Gly Leu Ser Ile Ile
                .90                95                100

gtt ccg cag gca cca agc ctt ccg tgg aac ctt ggc gat acc cgt ggc 451
Val Pro Gln Ala Pro Ser Leu Pro Trp Asn Leu Gly Asp Thr Arg Gly
                105                110                115

acc gta atg ctg cgc atg cca ctg cac cca gtt gcc att gaa ttg ctg 499
Thr Val Met Leu Arg Met Pro Leu His Pro Val Ala Ile Glu Leu Leu
                120                125                130

cgc caa acc gga cca atg gct gtc tcc tcc gcc aac atc tcc gga cat 547
Arg Gln Thr Gly Pro Met Ala Val Ser Ser Ala Asn Ile Ser Gly His
                135                140                145

act cct cca acc acc gtg ctg gag gct cgt cag cag ctc aac caa aat 595
Thr Pro Pro Thr Thr Val Leu Glu Ala Arg Gln Gln Leu Asn Gln Asn
                150                155                160                165

gtc gct gtc tac ctc gat ggt ggc gaa tgc gcg ctg gcc acc cct tca 643
Val Ala Val Tyr Leu Asp Gly Gly Glu Cys Ala Leu Ala Thr Pro Ser
                170                175                180

acc atc gtg gat att tca ggc ccc gca cca aag att ttg cgt gag ggt 691
Thr Ile Val Asp Ile Ser Gly Pro Ala Pro Lys Ile Leu Arg Glu Gly
                185                190                195

gcc atc agc gca gaa cgc gtt ggc gaa gta ctt gga gtg tcg gca gaa 739
Ala Ile Ser Ala Glu Arg Val Gly Glu Val Leu Gly Val Ser Ala Glu

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Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe  
 100 105 110  
 Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu  
 115 120 125  
 Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met  
 130 135 140  
 Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val  
 145 150 155 160  
 Gly Ala Ala Ala Val Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln  
 165 170 175  
 Ile Gly Ile Gln Ser Ala Gln Ile Lys Ala Ile Glu Asn Asp His His  
 180 185 190  
 Trp His Glu Gly Asn Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly  
 195 200 205  
 Leu Gly Ala Ala Arg Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu  
 210 215 220  
 Glu Ile Asp Glu Arg Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro  
 225 230 235 240  
 Leu Gly Pro Tyr Arg Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr  
 245 250 255  
 Leu Asp Tyr Gln Ala Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser  
 260 265 270  
 Tyr Val Leu Leu Thr Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp  
 275 280 285  
 Arg Gly Gly Leu Asn Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu  
 290 295 300  
 Val Ala Gly Val Asp Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu  
 305 310 315 320  
 His Leu Ser Arg Asn Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val  
 325 330 335  
 Ser Pro Val Gly His Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp  
 340 345 350  
 Arg Ile Val Arg Asn Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn  
 355 360 365  
 Pro Ser  
 370

&lt;210&gt; 181

&lt;211&gt; 771

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr Leu Asp Tyr Gln Ala  
 250 255 260

gac aag cta gta cag cgt ttc gac gcc ggc tcc tac gtc ttg ctc acc 931  
 Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser Tyr Val Leu Leu Thr  
 265 270 275

gac gcc ctc aac cgc cac gac att ggt cgc gac cgc gga ggc ctc aac 979  
 Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp Arg Gly Gly Leu Asn  
 280 285 290

aag gca ctc gaa tcc atc aaa gtt cca gtc ctt gtc gca ggc gta gat  
 1027

Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu Val Ala Gly Val Asp  
 295 300 305

acc gat att ttg tac ccc tac cac cag caa gaa cac ctc tcc aga aac  
 1075

Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu His Leu Ser Arg Asn  
 310 315 320 325

ctg gga aat cta ctg gca atg gca aaa atc gta tcc cct gtc ggc cac  
 1123

Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val Ser Pro Val Gly His  
 330 335 340

gat gct ttc ctc acc gaa agc cgc caa atg gat cgc atc gtg agg aac  
 1171

Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp Arg Ile Val Arg Asn  
 345 350 355

ttc ttc agc ctc atc tcc cca gac gaa gac aac cct tcg  
 1210

Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn Pro Ser  
 360 365 370

<210> 180  
 <211> 370  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 180

Met Pro Thr Leu Ala Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly  
 1 5 10 15

Asp Val Ser Thr Glu Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala  
 20 25 30

Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn  
 35 40 45

Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp  
 50 55 60

Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile  
 65 70 75 80

Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr  
 85 90 95

cct tca ggt caa ctt gaa atc caa gcg atc ggt gat gtc tcc acc gaa	163
Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly Asp Val Ser Thr Glu	
10 15 20	
gcc gga gca atc att aca aac gct gaa atc gcc tat cac cgc tgg ggt	211
Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala Tyr His Arg Trp Gly	
25 30 35	
gaa tac cgc gta gat aaa gaa gga cgc agc aat gtc gtt ctc atc gaa	259
Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn Val Val Leu Ile Glu	
40 45 50	
cac gcc ctc act gga gat tcc aac gca gcc gat tgg tgg gct gac ttg	307
His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp Trp Trp Ala Asp Leu	
55 60 65	
ctc ggt ccc ggc aaa gcc atc aac act gat att tac tgc gtg atc tgt	355
Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile Tyr Cys Val Ile Cys	
70 75 80 85	
acc aac gtc atc ggt ggt tgc aac ggt tcc acc gga cct ggc tcc atg	403
Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr Gly Pro Gly Ser Met	
90 95 100	
cat cca gat gga aat ttc tgg ggt aat cgc ttc ccc gcc acg tcc att	451
His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe Pro Ala Thr Ser Ile	
105 110 115	
cgt gat cag gta aac gcc gaa aaa caa ttc ctc gac gca ctc ggc atc	499
Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu Asp Ala Leu Gly Ile	
120 125 130	
acc acg gtc gcc gca gta ctt ggt ggt tcc atg ggt ggt gcc cgc acc	547
Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met Gly Gly Ala Arg Thr	
135 140 145	
cta gag tgg gcc gca atg tac cca gaa act gtt ggc gca gct gct gtt	595
Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val Gly Ala Ala Ala Val	
150 155 160 165	
ctt gca gtt tct gca cgc gcc agc gcc tgg caa atc ggc att caa tcc	643
Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln Ile Gly Ile Gln Ser	
170 175 180	
gcc caa att aag gcg att gaa aac gac cac cac tgg cac gaa ggc aac	691
Ala Gln Ile Lys Ala Ile Glu Asn Asp His His Trp His Glu Gly Asn	
185 190 195	
tac tac gaa tcc ggc tgc aac cca gcc acc gga ctc ggc gcc gcc cga	739
Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly Leu Gly Ala Ala Arg	
200 205 210	
cgc atc gcc cac ctc acc tac cgt ggc gaa cta gaa atc gac gaa cgc	787
Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu Glu Ile Asp Glu Arg	
215 220 225	
ttc ggc acc aaa gcc caa aag aac gaa aac cca ctc ggt ccc tac cgc	835
Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro Leu Gly Pro Tyr Arg	
230 235 240 245	
aag ccc gac cag cgc ttc gcc gtg gaa tcc tac ttg gac tac caa gca	883

250								255				260						
gtc	cta	ccc	tct	gga	tgt	gga	aac	atg	ttg	tca	ttt	gag	ctt	gat	gca	931		
Val	Leu	Pro	Ser	Gly	Cys	Gly	Asn	Met	Leu	Ser	Phe	Glu	Leu	Asp	Ala			
265								270				275						
aca	cct	gaa	cga	act	gat	gag	att	ctc	gaa	agc	ctg	tca	ctt	tta	acc	979		
Thr	Pro	Glu	Arg	Thr	Asp	Glu	Ile	Leu	Glu	Ser	Leu	Ser	Leu	Leu	Thr			
280								285				290						
cac	gcg	acc	agt	tgg	gga	ggt	gtg	gaa	aca	gcc	att	gaa	cgt	cgc	acc			
1027																		
His	Ala	Thr	Ser	Trp	Gly	Gly	Val	Glu	Thr	Ala	Ile	Glu	Arg	Arg	Thr			
295								300				305						
agg	cgg	gat	gct	gaa	gtg	gtg	gca	gaa	gta	ccg	atg	act	ctt	tgc	cgc			
1075																		
Arg	Arg	Asp	Ala	Glu	Val	Val	Ala	Glu	Val	Pro	Met	Thr	Leu	Cys	Arg			
310	315								320				325					
gtt	tcc	gta	gga	att	gaa	gac	gtt	gaa	gat	cta	tgg	gaa	gac	ctc	aac			
1123																		
Val	Ser	Val	Gly	Ile	Glu	Asp	Val	Glu	Asp	Leu	Trp	Glu	Asp	Leu	Asn			
330								335				340						
gcc	tca	atc	gac	aaa	gtt	ctg	ggt	tagaactcgt	agccagtaac cag									
1170																		
Ala	Ser	Ile	Asp	Lys	Val	Leu	Gly											
345																		

<210> 196  
<211> 349  
<212> PRT  
<213> Corynebacterium glutamicum

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<400> 196
Met Asn Pro Pro Ile Thr Leu Ser Ser Thr Tyr Val His Asp Ser Glu
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Lys Ala Tyr Gly Arg Asp Gly Asn Asp Gly Trp Gly Ala Phe Glu Ala
      20              25              30

Ala Met Gly Thr Leu Asp Gly Gly Phe Ala Val Ser Tyr Ser Ser Gly
      35              40              45

Leu Ala Ala Ala Thr Ser Ile Ala Asp Leu Val Pro Thr Gly Gly Thr
  50              55              60

Val Val Leu Pro Lys Ala Ala Tyr Tyr Gly Val Thr Asn Ile Phe Ala
  65              70              75              80

Arg Met Glu Ala Arg Gly Arg Leu Lys Val Arg Thr Val Asp Ala Asp
      85              90              95

Asn Thr Glu Glu Val Ile Ala Ala Ala Gln Gly Ala Asp Val Val Trp
      100              105              110

Val Glu Ser Ile Ala Asn Pro Thr Met Val Val Ala Asp Ile Pro Ala
      115              120              125

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Thr	Leu	Ser	Ser	Thr	Tyr	Val	His	Asp	Ser	Glu	Lys	Ala	Tyr	Gly	Arg	
				10					15					20		
gat	ggc	aat	gat	gga	tgg	ggt	gca	ttt	gag	gct	gcc	atg	gga	act	cta	211
Asp	Gly	Asn	Asp	Gly	Trp	Gly	Ala	Phe	Glu	Ala	Ala	Met	Gly	Thr	Leu	
			25					30					35			
gat	ggt	ggg	ttc	gcg	gta	tct	tat	tct	tca	ggt	ttg	gca	gcg	gca	acg	259
Asp	Gly	Gly	Phe	Ala	Val	Ser	Tyr	Ser	Ser	Gly	Leu	Ala	Ala	Ala	Thr	
		40				45					50					
tcg	att	gct	gat	ttg	gtt	cct	act	ggt	ggc	aca	gtt	gtt	tta	cct	aaa	307
Ser	Ile	Ala	Asp	Leu	Val	Pro	Thr	Gly	Gly	Thr	Val	Val	Leu	Pro	Lys	
	55					60					65					
gct	gcc	tat	tat	ggc	gtg	acc	aat	att	ttc	gcc	agg	atg	gaa	gcc	cgc	355
Ala	Ala	Tyr	Tyr	Gly	Val	Thr	Asn	Ile	Phe	Ala	Arg	Met	Glu	Ala	Arg	
	70				75					80					85	
gga	agg	ctg	aag	gtt	cga	act	ggt	gat	gca	gac	aat	acc	gaa	gaa	gtg	403
Gly	Arg	Leu	Lys	Val	Arg	Thr	Val	Asp	Ala	Asp	Asn	Thr	Glu	Glu	Val	
			90						95					100		
att	gct	gct	gct	caa	ggt	gca	gat	gtg	gtg	tgg	gtg	gaa	tcg	atc	gct	451
Ile	Ala	Ala	Ala	Gln	Gly	Ala	Asp	Val	Val	Trp	Val	Glu	Ser	Ile	Ala	
			105					110					115			
aat	ccg	acg	atg	gtg	gta	gct	gat	atc	cct	gca	ata	gtc	gac	ggt	gtg	499
Asn	Pro	Thr	Met	Val	Val	Ala	Asp	Ile	Pro	Ala	Ile	Val	Asp	Gly	Val	
		120					125					130				
cgt	ggg	ctt	gga	gtt	ttg	act	gtc	ggt	gac	gcg	act	ttc	gca	acg	cca	547
Arg	Gly	Leu	Gly	Val	Leu	Thr	Val	Val	Asp	Ala	Thr	Phe	Ala	Thr	Pro	
	135					140					145					
ctt	cgt	caa	cgt	cca	ttg	gaa	ctt	ggt	gct	gat	att	gtg	ctt	tac	tcg	595
Leu	Arg	Gln	Arg	Pro	Leu	Glu	Leu	Gly	Ala	Asp	Ile	Val	Leu	Tyr	Ser	
	150				155					160					165	
gca	acc	aaa	ctt	atc	ggt	gga	cac	tct	gat	ctt	ctt	ctt	gga	gtc	gca	643
Ala	Thr	Lys	Leu	Ile	Gly	Gly	His	Ser	Asp	Leu	Leu	Leu	Gly	Val	Ala	
			170						175					180		
gtg	tgc	aag	tct	gag	cac	cat	gcg	cag	ttt	ctt	gcc	act	cac	cgt	cat	691
Val	Cys	Lys	Ser	Glu	His	His	Ala	Gln	Phe	Leu	Ala	Thr	His	Arg	His	
			185					190					195			
gat	cat	ggt	tca	gtg	ccg	gga	ggt	ctt	gaa	gcg	ttt	ctt	gct	ctc	cgt	739
Asp	His	Gly	Ser	Val	Pro	Gly	Gly	Leu	Glu	Ala	Phe	Leu	Ala	Leu	Arg	
		200					205					210				
gga	ttg	tat	tcc	ttg	gcg	gtg	cgt	ctt	gat	cga	gca	gaa	tcc	aac	gca	787
Gly	Leu	Tyr	Ser	Leu	Ala	Val	Arg	Leu	Asp	Arg	Ala	Glu	Ser	Asn	Ala	
	215					220					225					
gca	gaa	ctt	tcg	cgg	cga	ctt	aac	gcg	cat	cct	tcg	gtt	acc	cgc	gtc	835
Ala	Glu	Leu	Ser	Arg	Arg	Leu	Asn	Ala	His	Pro	Ser	Val	Thr	Arg	Val	
	230				235					240				245		
aat	tat	cca	gga	ctt	cct	gat	gat	ccc	caa	cat	gaa	aaa	gcc	gtg	cga	883
Asn	Tyr	Pro	Gly	Leu	Pro	Asp	Asp	Pro	Gln	His	Glu	Lys	Ala	Val	Arg	

<213> Corynebacterium glutamicum

<400> 194

Gln Pro Leu Lys Leu Gly Ala His Ala Val Leu His Ser Thr Thr Lys  
1 5 10 15

Tyr Ile Gly Gly His Ser Asp Val Val Gly Gly Leu Val Val Thr Asn  
20 25 30

Asp Gln Glu Met Asp Glu Glu Leu Leu Phe Met Gln Gly Gly Ile Gly  
35 40 45

Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu Thr Ala Arg Gly Leu Lys  
50 55 60

Thr Leu Ala Val Arg Met Asp Arg His Cys Asp Asn Ala Glu Lys Ile  
65 70 75 80

Ala Glu Phe Leu Asp Ser Arg Pro Glu Val Ser Thr Val Leu Tyr Pro  
85 90 95

Gly Leu Lys Asn His Pro Gly His Glu Val Ala Ala Lys Gln Met Lys  
100 105 110

Arg Phe Gly Gly Met Ile Ser Val Arg Phe Ala Gly Gly Glu Glu Ala  
115 120 125

Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu Ile Cys Leu Ala Glu Ser  
130 135 140

Leu Gly Gly Val Glu Ser Leu Leu Glu His Pro Ala Thr Met Thr His  
145 150 155 160

Gln Ser Ala Ala Gly Ser Gln Leu Glu Val Pro Arg Asp Leu Val Arg  
165 170 175

Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp Leu Leu Ala Asp Val Glu  
180 185 190

Gln Ala Leu Asn Asn Leu  
195

<210> 195

<211> 1170

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1147)

<223> RXA02532

<400> 195

gatgaatttt taccacccat ctgtacctat taaccctgcg tggcgtccac ccacagtaac 60

tgtgcaagcg ggacggccag ccagaactcc tgggtgcgccg atg aac cca cct atc 115  
Met Asn Pro Pro Ile  
1 5

acg ttg tcc agc act tat gtt cat gat tca gaa aaa gct tat ggg cgc 163

&lt;221&gt; CDS

&lt;222&gt; (1)..(594)

&lt;223&gt; FRXA00254

&lt;400&gt; 193

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cag cca cta aaa ctc ggc gca cac gca gtc ttg cac tcc acc acc aag      48
Gln Pro Leu Lys Leu Gly Ala His Ala Val Leu His Ser Thr Thr Lys
  1                   5                   10                   15

tac atc gga gga cac tcc gac gtt gtt ggc ggc ctt gtg gtt acc aac      96
Tyr Ile Gly Gly His Ser Asp Val Val Gly Gly Leu Val Val Thr Asn
                20                   25                   30

gac cag gaa atg gac gaa gaa ctg ctg ttc atg cag ggc ggc atc gga      144
Asp Gln Glu Met Asp Glu Glu Leu Leu Phe Met Gln Gly Gly Ile Gly
                35                   40                   45

ccg atc cca tca gtt ttc gat gca tac ctg acc gcc cgt ggc ctc aag      192
Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu Thr Ala Arg Gly Leu Lys
                50                   55                   60

acc ctt gca gtg cgc atg gat cgc cac tgc gac aac gca gaa aag atc      240
Thr Leu Ala Val Arg Met Asp Arg His Cys Asp Asn Ala Glu Lys Ile
                65                   70                   75                   80

gcg gaa ttc ctg gac tcc cgc cca gag gtc tcc acc gtg ctc tac cca      288
Ala Glu Phe Leu Asp Ser Arg Pro Glu Val Ser Thr Val Leu Tyr Pro
                85                   90                   95

ggt ctg aag aac cac cca ggc cac gaa gtc gca gcg aag cag atg aag      336
Gly Leu Lys Asn His Pro Gly His Glu Val Ala Ala Lys Gln Met Lys
                100                  105                  110

cgc ttc ggc ggc atg atc tcc gtc cgt ttc gca ggc ggc gaa gaa gca      384
Arg Phe Gly Gly Met Ile Ser Val Arg Phe Ala Gly Gly Glu Glu Ala
                115                  120                  125

gct aag aag ttc tgt acc tcc acc aaa ctg atc tgt ctg gcc gag tcc      432
Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu Ile Cys Leu Ala Glu Ser
                130                  135                  140

ctc ggt ggc gtg gaa tcc ctc ctg gag cac cca gca acc atg acc cac      480
Leu Gly Gly Val Glu Ser Leu Leu Glu His Pro Ala Thr Met Thr His
                145                  150                  155                  160

cag tca gct gcc ggc tct cag ctc gag gtt ccc cgc gac ctc gtg cgc      528
Gln Ser Ala Ala Gly Ser Gln Leu Glu Val Pro Arg Asp Leu Val Arg
                165                  170                  175

atc tcc att ggt att gaa gac att gaa gac ctg ctc gca gat gtc gag      576
Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp Leu Leu Ala Asp Val Glu
                180                  185                  190

cag gcc ctc aat aac ctt tagaaactat ttggcggcaa gca                      617
Gln Ala Leu Asn Asn Leu
                195

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&lt;210&gt; 194

&lt;211&gt; 198

&lt;212&gt; PRT



His Gln Ser Ala Ala Gly Ser Gln Leu Glu Val Pro Arg Asp Leu Val  
 150 155 160 165  
 cgc atc tcc att ggt att gaa gac att gaa gac ctg ctc gca gat gtc 643  
 Arg Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp Leu Leu Ala Asp Val  
 170 175 180  
 gag cag gcc ctc aat aac ctt tagaaactat ttggcggcaa gca 687  
 Glu Gln Ala Leu Asn Asn Leu  
 185

<210> 192  
 <211> 188  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 192  
 Leu His Ser Thr Thr Lys Tyr Ile Glu Gly His Ser Asp Val Val Gly  
 1 5 10 15  
 Gly Leu Val Gly Thr Asn Asp Gln Glu Met Asp Glu Glu Leu Leu Phe  
 20 25 30  
 Met Gln Gly Gly Ile Gly Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu  
 35 40 45  
 Thr Ala Arg Gly Leu Lys Thr Leu Ala Val Arg Met Asp Arg His Cys  
 50 55 60  
 Asp Asn Ala Glu Lys Ile Ala Glu Phe Leu Asp Ser Arg Pro Glu Val  
 65 70 75 80  
 Ser Thr Val Leu Tyr Pro Gly Leu Lys Asn His Pro Gly His Glu Val  
 85 90 95  
 Ala Ala Lys Gln Met Lys Arg Phe Gly Gly Met Ile Ser Val Arg Phe  
 100 105 110  
 Ala Gly Gly Glu Glu Ala Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu  
 115 120 125  
 Ile Cys Leu Ala Glu Ser Leu Gly Gly Val Glu Ser Leu Leu Glu His  
 130 135 140  
 Pro Ala Thr Met Thr His Gln Ser Ala Ala Gly Ser Gln Leu Glu Val  
 145 150 155 160  
 Pro Arg Asp Leu Val Arg Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp  
 165 170 175  
 Leu Leu Ala Asp Val Glu Gln Ala Leu Asn Asn Leu  
 180 185

<210> 193  
 <211> 617  
 <212> DNA  
 <213> Corynebacterium glutamicum  
 <220>

Arg Ile Val Arg Asn Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn  
 355 360 365

Pro Ser  
 370

<210> 191  
 <211> 687  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(664)  
 <223> RXS03158

<400> 191  
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 acctgcagca gccactaaaa ctgcggcgac acgcaagtcc ttg cac tcc acc acc 115  
 Leu His Ser Thr Thr  
 1 5  
 aag tac atc gaa gga cac tcc gac gtt gtt ggc ggc ctt gtg ggt acc 163  
 Lys Tyr Ile Glu Gly His Ser Asp Val Val Gly Gly Leu Val Gly Thr  
 10 15 20  
 aac gac cag gaa atg gac gaa gaa ctg ctg ttc atg cag ggc ggc atc 211  
 Asn Asp Gln Glu Met Asp Glu Glu Leu Leu Phe Met Gln Gly Gly Ile  
 25 30 35  
 gga ccg atc cca tca gtt ttc gat gca tac ctg acc gcc cgt ggc ctc 259  
 Gly Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu Thr Ala Arg Gly Leu  
 40 45 50  
 aag acc ctt gca gtg cgc atg gat cgc cac tgc gac aac gca gaa aag 307  
 Lys Thr Leu Ala Val Arg Met Asp Arg His Cys Asp Asn Ala Glu Lys  
 55 60 65  
 atc gcg gaa ttc ctg gac tcc cgc cca gag gtc tcc acc gtg ctc tac 355  
 Ile Ala Glu Phe Leu Asp Ser Arg Pro Glu Val Ser Thr Val Leu Tyr  
 70 75 80 85  
 cca ggt ctg aag aac cac cca ggc cac gaa gtc gca gcg aag cag atg 403  
 Pro Gly Leu Lys Asn His Pro Gly His Glu Val Ala Ala Lys Gln Met  
 90 95 100  
 aag cgc ttc ggc ggc atg atc tcc gtc cgt ttc gca ggc ggc gaa gaa 451  
 Lys Arg Phe Gly Gly Met Ile Ser Val Arg Phe Ala Gly Gly Glu Glu  
 105 110 115  
 gca gct aag aag ttc tgt acc tcc acc aaa ctg atc tgt ctg gcc gag 499  
 Ala Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu Ile Cys Leu Ala Glu  
 120 125 130  
 tcc ctc ggt ggc gtg gaa tcc ctc ctg gag cac cca gca acc atg acc 547  
 Ser Leu Gly Gly Val Glu Ser Leu Leu Glu His Pro Ala Thr Met Thr  
 135 140 145  
 cac cag tca gct gcc ggc tct cag ctc gag gtt ccc cgc gac ctc gtg 595

Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn  
 35 40 45  
 Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp  
 50 55 60  
 Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile  
 65 70 75 80  
 Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr  
 85 90 95  
 Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe  
 100 105 110  
 Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu  
 115 120 125  
 Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met  
 130 135 140  
 Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val  
 145 150 155 160  
 Gly Ala Ala Ala Val Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln  
 165 170 175  
 Ile Gly Ile Gln Ser Ala Gln Ile Lys Ala Ile Glu Asn Asp His His  
 180 185 190  
 Trp His Glu Gly Asn Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly  
 195 200 205  
 Leu Gly Ala Ala Arg Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu  
 210 215 220  
 Glu Ile Asp Glu Arg Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro  
 225 230 235 240  
 Leu Gly Pro Tyr Arg Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr  
 245 250 255  
 Leu Asp Tyr Gln Ala Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser  
 260 265 270  
 Tyr Val Leu Leu Thr Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp  
 275 280 285  
 Arg Gly Gly Leu Asn Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu  
 290 295 300  
 Val Ala Gly Val Asp Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu  
 305 310 315 320  
 His Leu Ser Arg Asn Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val  
 325 330 335  
 Ser Pro Val Gly His Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp  
 340 345 350

tac tac gaa tcc ggc tgc aac cca gcc acc gga ctc ggc gcc gcc cga 739  
 Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly Leu Gly Ala Ala Arg  
 200 205 210

cgc atc gcc cac ctc acc tac cgt ggc gaa cta gaa atc gac gaa cgc 787  
 Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu Glu Ile Asp Glu Arg  
 215 220 225

ttc ggc acc aaa gcc caa aag aac gaa aac cca ctc ggt ccc tac cgc 835  
 Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro Leu Gly Pro Tyr Arg  
 230 235 240 245

aag ccc gac cag cgc ttc gcc gtg gaa tcc tac ttg gac tac caa gca 883  
 Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr Leu Asp Tyr Gln Ala  
 250 255 260

gac aag cta gta cag cgt ttc gac gcc ggc tcc tac gtc ttg ctc acc 931  
 Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser Tyr Val Leu Leu Thr  
 265 270 275

gac gcc ctc aac cgc cac gac att ggt cgc gac cgc gga ggc ctc aac 979  
 Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp Arg Gly Gly Leu Asn  
 280 285 290

aag gca ctc gaa tcc atc aaa gtt cca gtc ctt gtc gca ggc gta gat  
 1027  
 Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu Val Ala Gly Val Asp  
 295 300 305

acc gat att ttg tac ccc tac cac cag caa gaa cac ctc tcc aga aac  
 1075  
 Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu His Leu Ser Arg Asn  
 310 315 320 325

ctg gga aat cta ctg gca atg gca aaa atc gta tcc cct gtc ggc cac  
 1123  
 Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val Ser Pro Val Gly His  
 330 335 340

gat gct ttc ctc acc gaa agc cgc caa atg gat cgc atc gtg agg aac  
 1171  
 Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp Arg Ile Val Arg Asn  
 345 350 355

ttc ttc agc ctc atc tcc cca gac gaa gac aac cct tcg  
 1210  
 Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn Pro Ser  
 360 365 370

<210> 190

<211> 370

<212> PRT

<213> Corynebacterium glutamicum

<400> 190

Met Pro Thr Leu Ala Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly  
 1 5 10 15

Asp Val Ser Thr Glu Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala  
 20 25 30

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1210)

&lt;223&gt; FRXA00403

&lt;400&gt; 189

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tttttcagac tcgtgagaat gcaaactaga ctagacagag ctgtccatat acactggacg 60

aagtttttagt cttgtccacc cagaacaggc ggttattttc atg ccc acc ctc gcg 115
                                         Met Pro Thr Leu Ala
                                         1           5

cct tca ggt caa ctt gaa atc caa gcg atc ggt gat gtc tcc acc gaa 163
Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly Asp Val Ser Thr Glu
                        10                        15                        20

gcc gga gca atc att aca aac gct gaa atc gcc tat cac cgc tgg ggt 211
Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala Tyr His Arg Trp Gly
                        25                        30                        35

gaa tac cgc gta gat aaa gaa gga cgc agc aat gtc gtt ctc atc gaa 259
Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn Val Val Leu Ile Glu
                        40                        45                        50

cac gcc ctc act gga gat tcc aac gca gcc gat tgg tgg gct gac ttg 307
His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp Trp Trp Ala Asp Leu
                        55                        60                        65

ctc ggt ccc ggc aaa gcc atc aac act gat att tac tgc gtg atc tgt 355
Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile Tyr Cys Val Ile Cys
70                        75                        80                        85

acc aac gtc atc ggt ggt tgc aac ggt tcc acc gga cct ggc tcc atg 403
Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr Gly Pro Gly Ser Met
                        90                        95                        100

cat cca gat gga aat ttc tgg ggt aat cgc ttc ccc gcc acg tcc att 451
His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe Pro Ala Thr Ser Ile
                        105                        110                        115

cgt gat cag gta aac gcc gaa aaa caa ttc ctc gac gca ctc ggc atc 499
Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu Asp Ala Leu Gly Ile
                        120                        125                        130

acc acg gtc gcc gca gta ctt ggt ggt tcc atg ggt ggt gcc cgc acc 547
Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met Gly Gly Ala Arg Thr
                        135                        140                        145

cta gag tgg gcc gca atg tac cca gaa act gtt ggc gca gct gct gtt 595
Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val Gly Ala Ala Ala Val
150                        155                        160                        165

ctt gca gtt tct gca cgc gcc agc gcc tgg caa atc ggc att caa tcc 643
Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln Ile Gly Ile Gln Ser
                        170                        175                        180

gcc caa att aag gcg att gaa aac gac cac cac tgg cac gaa ggc aac 691
Ala Gln Ile Lys Ala Ile Glu Asn Asp His His Trp His Glu Gly Asn
                        185                        190                        195

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85					90					95					
Gly	Pro	Gly	Ser	Met	His	Pro	Asp	Gly	Asn	Phe	Trp	Gly	Asn	Arg	Phe
			100					105					110		
Pro	Ala	Thr	Ser	Ile	Arg	Asp	Gln	Val	Asn	Ala	Glu	Lys	Gln	Phe	Leu
		115					120					125			
Asp	Ala	Leu	Gly	Ile	Thr	Thr	Val	Ala	Ala	Val	Leu	Gly	Gly	Ser	Met
		130				135					140				
Gly	Gly	Ala	Arg	Thr	Leu	Glu	Trp	Ala	Ala	Met	Tyr	Pro	Glu	Thr	Val
145					150					155					160
Gly	Ala	Ala	Ala	Val	Leu	Ala	Val	Ser	Ala	Arg	Ala	Ser	Ala	Trp	Gln
				165					170					175	
Ile	Gly	Ile	Gln	Ser	Ala	Gln	Ile	Lys	Ala	Ile	Glu	Asn	Asp	His	His
			180					185					190		
Trp	His	Glu	Gly	Asn	Tyr	Tyr	Glu	Ser	Gly	Cys	Asn	Pro	Ala	Thr	Gly
		195					200					205			
Leu	Gly	Ala	Ala	Arg	Arg	Ile	Ala	His	Leu	Thr	Tyr	Arg	Gly	Glu	Leu
	210					215					220				
Glu	Ile	Asp	Glu	Arg	Phe	Gly	Thr	Lys	Ala	Gln	Lys	Asn	Glu	Asn	Pro
225					230					235					240
Leu	Gly	Pro	Tyr	Arg	Lys	Pro	Asp	Gln	Arg	Phe	Ala	Val	Glu	Ser	Tyr
				245					250					255	
Leu	Asp	Tyr	Gln	Ala	Asp	Lys	Leu	Val	Gln	Arg	Phe	Asp	Ala	Gly	Ser
			260					265					270		
Tyr	Val	Leu	Leu	Thr	Asp	Ala	Leu	Asn	Arg	His	Asp	Ile	Gly	Arg	Asp
		275					280					285			
Arg	Gly	Gly	Leu	Asn	Lys	Ala	Leu	Glu	Ser	Ile	Lys	Val	Pro	Val	Leu
	290					295					300				
Val	Ala	Gly	Val	Asp	Thr	Asp	Ile	Leu	Tyr	Pro	Tyr	His	Gln	Gln	Glu
305					310					315					320
His	Leu	Ser	Arg	Asn	Leu	Gly	Asn	Leu	Leu	Ala	Met	Ala	Lys	Ile	Val
				325				330						335	
Ser	Pro	Val	Gly	His	Asp	Ala	Phe	Leu	Thr	Glu	Ser	Arg	Gln	Met	Asp
			340					345					350		
Arg	Ile	Val	Arg	Asn	Phe	Phe	Ser	Leu	Ile	Ser	Pro	Asp	Glu	Asp	Asn
		355					360					365			
Pro	Ser	Thr	Tyr	Ile	Glu	Phe	Tyr	Ile							
		370				375									

&lt;210&gt; 189

&lt;211&gt; 1210

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

ggc gat ggc cct gag tcc cgc tac cag cgc atc atg aaa ctg gta aag  
1555

Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile Met Lys Leu Val Lys  
470 475 480 485

cag cac ggt gcg gcc gtg gtt gcg ctg acc att gat gag gaa ggc cag  
1603

Gln His Gly Ala Ala Val Val Ala Leu Thr Ile Asp Glu Glu Gly Gln  
490 495 500

gca cgt acc gct gag cac aag gtg cgc att gct aaa cga ctg att gac  
1651

Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala Lys Arg Leu Ile Asp  
505 510 515

gat atc acc ggc agc tac ggc ctg gat atc aaa gac atc gtt gtg gac  
1699

Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys Asp Ile Val Val Asp  
520 525 530

tgc ctg acc ttc ccg atc tct act ggc cag gaa gaa acc agg cga gat  
1747

Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu Glu Thr Arg Arg Asp  
535 540 545

ggc att gaa acc atc gaa gcc atc cgc gag ctg aag aag ctc tac cca  
1795

Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu Lys Lys Leu Tyr Pro  
550 555 560 565

gaa atc cac acc acc ctg ggt ctg tcc aat att tcc ttc ggc ctg aac  
1843

Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile Ser Phe Gly Leu Asn  
570 575 580

cct gct gca cgc cag gtt ctt aac tct gtg ttc ctc aat gag tgc att  
1891

Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe Leu Asn Glu Cys Ile  
585 590 595

gag gct ggt ctg gac tct gcg att gcg cac agc tcc aag att ttg ccg  
1939

Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser Ser Lys Ile Leu Pro  
600 605 610

atg aac cgc att gat gat cgc cag cgc gaa gtg gcg ttg gat atg gtc  
1987

Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val Ala Leu Asp Met Val  
615 620 625

tat gat cgc cgc acc gag gat tac gat ccg ctg cag gaa ttc atg cag  
2035

Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu Gln Glu Phe Met Gln  
630 635 640 645

ctg ttt gag ggc gtt tct gct gcc gat gcc aag gat gct cgc gct gaa  
2083

Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys Asp Ala Arg Ala Glu  
650 655 660

gaa tac cca ctt gag gct gag gat ttg gcg cag gcg ctg gct gga ttc 979  
 Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln Ala Leu Ala Gly Phe  
 280 285 290

gtc tcc gaa tat ggc ctg tcc atg gtg ggt ggt tgt tgt ggc acc aca  
 1027  
 Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly Cys Cys Gly Thr Thr  
 295 300 305

cct gag cac atc cgt gcg gtc cgc gat gcg gtg gtt ggt gtt cca gag  
 1075  
 Pro Glu His Ile Arg Ala Val Arg Asp Ala Val Val Gly Val Pro Glu  
 310 315 320 325

cag gaa acc tcc aca ctg acc aag atc cct gca ggc cct gtt gag cag  
 1123  
 Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala Gly Pro Val Glu Gln  
 330 335 340

gcc tcc cgc gag gtg gag aaa gag gac tcc gtc gcg tcg ctg tac acc  
 1171  
 Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val Ala Ser Leu Tyr Thr  
 345 350 355

tcg gtg cca ttg tcc cag gaa acc ggc att tcc atg atc ggt gag cgc  
 1219  
 Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser Met Ile Gly Glu Arg  
 360 365 370

acc aac tcc aac ggt tcc aag gca ttc cgt gag gca atg ctg tct ggc  
 1267  
 Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu Ala Met Leu Ser Gly  
 375 380 385

gat tgg gaa aag tgt gtg gat att gcc aag cag caa acc cgc gat ggt  
 1315  
 Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln Gln Thr Arg Asp Gly  
 390 395 400 405

gca cac atg ctg gat ctt tgt gtg gat tac gtg gga cga gac ggc acc  
 1363  
 Ala His Met Leu Asp Leu Cys Val Asp Tyr Val Gly Arg Asp Gly Thr  
 410 415 420

gcc gat atg gcg acc ttg gca gca ctt ctt gct acc agc tcc act ttg  
 1411  
 Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala Thr Ser Ser Thr Leu  
 425 430 435

cca atc atg att gac tcc acc gag cca gag gtt att cgc aca ggc ctt  
 1459  
 Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val Ile Arg Thr Gly Leu  
 440 445 450

gag cac ttg ggt gga cga agc atc gtt aac tcc gtc aac ttt gaa gac  
 1507  
 Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser Val Asn Phe Glu Asp  
 455 460 465



25	30	35	
caa ggc ttt gac ctg gac gtg gaa aag gat ttc ctt gat ctg gag ggg Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe Leu Asp Leu Glu Gly 40 45 50			259
tgt aat gag att ctc aac gac acc cgc cct gat gtg ttg agg cag att Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp Val Leu Arg Gln Ile 55 60 65			307
cac cgc gcc tac ttt gag gcg gga gct gac ttg gtt gag acc aat act His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu Val Glu Thr Asn Thr 70 75 80 85			355
ttt ggt tgc aac ctg ccg aac ttg gcg gat tat gac atc gct gat cgt Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr Asp Ile Ala Asp Arg 90 95 100			403
tgc cgt gag ctt gcc tac aag ggc act gca gtg gct agg gaa gtg gct Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val Ala Arg Glu Val Ala 105 110 115			451
gat gag atg ggg ccg ggc cga aac ggc atg cgg cgt ttc gtg gtt ggt Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg Arg Phe Val Val Gly 120 125 130			499
tcc ctg gga cct gga acg aag ctt cca tcg ctg ggc cat gca ccg tat Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu Gly His Ala Pro Tyr 135 140 145			547
gca gat ttg cgt ggg cac tac aag gaa gca gcg ctt ggc atc atc gac Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala Leu Gly Ile Ile Asp 150 155 160 165			595
ggg ggt ggc gat gcc ttt ttg att gag act gct cag gac ttg ctt cag Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala Gln Asp Leu Leu Gln 170 175 180			643
gtc aag gct gcg gtt cac ggc gtt caa gat gcc atg gct gaa ctt gat Val Lys Ala Ala Val His Gly Val Gln Asp Ala Met Ala Glu Leu Asp 185 190 195			691
aca ttc ttg ccc att att tgc cac gtc acc gta gag acc acc ggc acc Thr Phe Leu Pro Ile Ile Cys His Val Thr Val Glu Thr Thr Gly Thr 200 205 210			739
atg ctc atg ggt tct gag atc ggt gcc gcg ttg aca gcg ctg cag cca Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu Thr Ala Leu Gln Pro 215 220 225			787
ctg ggt atc gac atg att ggt ctg aac tgc gcc acc ggc cca gat gag Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala Thr Gly Pro Asp Glu 230 235 240 245			835
atg agc gag cac ctg cgt tac ctg tcc aag cac gcc gat att cct gtg Met Ser Glu His Leu Arg Tyr Leu Ser Lys His Ala Asp Ile Pro Val 250 255 260			883
tcg gtg atg cct aac gca ggt ctt cct gtc ctg ggt aaa aac ggt gca Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu Gly Lys Asn Gly Ala 265 270 275			931

&lt;400&gt; 210

Ala Glu Arg Met Arg Phe Ser Phe Pro Arg Gln Gln Arg Gly Arg Phe  
 1 5 10 15

Leu Cys Ile Ala Asp Phe Ile Arg Pro Arg Glu Gln Ala Val Lys Asp  
 20 25 30

Gly Gln Val Asp Val Met Pro Phe Gln Leu Val Thr Met Gly Asn Pro  
 35 40 45

Ile Ala Asp Phe Ala Asn Glu Leu Phe Ala Ala Asn Glu Tyr Arg Glu  
 50 55 60

Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala  
 65 70 75 80

Glu Tyr Trp His Ser Arg Val Arg Ser Glu Leu Lys Leu Asn Asp Gly  
 85 90 95

Gly Ser Val Ala Asp Phe Asp Pro Glu Asp Lys Thr Lys Phe Phe Asp  
 100 105 110

Leu Asp Tyr Arg Gly Ala Arg Phe Ser Phe Gly Tyr Gly Ser Cys Pro  
 115 120 125

Asp Leu Glu Asp Arg Ala Lys Leu Val Glu Leu Leu Glu Pro Gly Arg  
 130 135 140

Ile Gly Val Glu Leu Ser Glu Glu Leu Gln Leu His Pro Glu Gln Ser  
 145 150 155 160

Thr Asp Ala Phe Val Leu Tyr His Pro Glu Ala Lys Tyr Phe Asn Val  
 165 170 175

&lt;210&gt; 211

&lt;211&gt; 2599

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(2599)

&lt;223&gt; RXN02198

&lt;400&gt; 211

agactagtgg cgctttgcct gtgttgctta ggcggcggtg aaaatgaact acgaatgaaa 60

agttcgggaa ttgtctaatac cgtactaagc tgtctacaca atg tct act tca gtt 115  
 Met Ser Thr Ser Val  
 1 5

act tca cca gcc cac aac aac gca cat tcc tcc gaa ttt ttg gat gcg 163  
 Thr Ser Pro Ala His Asn Asn Ala His Ser Ser Glu Phe Leu Asp Ala  
 10 15 20

ttg gca aac cat gtg ttg atc ggc gac ggc gcc atg ggc acc cag ctc 211  
 Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala Met Gly Thr Gln Leu

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(528)

&lt;223&gt; RXA02197

&lt;400&gt; 209

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gcc gaa cgc atg cgc ttt agc ttc cca cgc cag cag cgc ggc agg ttc   48
Ala Glu Arg Met Arg Phe Ser Phe Pro Arg Gln Gln Arg Gly Arg Phe
   1             5             10             15

ttg tgc atc gcg gat ttc att cgc cca cgc gag caa gct gtc aag gac   96
Leu Cys Ile Ala Asp Phe Ile Arg Pro Arg Glu Gln Ala Val Lys Asp
           20           25           30

ggc caa gtg gac gtc atg cca ttc cag ctg gtc acc atg ggt aat cct  144
Gly Gln Val Asp Val Met Pro Phe Gln Leu Val Thr Met Gly Asn Pro
       35           40           45

att gct gat ttc gcc aac gag ttg ttc gca gcc aat gaa tac cgc gag  192
Ile Ala Asp Phe Ala Asn Glu Leu Phe Ala Ala Asn Glu Tyr Arg Glu
   50           55           60

tac ttg gaa gtt cac ggc atc ggc gtg cag ctc acc gaa gca ttg gcc  240
Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala
   65           70           75           80

gag tac tgg cac tcc cga gtg cgc agc gaa ctc aag ctg aac gac ggt  288
Glu Tyr Trp His Ser Arg Val Arg Ser Glu Leu Lys Leu Asn Asp Gly
           85           90           95

gga tct gtc gct gat ttt gat cca gaa gac aag acc aag ttc ttc gac  336
Gly Ser Val Ala Asp Phe Asp Pro Glu Asp Lys Thr Lys Phe Phe Asp
       100           105           110

ctg gat tac cgc ggc gcc cgc ttc tcc ttt ggt tac ggt tct tgc cct  384
Leu Asp Tyr Arg Gly Ala Arg Phe Ser Phe Gly Tyr Gly Ser Cys Pro
       115           120           125

gat ctg gaa gac cgc gca aag ctg gtg gaa ttg ctc gag cca ggc cgt  432
Asp Leu Glu Asp Arg Ala Lys Leu Val Glu Leu Glu Glu Pro Gly Arg
       130           135           140

atc ggc gtg gag ttg tcc gag gaa ctc cag ctg cac cca gag cag tcc  480
Ile Gly Val Glu Leu Ser Glu Glu Leu Gln Leu His Pro Glu Gln Ser
       145           150           155           160

aca gac gcg ttt gtg ctc tac cac cca gag gca aag tac ttt aac gtc  528
Thr Asp Ala Phe Val Leu Tyr His Pro Glu Ala Lys Tyr Phe Asn Val
           165           170           175

taacaccttt gagaggaaa act                                     551

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&lt;210&gt; 210

&lt;211&gt; 176

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

105	110	115	
tac ggt ggc acc gag act cta ttc ctt atc act ctt aac cgc ctg ggt			499
Tyr Gly Gly Thr Glu Thr Leu Phe Leu Ile Thr Leu Asn Arg Leu Gly			
120	125	130	
atc gat gtt tcc ttc gtg gaa aac ccc gac gac cct gag tcc tgg cag			547
Ile Asp Val Ser Phe Val Glu Asn Pro Asp Asp Pro Glu Ser Trp Gln			
135	140	145	
gca gcc gtt cag cca aac acc aaa gca ttc ttc ggc gag act ttc gcc			595
Ala Ala Val Gln Pro Asn Thr Lys Ala Phe Gly Glu Thr Phe Ala			
150	155	160	165
aac cca cag gca gac gtc			613
Asn Pro Gln Ala Asp Val			
170			
<210> 208			
<211> 171			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 208			
Met Pro Lys Tyr Asp Asn Ser Asn Ala Asp Gln Trp Gly Phe Glu Thr			
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Arg Ser Ile His Ala Gly Gln Ser Val Asp Ala Gln Thr Ser Ala Arg			
20	25	30	
Asn Leu Pro Ile Tyr Gln Ser Thr Ala Phe Val Phe Asp Ser Ala Glu			
35	40	45	
His Ala Lys Gln Arg Phe Ala Leu Glu Asp Leu Gly Pro Val Tyr Ser			
50	55	60	
Arg Leu Thr Asn Pro Thr Val Glu Ala Leu Glu Asn Arg Ile Ala Ser			
65	70	75	80
Leu Glu Gly Gly Val His Ala Val Ala Phe Ser Ser Gly Gln Ala Ala			
85	90	95	
Thr Thr Asn Ala Ile Leu Asn Leu Ala Gly Ala Gly Asp His Ile Val			
100	105	110	
Thr Ser Pro Arg Leu Tyr Gly Gly Thr Glu Thr Leu Phe Leu Ile Thr			
115	120	125	
Leu Asn Arg Leu Gly Ile Asp Val Ser Phe Val Glu Asn Pro Asp Asp			
130	135	140	
Pro Glu Ser Trp Gln Ala Ala Val Gln Pro Asn Thr Lys Ala Phe Phe			
145	150	155	160
Gly Glu Thr Phe Ala Asn Pro Gln Ala Asp Val			
165	170		

<210> 209  
 <211> 551

115	120	125
Leu His Ser Asn Leu Ala Asn Ile Gly Asp Val Arg Ser Leu Val Val		
130	135	140
His Pro Ala Thr Thr Thr His Ser Gln Ser Asp Glu Ala Gly Leu Ala		
145	150	155
Arg Ala Gly Val Thr Gln Ser Thr Val Arg Leu Ser Val Gly Ile Glu		
	165	170
		175
Thr Ile Asp Asp Ile Ile Ala Asp Leu Glu Gly Gly Phe Ala Ala Ile		
	180	185
		190

<210> 207  
 <211> 613  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(613)  
 <223> RXA00405

<400> 207  
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ggagaagaat ttcctaataa aaactcttaa ggacctccaa atg cca aag tac gac 115  
 Met Pro Lys Tyr Asp  
 1 5

aat tcc aat gct gac cag tgg ggc ttt gaa acc cgc tcc att cac gca 163  
 Asn Ser Asn Ala Asp Gln Trp Gly Phe Glu Thr Arg Ser Ile His Ala  
 10 15 20

ggc cag tca gta gac gca cag acc agc gca cga aac ctt ccg atc tac 211  
 Gly Gln Ser Val Asp Ala Gln Thr Ser Ala Arg Asn Leu Pro Ile Tyr  
 25 30 35

caa tcc acc gct ttc gtg ttc gac tcc gct gag cac gcc aag cag cgt 259  
 Gln Ser Thr Ala Phe Val Phe Asp Ser Ala Glu His Ala Lys Gln Arg  
 40 45 50

ttc gca ctt gag gat cta ggc cct gtt tac tcc cgc ctc acc aac cca 307  
 Phe Ala Leu Glu Asp Leu Gly Pro Val Tyr Ser Arg Leu Thr Asn Pro  
 55 60 65

acc gtt gag gct ttg gaa aac cgc atc gct tcc ctc gaa ggt ggc gtc 355  
 Thr Val Glu Ala Leu Glu Asn Arg Ile Ala Ser Leu Glu Gly Gly Val  
 70 75 80 85

cac gct gta gcg ttc tcc tcc gga cag gcc gca acc acc aac gcc att 403  
 His Ala Val Ala Phe Ser Ser Gly Gln Ala Ala Thr Thr Asn Ala Ile  
 90 95 100

ttg aac ctg gca gga gcg ggc gac cac atc gtc acc tcc cca cgc ctc 451  
 Leu Asn Leu Ala Gly Ala Gly Asp His Ile Val Thr Ser Pro Arg Leu

65	70	75	80	
gaa aag gtt aac ttc gca ggc ctg aag gat tcc cct tgg tac gca acc				288
Glu Lys Val Asn Phe Ala Gly Leu Lys Asp Ser Pro Trp Tyr Ala Thr	85	90	95	
aag gaa aag ctt ggc ctg aag tac acc ggc tcc gtt ctc acc ttc gag				336
Lys Glu Lys Leu Gly Leu Lys Tyr Thr Gly Ser Val Leu Thr Phe Glu	100	105	110	
atc aag ggc ggc aag gat gag gct tgg gca ttt atc gac gcc ctg aag				384
Ile Lys Gly Gly Lys Asp Glu Ala Trp Ala Phe Ile Asp Ala Leu Lys	115	120	125	
cta cac tcc aac ctt gca aac atc ggc gat gtt cgc tcc ctc gtt gtt				432
Leu His Ser Asn Leu Ala Asn Ile Gly Asp Val Arg Ser Leu Val Val	130	135	140	
cac cca gca acc acc acc cat tca cag tcc gac gaa gct ggc ctg gca				480
His Pro Ala Thr Thr Thr His Ser Gln Ser Asp Glu Ala Gly Leu Ala	145	150	155	160
cgc gcg ggc gtt acc cag tcc acc gtc cgc ctg tcc gtt ggc atc gag				528
Arg Ala Gly Val Thr Gln Ser Thr Val Arg Leu Ser Val Gly Ile Glu	165	170	175	
acc att gat gat atc atc gct gac ctc gaa ggc ggc ttt gct gca atc				576
Thr Ile Asp Asp Ile Ile Ala Asp Leu Glu Gly Gly Phe Ala Ala Ile	180	185	190	
tagctttaaa tagactcacc cca				599
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<212> PRT				
<213> Corynebacterium glutamicum				
<400> 206				
Val Leu Pro Tyr Phe Val Thr Pro Asp Ala Ala Tyr His Gly Leu Lys	1	5	10	15
Tyr Ala Asp Leu Gly Ala Pro Ala Phe Gly Leu Lys Val Arg Val Gly	20	25	30	
Leu Leu Arg Asp Thr Gly Ser Thr Leu Ser Ala Phe Asn Ala Trp Ala	35	40	45	
Ala Val Gln Gly Ile Asp Thr Leu Ser Leu Arg Leu Glu Arg His Asn	50	55	60	
Glu Asn Ala Ile Lys Val Ala Glu Phe Leu Asn Asn His Glu Lys Val	65	70	75	80
Glu Lys Val Asn Phe Ala Gly Leu Lys Asp Ser Pro Trp Tyr Ala Thr	85	90	95	
Lys Glu Lys Leu Gly Leu Lys Tyr Thr Gly Ser Val Leu Thr Phe Glu	100	105	110	
Ile Lys Gly Gly Lys Asp Glu Ala Trp Ala Phe Ile Asp Ala Leu Lys				

Leu Ser Ala Phe Asn Ala Trp Ala Ala Val Gln Gly Ile Asp Thr Leu  
 50 55 60  
 Ser Leu Arg Leu Glu Arg His Asn Glu Asn Ala Ile Lys Val Ala Glu  
 65 70 75 80  
 Phe Leu Asn Asn His Glu Lys Val Glu Lys Val Asn Phe Ala Gly Leu  
 85 90 95  
 Lys Asp Ser Pro Trp Tyr Ala Thr Lys Glu Lys Leu Gly Leu Lys Tyr  
 100 105 110  
 Thr Gly Ser Val Leu Thr Phe Glu Ile Lys Gly Gly Lys Asp Glu Ala  
 115 120 125  
 Trp Ala Phe Ile Asp Ala Leu Lys Leu His Ser Asn Leu Ala Asn Ile  
 130 135 140  
 Gly Asp Val Arg Ser Leu Val Val His Pro Ala Thr Thr Thr His Ser  
 145 150 155 160  
 Gln Ser Asp Glu Ala Gly Leu Ala Arg Ala Gly Val Thr Gln Ser Thr  
 165 170 175  
 Val Arg Leu Ser Val Gly Ile Glu Thr Ile Asp Asp Ile Ile Ala Asp  
 180 185 190  
 Leu Glu Gly Gly Phe Ala Ala Ile  
 195 200

&lt;210&gt; 205

&lt;211&gt; 599

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(576)

&lt;223&gt; FRXA00402

&lt;400&gt; 205

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 Val Leu Pro Tyr Phe Val Thr Pro Asp Ala Ala Tyr His Gly Leu Lys  
 1 5 10 15  
 tac gca gac ctt ggt gca cca gcc ttc ggc ctc aag gtt cgc gtt ggc 96  
 Tyr Ala Asp Leu Gly Ala Pro Ala Phe Gly Leu Lys Val Arg Val Gly  
 20 25 30  
 ctt cta cgc gac acc ggc tcc acc ctc tcc gca ttc aac gca tgg gct 144  
 Leu Leu Arg Asp Thr Gly Ser Thr Leu Ser Ala Phe Asn Ala Trp Ala  
 35 40 45  
 gca gtc cag ggc atc gac acc ctt tcc ctg cgc ctg gag cgc cac aac 192  
 Ala Val Gln Gly Ile Asp Thr Leu Ser Leu Arg Leu Glu Arg His Asn  
 50 55 60  
 gaa aac gcc atc aag gtt gca gaa ttc ctc aac aac cac gag aag gtg 240  
 Glu Asn Ala Ile Lys Val Ala Glu Phe Leu Asn Asn His Glu Lys Val

20	25	30	
ttc ggc ctc aag gtt cgc gtt ggc ctt cta cgc gac acc ggc tcc acc Phe Gly Leu Lys Val Arg Val Gly Leu Leu Arg Asp Thr Gly Ser Thr 35 40 45			144
ctc tcc gca ttc aac gca tgg gct gca gtc cag ggc atc gac acc ctt Leu Ser Ala Phe Asn Ala Trp Ala Ala Val Gln Gly Ile Asp Thr Leu 50 55 60			192
tcc ctg cgc ctg gag cgc cac aac gaa aac gcc atc aag gtt gca gaa Ser Leu Arg Leu Glu Arg His Asn Glu Asn Ala Ile Lys Val Ala Glu 65 70 75 80			240
ttc ctc aac aac cac gag aag gtg gaa aag gtt aac ttc gca ggc ctg Phe Leu Asn Asn His Glu Lys Val Glu Lys Val Asn Phe Ala Gly Leu 85 90 95			288
aag gat tcc cct tgg tac gca acc aag gaa aag ctt ggc ctg aag tac Lys Asp Ser Pro Trp Tyr Ala Thr Lys Glu Lys Leu Gly Leu Lys Tyr 100 105 110			336
acc ggc tcc gtt ctc acc ttc gag atc aag ggc ggc aag gat gag gct Thr Gly Ser Val Leu Thr Phe Glu Ile Lys Gly Gly Lys Asp Glu Ala 115 120 125			384
tgg gca ttt atc gac gcc ctg aag cta cac tcc aac ctt gca aac atc Trp Ala Phe Ile Asp Ala Leu Lys Leu His Ser Asn Leu Ala Asn Ile 130 135 140			432
ggc gat gtt cgc tcc ctc gtt gtt cac cca gca acc acc acc cat tca Gly Asp Val Arg Ser Leu Val Val His Pro Ala Thr Thr Thr His Ser 145 150 155 160			480
cag tcc gac gaa gct ggc ctg gca cgc gcg ggc gtt acc cag tcc acc Gln Ser Asp Glu Ala Gly Leu Ala Arg Ala Gly Val Thr Gln Ser Thr 165 170 175			528
gtc cgc ctg tcc gtt ggc atc gag acc att gat gat atc atc gct gac Val Arg Leu Ser Val Gly Ile Glu Thr Ile Asp Asp Ile Ile Ala Asp 180 185 190			576
ctc gaa ggc ggc ttt gct gca atc tagctttaaa tagactcacc cca Leu Glu Gly Gly Phe Ala Ala Ile 195 200			623
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Asp Ala Ala Tyr His Gly Leu Lys Tyr Ala Asp Leu Gly Ala Pro Ala 20 25 30			
Phe Gly Leu Lys Val Arg Val Gly Leu Leu Arg Asp Thr Gly Ser Thr 35 40 45			



Glu Leu Ala Asn Gly His Arg Val Leu Ser Asp Arg Gly Ala Met Arg  
 115 120 125  
 Asp Leu Thr Gln Ala Leu Ile Ala Gly Ile Asp Ala His Ala Arg Lys  
 130 135 140  
 Val Ala Gly Arg Phe Arg Ala Glu Val Gln Val Gln Ile Asp Glu Pro  
 145 150 155 160  
 Glu Leu Lys Ser Leu Ile Asp Gly Ser Leu Pro Gly Thr Ser Thr Phe  
 165 170 175  
 Asp Ile Ile Pro Ala Val Asn Val Ala Asp Ala Ser Glu Arg Leu Gln  
 180 185 190  
 Gln Val Phe Ser Ser Ile Glu Gly Pro Thr Tyr Leu Asn Leu Thr Gly  
 195 200 205  
 Gln Ile Pro Thr Trp Asp Val Ala Arg Gly Ala Gly Ala Asp Thr Val  
 210 215 220  
 Gln Ile Ser Met Asp Gln Val Arg Gly Asn Glu His Leu Asp Gly Phe  
 225 230 235 240  
 Gly Glu Thr Ile Thr Ser Gly Ile Arg Leu Gly Leu Gly Ile Thr Thr  
 245 250 255  
 Gly Lys Asp Val Val Asp Glu Leu Leu Glu Arg Pro Arg Gln Lys Ala  
 260 265 270  
 Val Glu Val Ala Arg Phe Phe Asp Arg Leu Gly Val Gly Arg Asn Tyr  
 275 280 285  
 Leu Val Asp Ala Val Asp Ile His Pro Gly Glu Asp Leu Val Gln Gly  
 290 295 300  
 Thr Ile Thr Glu Ala Ala Gln Ala Tyr Arg Met Ala Arg Val Met Ser  
 305 310 315 320  
 Glu Met Leu Ser Lys Asp Ser Cys Asp Leu  
 325 330

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 <213> Corynebacterium glutamicum

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 <222> (1)..(600)  
 <223> RXN00402

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 gat gct gct tac cac gga ttg aag tac gca gac ctt ggt gca cca gcc 96  
 Asp Ala Ala Tyr His Gly Leu Lys Tyr Ala Asp Leu Gly Ala Pro Ala

Asp Val Ala Arg Gly Ala Gly Ala Asp Thr Val Gln Ile Ser Met Asp  
 215 220 225  
 caa gtc cgt gga aat gaa cat ttg gat ggt ttt ggt gaa acc atc acc 835  
 Gln Val Arg Gly Asn Glu His Leu Asp Gly Phe Gly Glu Thr Ile Thr  
 230 235 240 245  
 agt gga att cgt ctt ggt ttg ggc att acg aca gga aaa gat gtc gta 883  
 Ser Gly Ile Arg Leu Gly Leu Gly Ile Thr Thr Gly Lys Asp Val Val  
 250 255 260  
 gat gaa ctg ctc gag cga ccg cgg caa aag gcc gtt gag gta gca cgc 931  
 Asp Glu Leu Leu Glu Arg Pro Arg Gln Lys Ala Val Glu Val Ala Arg  
 265 270 275  
 ttt ttt gat cgt tta ggt gtg ggc cga aac tat ctc gtg gat gct gtt 979  
 Phe Phe Asp Arg Leu Gly Val Gly Arg Asn Tyr Leu Val Asp Ala Val  
 280 285 290  
 gat att cat ccg ggt gag gat ttg gtg cag ggg acc atc acc gag gcc  
 1027  
 Asp Ile His Pro Gly Glu Asp Leu Val Gln Gly Thr Ile Thr Glu Ala  
 295 300 305  
 gcg cag gct tat cgc atg gcc cgg gtg atg tcg gag atg ttg tcg aag  
 1075  
 Ala Gln Ala Tyr Arg Met Ala Arg Val Met Ser Glu Met Leu Ser Lys  
 310 315 320 325  
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 1113  
 Asp Ser Cys Asp Leu  
 330

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 <213> Corynebacterium glutamicum

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 Gln Leu Pro Ala Arg Gly Leu Gly Ala Asp Leu Ile Gly Arg Thr Val  
 35 40 45  
 Gly Leu Leu Asp Met Ile Asn Val Asp Arg Gly Ala Arg Ser Trp Val  
 50 55 60  
 Met Ser Thr Arg Pro Ser Arg Leu Thr His Leu Thr Gly Asp Phe Leu  
 65 70 75 80  
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 85 90 95  
 Lys Leu Lys Ile Gln Val Ala Gly Pro Trp Thr Leu Gly Ala Arg Ile  
 100 105 110

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 Leu Gly Ala Tyr Gly  
 1 5

tta ggt gag ctt cct gga aaa tcc gcc gcg gaa gcc gcc gac att att 163  
 Leu Gly Glu Leu Pro Gly Lys Ser Ala Ala Glu Ala Ala Asp Ile Ile  
 10 15 20

cag ggt gaa acg ggc gat ctt ctc cat att cct cag ctt ccg gcg cga 211  
 Gln Gly Glu Thr Gly Asp Leu Leu His Ile Pro Gln Leu Pro Ala Arg  
 25 30 35

ggg ttg ggt gct gat ctg atc ggt cga acc gtc ggt ctg ctg gac atg 259  
 Gly Leu Gly Ala Asp Leu Ile Gly Arg Thr Val Gly Leu Leu Asp Met  
 40 45 50

atc aac gtt gat cgc ggg gcc cga tct tgg gtg atg agc aca cgc ccc 307  
 Ile Asn Val Asp Arg Gly Ala Arg Ser Trp Val Met Ser Thr Arg Pro  
 55 60 65

agc aga ttg acg cac ctg acc ggc gat ttc ctt gac atg gat ttg gat 355  
 Ser Arg Leu Thr His Leu Thr Gly Asp Phe Leu Asp Met Asp Leu Asp  
 70 75 80 85

gcg tgc gag gaa acc tgg gga acg ggc gtc gac aag cta aaa atc caa 403  
 Ala Cys Glu Glu Thr Trp Gly Thr Gly Val Asp Lys Leu Lys Ile Gln  
 90 95 100

gtt gct ggt ccc tgg act tta ggt gcg cgc att gag ttg gcc aat ggc 451  
 Val Ala Gly Pro Trp Thr Leu Gly Ala Arg Ile Glu Leu Ala Asn Gly  
 105 110 115

cat cgc gtt ttg tct gat cgc ggt gcg atg cgt gat ctc acg cag gcg 499  
 His Arg Val Leu Ser Asp Arg Gly Ala Met Arg Asp Leu Thr Gln Ala  
 120 125 130

ctg atc gcc ggc atc gat gcg cat gca cgc aag gtt gct ggg cga ttt 547  
 Leu Ile Ala Gly Ile Asp Ala His Ala Arg Lys Val Ala Gly Arg Phe  
 135 140 145

cgc gcc gaa gtg cag gtg caa att gat gag ccg gag ctg aaa tcg ctt 595  
 Arg Ala Glu Val Gln Val Gln Ile Asp Glu Pro Glu Leu Lys Ser Leu  
 150 155 160 165

atc gac ggc tcc ctc cct ggc act tcc acc ttt gac att att cct gcg 643  
 Ile Asp Gly Ser Leu Pro Gly Thr Ser Thr Phe Asp Ile Ile Pro Ala  
 170 175 180

gtg aat gtc gct gat gcc agt gaa cgt ttg cag cag gtc ttt agc tcg 691  
 Val Asn Val Ala Asp Ala Ser Glu Arg Leu Gln Gln Val Phe Ser Ser  
 185 190 195

att gag ggg ccg aca tat ctc aac ctc acc ggc cag att cct act tgg 739  
 Ile Glu Gly Pro Thr Tyr Leu Asn Leu Thr Gly Gln Ile Pro Thr Trp  
 200 205 210

gat gtg gct cgg ggt gcg ggc gcc gat act gtg cag att tcc atg gat 787

gng cac acg cag  
Xaa His Thr Gln  
200

703

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Ala Gly Tyr Glu Pro Asp Asp Tyr Tyr Gly Ser Ile Asn Thr Pro Ile  
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Tyr Ala Ser Thr Thr Phe Ala Gln Asn Ala Pro Asn Glu Leu Arg Lys  
35 40 45  
Gly Tyr Glu Tyr Thr Arg Val Gly Asn Pro Thr Ile Val Ala Leu Glu  
50 55 60  
Gln Thr Val Ala Ala Leu Glu Gly Ala Lys Tyr Gly Arg Ala Phe Ser  
65 70 75 80  
Ser Gly Met Ala Ala Thr Asp Ile Leu Phe Arg Ile Ile Leu Lys Pro  
85 90 95  
Gly Asp His Ile Val Leu Gly Asn Asp Ala Tyr Gly Gly Thr Tyr Arg  
100 105 110  
Leu Ile Asp Thr Val Phe Thr Ala Trp Gly Val Glu Tyr Thr Val Val  
115 120 125  
Asp Thr Ser Val Val Glu Glu Val Lys Ala Ala Ile Lys Asp Asn Thr  
130 135 140  
Lys Ala Asp Leu Gly Gly Asn Pro Asn Gln Pro Ser Thr Leu Ala Leu  
145 150 155 160  
Pro Asp Ile Glu Ala Val Cys Lys Thr Ser Pro Glu Arg His Gln Pro  
165 170 175  
Gln Ala Cys Cys Leu Thr Thr Pro Ser His Ser Pro Tyr Leu Gln Xaa  
180 185 190  
Pro Leu Lys Xaa Xaa Xaa His Thr Gln  
195 200

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<220>  
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&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(703)

&lt;223&gt; FRXA02768

&lt;400&gt; 199

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tttagggcca tagaattctg attacaggag ttgatctacc ttg tct ttt gac cca 115
                                         Leu Ser Phe Asp Pro
                                         1           5

aac acc cag ggt ttc tcc act gca tgc att cac gct ggg tat gag cca 163
Asn Thr Gln Gly Phe Ser Thr Ala Ser Ile His Ala Gly Tyr Glu Pro
                        10                        15                        20

gac gac tac tac ggt tgc att aac acc cca atc tat gcc tcc acc acc 211
Asp Asp Tyr Tyr Gly Ser Ile Asn Thr Pro Ile Tyr Ala Ser Thr Thr
                        25                        30                        35

ttc gcg cag aac gct cca aac gaa ctg cgc aaa ggc tac gag tac acc 259
Phe Ala Gln Asn Ala Pro Asn Glu Leu Arg Lys Gly Tyr Glu Tyr Thr
                        40                        45                        50

cgt gtg ggc aac ccc acc atc gtg gca tta gag cag acc gtc gca gca 307
Arg Val Gly Asn Pro Thr Ile Val Ala Leu Glu Gln Thr Val Ala Ala
                        55                        60                        65

ctc gaa ggc gca aag tat ggc cgc gca ttc tcc tcc ggc atg gct gca 355
Leu Glu Gly Ala Lys Tyr Gly Arg Ala Phe Ser Ser Gly Met Ala Ala
                        70                        75                        80                        85

acc gac atc ctg ttc cgc atc atc ctc aag ccg ggc gat cac atc gtc 403
Thr Asp Ile Leu Phe Arg Ile Ile Leu Lys Pro Gly Asp His Ile Val
                        90                        95                        100

ctc ggc aac gat gct tac ggc gga acc tac cgc ctg atc gac acc gta 451
Leu Gly Asn Asp Ala Tyr Gly Gly Thr Tyr Arg Leu Ile Asp Thr Val
                        105                        110                        115

ttc acc gca tgg ggc gtc gaa tac acc gtt gtt gat acc tcc gtc gtg 499
Phe Thr Ala Trp Gly Val Glu Tyr Thr Val Val Asp Thr Ser Val Val
                        120                        125                        130

gaa gag gtc aag gca gcg atc aag gac aac acc aag gct gat ctt ggt 547
Glu Glu Val Lys Ala Ala Ile Lys Asp Asn Thr Lys Ala Asp Leu Gly
                        135                        140                        145

gga aac ccc aac caa ccc agc act ttg gca tta ccc gac atc gaa gca 595
Gly Asn Pro Asn Gln Pro Ser Thr Leu Ala Leu Pro Asp Ile Glu Ala
                        150                        155                        160                        165

gtg tgc aaa act tca ccc gaa agg cac caa ccc caa gct tgt tgt ttg 643
Val Cys Lys Thr Ser Pro Glu Arg His Gln Pro Gln Ala Cys Cys Leu
                        170                        175                        180

aca aca cct tgc cat tcc cca tac ctg cag can cca ctt aaa ant tnn 691
Thr Thr Pro Ser His Ser Pro Tyr Leu Gln Xaa Pro Leu Lys Xaa Xaa
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                   20                  25                  30  
 Tyr Ala Ser Thr Thr Phe Ala Gln Asn Ala Pro Asn Glu Leu Arg Lys  
           35                  40                  45  
 Gly Tyr Glu Tyr Thr Arg Val Gly Asn Pro Thr Ile Val Ala Leu Glu  
   50                  55                  60  
 Gln Thr Val Ala Ala Leu Glu Gly Ala Lys Tyr Gly Arg Ala Phe Ser  
   65                  70                  75                  80  
 Ser Gly Met Ala Ala Thr Asp Ile Leu Phe Arg Ile Ile Leu Lys Pro  
                   85                  90                  95  
 Gly Asp His Ile Val Leu Gly Asn Asp Ala Tyr Gly Gly Thr Tyr Arg  
           100                  105                  110  
 Leu Ile Asp Thr Val Phe Thr Ala Trp Gly Val Glu Tyr Thr Val Val  
   115                  120                  125  
 Asp Thr Ser Val Val Glu Glu Val Lys Ala Ala Ile Lys Asp Asn Thr  
   130                  135                  140  
 Lys Leu Ile Trp Val Glu Thr Pro Thr Asn Pro Ala Leu Gly Ile Thr  
   145                  150                  155                  160  
 Asp Ile Glu Ala Val Ala Lys Leu Thr Glu Gly Thr Asn Ala Lys Leu  
                   165                  170                  175  
 Val Val Asp Asn Thr Leu Ala Ser Pro Tyr Leu Gln Gln Pro Leu Lys  
           180                  185                  190  
 Leu Gly Ala His Ala Ser Pro Cys Thr Pro Pro Pro Ser Thr Ser Lys  
   195                  200                  205  
 Asp Thr Pro Thr Leu Leu Ala Ala Leu Trp Val Pro Thr Thr Arg Lys  
   210                  215                  220  
 Trp Thr Lys Asn Cys Cys Ser Cys Arg Ala Ala Ser Asp Arg Ser His  
   225                  230                  235                  240  
 Gln Phe Ser Met His Thr  
                   245

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Asp Asp Tyr Tyr Gly Ser Ile Asn Thr Pro Ile Tyr Ala Ser Thr Thr	
25 30 35	
ttc gcg cag aac gct cca aac gaa ctg cgc aaa ggc tac gag tac acc	259
Phe Ala Gln Asn Ala Pro Asn Glu Leu Arg Lys Gly Tyr Glu Tyr Thr	
40 45 50	
cgt gtg ggc aac ccc acc atc gtg gca tta gag cag acc gtc gca gca	307
Arg Val Gly Asn Pro Thr Ile Val Ala Leu Glu Gln Thr Val Ala Ala	
55 60 65	
ctc gaa ggc gca aag tat ggc cgc gca ttc tcc tcc ggc atg gct gca	355
Leu Glu Gly Ala Lys Tyr Gly Arg Ala Phe Ser Ser Gly Met Ala Ala	
70 75 80 85	
acc gac atc ctg ttc cgc atc atc ctc aag ccg ggc gat cac atc gtc	403
Thr Asp Ile Leu Phe Arg Ile Ile Leu Lys Pro Gly Asp His Ile Val	
90 95 100	
ctc ggc aac gat gct tac ggc gga acc tac cgc ctg atc gac acc gta	451
Leu Gly Asn Asp Ala Tyr Gly Gly Thr Tyr Arg Leu Ile Asp Thr Val	
105 110 115	
ttc acc gca tgg ggc gtc gaa tac acc gtt gtt gat acc tcc gtc gtg	499
Phe Thr Ala Trp Gly Val Glu Tyr Thr Val Val Asp Thr Ser Val Val	
120 125 130	
gaa gag gtc aag gca gcg atc aag gac aac acc aag ctg atc tgg gtg	547
Glu Glu Val Lys Ala Ala Ile Lys Asp Asn Thr Lys Leu Ile Trp Val	
135 140 145	
gaa acc cca acc aac cca gca ctt ggc atc acc gac atc gaa gca gta	595
Glu Thr Pro Thr Asn Pro Ala Leu Gly Ile Thr Asp Ile Glu Ala Val	
150 155 160 165	
gca aag ctc acc gaa ggc acc aac gcc aag ttg gtt gtt gac aac acc	643
Ala Lys Leu Thr Glu Gly Thr Asn Ala Lys Leu Val Val Asp Asn Thr	
170 175 180	
ttg gca tcc cca tac ctg cag cag cca cta aaa ctc ggc gca cac gca	691
Leu Ala Ser Pro Tyr Leu Gln Gln Pro Leu Lys Leu Gly Ala His Ala	
185 190 195	
agt cct tgc act cca cca cca agt aca tcg aag gac act ccg acg ttg	739
Ser Pro Cys Thr Pro Pro Pro Ser Thr Ser Lys Asp Thr Pro Thr Leu	
200 205 210	
ttg gcg gcc ttg tgg gta cca acg acc agg aaa tgg acg aag aac tgc	787
Leu Ala Ala Leu Trp Val Pro Thr Thr Arg Lys Trp Thr Lys Asn Cys	
215 220 225	
tgt tca tgc agg gcg gca tcg gac cga tcc cat cag ttt tcg atg cat	835
Cys Ser Cys Arg Ala Ala Ser Asp Arg Ser His Gln Phe Ser Met His	
230 235 240 245	
acc tgaccgcccg tggcctcaag acc	861
Thr	

Ile Val Asp Gly Val Arg Gly Leu Gly Val Leu Thr Val Val Asp Ala  
 130 135 140  
 Thr Phe Ala Thr Pro Leu Arg Gln Arg Pro Leu Glu Leu Gly Ala Asp  
 145 150 155 160  
 Ile Val Leu Tyr Ser Ala Thr Lys Leu Ile Gly Gly His Ser Asp Leu  
 165 170 175  
 Leu Leu Gly Val Ala Val Cys Lys Ser Glu His His Ala Gln Phe Leu  
 180 185 190  
 Ala Thr His Arg His Asp His Gly Ser Val Pro Gly Gly Leu Glu Ala  
 195 200 205  
 Phe Leu Ala Leu Arg Gly Leu Tyr Ser Leu Ala Val Arg Leu Asp Arg  
 210 215 220  
 Ala Glu Ser Asn Ala Ala Glu Leu Ser Arg Arg Leu Asn Ala His Pro  
 225 230 235 240  
 Ser Val Thr Arg Val Asn Tyr Pro Gly Leu Pro Asp Asp Pro Gln His  
 245 250 255  
 Glu Lys Ala Val Arg Val Leu Pro Ser Gly Cys Gly Asn Met Leu Ser  
 260 265 270  
 Phe Glu Leu Asp Ala Thr Pro Glu Arg Thr Asp Glu Ile Leu Glu Ser  
 275 280 285  
 Leu Ser Leu Leu Thr His Ala Thr Ser Trp Gly Gly Val Glu Thr Ala  
 290 295 300  
 Ile Glu Arg Arg Thr Arg Arg Asp Ala Glu Val Val Ala Glu Val Pro  
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 Leu Ser Phe Asp Pro  
 1 5  
  
 aac acc cag ggt ttc tcc act gca tcg att cac gct ggg tat gag cca 163



145		150		155		160
Pro Ala Glu Ala	Asn Asp Ser Asp Glu Tyr Ile Ala Phe Leu Gly Met					
	165			170		175
Leu Arg Glu Val	Leu Ala Ala Glu Pro Gly Lys Trp Gly Lys Ile Ala					
	180		185			190
Glu Ala Val Lys Gly Val Thr Glu Glu Thr Thr Thr Gly Val His Arg						
	195		200			205
Leu Tyr His Phe Ala Glu Glu Gly Val Leu Pro Phe Pro Ala Met Asn						
	210		215		220	
Val Asn Asp Ala Val Thr Lys Ser Lys Phe Asp Asn Lys Tyr Gly Thr						
	225		230		235	240
Arg His Ser Leu Ile Asp Gly Ile Asn Arg Ala Thr Asp Met Leu Met						
	245		250			255
Gly Gly Lys Asn Val Leu Val Cys Gly Tyr Gly Asp Val Gly Lys Gly						
	260		265			270
Cys Ala Glu Ala Phe Asp Gly Gln Gly Ala Arg Val Lys Val Thr Glu						
	275		280			285
Ala Asp Pro Ile Asn Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser Val						
	290		295		300	
Val Thr Val Asp Glu Ala Ile Glu Asp Ala Asp Ile Val Ile Thr Ala						
	305		310		315	320
Thr Gly Asn Lys Asp Ile Ile Ser Phe Glu Gln Met Leu Lys Met Lys						
	325		330			335
Asp His Ala Leu Leu Gly Asn Ile Gly His Phe Asp Asn Glu Ile Asp						
	340		345			350
Met His Ser Leu Leu His Arg Asp Asp Val Thr Arg Thr Thr Ile Lys						
	355		360			365
Pro Gln Val Asp Glu Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile Val						
	370		375			380
Leu Ser Glu Gly Arg Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro						
	385		390		395	400
Ser Phe Val Met Ser Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile						
	405		410			415
Glu Leu Phe Gln Asn Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg Leu						
	420		425			430
Pro Lys Val Leu Asp Glu Lys Val Ala Arg Ile His Val Glu Ala Leu						
	435		440			445
Gly Gly Gln Leu Thr Glu Leu Thr Lys Glu Gln Ala Glu Tyr Ile Gly						
	450		455			460
Val Asp Val Ala Gly Pro Phe Lys Pro Glu His Tyr Arg Tyr						
	465		470		475	

Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile Glu Leu Phe Gln Asn  
 410 415 420

gaa gga cag tac gag aac gag gtc tac cgt ctg cct aag gtt ctc gac  
 1411

Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg Leu Pro Lys Val Leu Asp  
 425 430 435

gaa aag gtg gca cgc atc cac gtt gag gct ctc ggc ggt cag ctc acc  
 1459

Glu Lys Val Ala Arg Ile His Val Glu Ala Leu Gly Gly Gln Leu Thr  
 440 445 450

gaa ctg acc aag gag cag gct gag tac atc ggc gtt gac gtt gca ggc  
 1507

Glu Leu Thr Lys Glu Gln Ala Glu Tyr Ile Gly Val Asp Val Ala Gly  
 455 460 465

cca ttc aag ccg gag cac tac cgc tac taatgattgt cagcattgag  
 1554

Pro Phe Lys Pro Glu His Tyr Arg Tyr  
 470 475

gga  
 1557

<210> 220

<211> 478

<212> PRT

<213> Corynebacterium glutamicum

<400> 220

Met Ala Gln Val Met Asp Phe Lys Val Ala Asp Leu Ser Leu Ala Glu  
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Ala Gly Arg His Gln Ile Arg Leu Ala Glu Tyr Glu Met Pro Gly Leu  
 20 25 30

Met Gln Leu Arg Lys Glu Phe Ala Asp Glu Gln Pro Leu Lys Gly Ala  
 35 40 45

Arg Ile Ala Gly Ser Ile His Met Thr Val Gln Thr Ala Val Leu Ile  
 50 55 60

Glu Thr Leu Thr Ala Leu Gly Ala Glu Val Arg Trp Ala Ser Cys Asn  
 65 70 75 80

Ile Phe Ser Thr Gln Asp Glu Ala Ala Ala Ile Val Val Gly Ser  
 85 90 95

Gly Thr Val Glu Glu Pro Ala Gly Val Pro Val Phe Ala Trp Lys Gly  
 100 105 110

Glu Ser Leu Glu Glu Tyr Trp Trp Cys Ile Asn Gln Ile Phe Ser Trp  
 115 120 125

Gly Asp Glu Leu Pro Asn Met Ile Leu Asp Asp Gly Gly Asp Ala Thr  
 130 135 140

Met Ala Val Ile Arg Gly Arg Glu Tyr Glu Gln Ala Gly Leu Val Pro

gtc acc gag gaa acc acc acc ggt gtg cac cgc ctg tac cac ttc gct 739  
 Val Thr Glu Glu Thr Thr Thr Gly Val His Arg Leu Tyr His Phe Ala  
 200 205 210

gaa gaa ggc gtg ctg cct ttc cca gcg atg aac gtc aac gac gct gtc 787  
 Glu Glu Gly Val Leu Pro Phe Pro Ala Met Asn Val Asn Asp Ala Val  
 215 220 225

acc aag tcc aag ttt gat aac aag tac ggc acc cgc cac tcc ctg atc 835  
 Thr Lys Ser Lys Phe Asp Asn Lys Tyr Gly Thr Arg His Ser Leu Ile  
 230 235 240 245

gac ggc atc aac cgc gcc act gac atg ctc atg ggc ggc aag aac gtg 883  
 Asp Gly Ile Asn Arg Ala Thr Asp Met Leu Met Gly Gly Lys Asn Val  
 250 255 260

ctt gtc tgc ggt tac ggc gat gtc ggc aag ggc tgc gct gag gct ttc 931  
 Leu Val Cys Gly Tyr Gly Asp Val Gly Lys Gly Cys Ala Glu Ala Phe  
 265 270 275

gac ggc cag ggc gct cgc gtc aag gtc acc gaa gct gac cca atc aac 979  
 Asp Gly Gln Gly Ala Arg Val Lys Val Thr Glu Ala Asp Pro Ile Asn  
 280 285 290

gct ctt cag gct ctg atg gat ggc tac tct gtg gtc acc gtt gat gag  
 1027  
 Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser Val Val Thr Val Asp Glu  
 295 300 305

gcc atc gag gac gcc gac atc gtg atc acc gcg acc ggc aac aag gac  
 1075  
 Ala Ile Glu Asp Ala Asp Ile Val Ile Thr Ala Thr Gly Asn Lys Asp  
 310 315 320 325

atc att tcc ttc gag cag atg ctc aag atg aag gat cac gct ctg ctg  
 1123  
 Ile Ile Ser Phe Glu Gln Met Leu Lys Met Lys Asp His Ala Leu Leu  
 330 335 340

ggc aac atc ggt cac ttt gat aat gag atc gat atg cat tcc ctg ttg  
 1171  
 Gly Asn Ile Gly His Phe Asp Asn Glu Ile Asp Met His Ser Leu Leu  
 345 350 355

cac cgc gac gac gtc acc cgc acc acg atc aag cca cag gtc gac gag  
 1219  
 His Arg Asp Asp Val Thr Arg Thr Thr Ile Lys Pro Gln Val Asp Glu  
 360 365 370

ttc acc ttc tcc acc ggt cgc tcc atc atc gtc ctg tcc gaa ggt cgc  
 1267  
 Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile Val Leu Ser Glu Gly Arg  
 375 380 385

ctg ttg aac ctt ggc aac gcc acc gga cac cca tca ttt gtc atg tcc  
 1315  
 Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro Ser Phe Val Met Ser  
 390 395 400 405

aac tct ttc gcc gat cag acc att gcg cag atc gaa ctg ttc caa aac  
 1363

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<220>  
<221> CDS  
<222> (101)..(1534)  
<223> RXN00132
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tttcctaatt ttcatTTTTCT TAAAAGGAgC tcgccaggac atg gca cag gtt atg	115
	Met Ala Gln Val Met
	1 5
gac ttc aag gtt gcc gat ctt tca cta gca gag gca gga cgt cac cag	163
Asp Phe Lys Val Ala Asp Leu Ser Leu Ala GlU Ala Gly Arg His Gln	
	10 15 20
att cgt ctt gca gag tat gag atg cca ggt ctC atg cag ttg cgC aag	211
Ile Arg Leu Ala GlU Tyr GlU Met Pro Gly Leu Met Gln Leu Arg Lys	
	25 30 35
gaa ttc gca gac gag cag cct ttg aag ggc gcc cga att gct ggt tct	259
Glu Phe Ala Asp GlU Gln Pro Leu Lys Gly Ala Arg Ile Ala Gly Ser	
	40 45 50
atc cac atg acg gtc cag acc gcc gtg ctt att gag acc ctC act gct	307
Ile His Met Thr Val Gln Thr Ala Val Leu Ile GlU Thr Leu Thr Ala	
	55 60 65
ttg ggc gct gag gtt cgt tgg gct tcc tgc aac att ttc tcc acc cag	355
Leu Gly Ala GlU Val Arg Trp Ala Ser Cys Asn Ile Phe Ser Thr Gln	
	70 75 80 85
gat gag gct gca gcg gct atc gtt gtc ggc tcc ggc acc gtc gaa gag	403
Asp GlU Ala Ala Ala Ile Val Val Gly Ser Gly Thr Val GlU GlU	
	90 95 100
cca gct ggt gtt cca gta ttc gcg tgg aag ggt gag tca ctg gag gag	451
Pro Ala Gly Val Pro Val Phe Ala Trp Lys Gly GlU Ser Leu GlU GlU	
	105 110 115
tac tgg tgg tgc atc aac cag atc ttc agc tgg ggc gat gag ctg cca	499
Tyr Trp Trp Cys Ile Asn Gln Ile Phe Ser Trp Gly Asp GlU Leu Pro	
	120 125 130
aac atg atc ctC gac gac ggc ggt gac gcc acc atg gct gtt att cgC	547
Asn Met Ile Leu Asp Asp Gly Gly Asp Ala Thr Met Ala Val Ile Arg	
	135 140 145
ggt cgC gaa tac gag cag gct ggt ctg gtt cca cca gca gag gcc aac	595
Gly Arg GlU Tyr GlU Gln Ala Gly Leu Val Pro Pro Ala GlU Ala Asn	
	150 155 160 165
gat tcc gat gag tac atc gca ttc ttg ggc atg ctg cgT gag gtt ctt	643
Asp Ser Asp GlU Tyr Ile Ala Phe Leu Gly Met Leu Arg GlU Val Leu	
	170 175 180
gct gca gag cct ggc aag tgg ggc aag atc gct gag gcc gtt aag ggt	691
Ala Ala GlU Pro Gly Lys Trp Gly Lys Ile Ala GlU Ala Val Lys Gly	
	185 190 195

ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499  
 Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg  
 120 125 130  
  
 gac gta gtg gta tcg att ggt ggc att gac ttc att cct ggt cat tac 547  
 Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr  
 135 140 145  
  
 gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595  
 Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys  
 150 155 160 165  
  
 cag taatttggtt tgacgacgca gta 621  
 Gln

<210> 218  
 <211> 166  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 218  
 Met Thr Gln Ser Ala Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp  
 1 5 10 15  
  
 Ile Ile Gly Asp Asn Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu  
 20 25 30  
  
 Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe  
 35 40 45  
  
 Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly  
 50 55 60  
  
 Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val  
 65 70 75 80  
  
 Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val  
 85 90 95  
  
 Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr  
 100 105 110  
  
 Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr  
 115 120 125  
  
 Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe  
 130 135 140  
  
 Ile Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr  
 145 150 155 160  
  
 Glu Ala Pro Ile Lys Gln  
 165

<210> 219  
 <211> 1557  
 <212> DNA  
 <213> Corynebacterium glutamicum

Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr  
 100 105 110

Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr  
 115 120 125

Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe  
 130 135 140

Ile Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr  
 145 150 155 160

Glu Ala Pro Ile Lys Gln  
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<210> 217

<211> 621

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(598)

<223> FRXA02906

<400> 217

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tagcaggaca agcatactgt tttagttcta tgctgtgggc atg act caa agt gct 115  
 Met Thr Gln Ser Ala  
 1 5

cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac 163  
 Pro Glu Phe Ile Ile Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn  
 10 15 20

gcg caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa 211  
 Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu  
 25 30 35

ttc cac gga ata ata acc acc gtg aaa tgc ttc caa gac aac gcc ctc 259  
 Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu  
 40 45 50

ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc 307  
 Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile  
 55 60 65

gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca 355  
 Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala  
 70 75 80 85

gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403  
 Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala  
 90 95 100

att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc 451  
 Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala  
 105 110 115

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ttc cac gga ata ata acc acc gtg aaa tgc ttc caa gac aac gcc ctc 259
Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu
      40                      45                      50

ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc 307
Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile
      55                      60                      65

gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca 355
Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala
      70                      75                      80                      85

gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403
Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala
      90                      95                      100

att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc 451
Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala
      105                      110                      115

ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499
Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg
      120                      125                      130

gac gta gtg gta tcg att ggt ggc att gac ttc att cct ggt cat tac 547
Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr
      135                      140                      145

gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595
Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys
      150                      155                      160                      165

cag taatttggtt tgacgacgca gta 621
Gln

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&lt;210&gt; 216

&lt;211&gt; 166

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 216

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Met Thr Gln Ser Ala Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp
  1                      5                      10                      15

Ile Ile Gly Asp Asn Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu
      20                      25                      30

Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe
      35                      40                      45

Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly
      50                      55                      60

Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val
      65                      70                      75                      80

Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val
      85                      90                      95

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<210> 215
<211> 621
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(598)  
<223> RXN03074
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tagcaggaca agcatactgt tttagttcta tgctgtgggc atg act caa agt gct      115
                                         Met Thr Gln Ser Ala
                                           1             5
cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac      163
Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn
                        10                      15                20
gcg caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa      211
Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu
                    25                          30                  35
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Val Gly Val Pro Glu Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala  
 325 330 335  
 Gly Pro Val Glu Gln Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val  
 340 345 350  
 Ala Ser Leu Tyr Thr Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser  
 355 360 365  
 Met Ile Gly Glu Arg Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu  
 370 375 380  
 Ala Met Leu Ser Gly Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln  
 385 390 395 400  
 Gln Thr Arg Asp Gly Ala His Met Leu Asp Leu Cys Val Asp Tyr Val  
 405 410 415  
 Gly Arg Asp Gly Thr Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala  
 420 425 430  
 Thr Ser Ser Thr Leu Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val  
 435 440 445  
 Ile Arg Thr Gly Leu Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser  
 450 455 460  
 Val Asn Phe Glu Asp Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile  
 465 470 475 480  
 Met Lys Leu Val Lys Gln His Gly Ala Ala Val Val Ala Leu Thr Ile  
 485 490 495  
 Asp Glu Glu Gly Gln Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala  
 500 505 510  
 Lys Arg Leu Ile Asp Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys  
 515 520 525  
 Asp Ile Val Val Asp Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu  
 530 535 540  
 Glu Thr Arg Arg Asp Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu  
 545 550 555 560  
 Lys Lys Leu Tyr Pro Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile  
 565 570 575  
 Ser Phe Gly Leu Asn Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe  
 580 585 590  
 Leu Asn Glu Cys Ile Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser  
 595 600 605  
 Ser Lys Ile Leu Pro Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val  
 610 615 620  
 Ala Leu Asp Met Val Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu  
 625 630 635 640  
 Gln Glu Phe Met Gln Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys

<400> 214  
Met Ser Thr Ser Val Thr Ser Pro Ala His Asn Asn Ala His Ser Ser  
1 5 10 15  
Glu Phe Leu Asp Ala Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala  
20 25 30  
Met Gly Thr Gln Leu Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe  
35 40 45  
Leu Asp Leu Glu Gly Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp  
50 55 60  
Val Leu Arg Gln Ile His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu  
65 70 75 80  
Val Glu Thr Asn Thr Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr  
85 90 95  
Asp Ile Ala Asp Arg Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val  
100 105 110  
Ala Arg Glu Val Ala Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg  
115 120 125  
Arg Phe Val Val Gly Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu  
130 135 140  
Gly His Ala Pro Tyr Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala  
145 150 155 160  
Leu Gly Ile Ile Asp Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala  
165 170 175  
Gln Asp Leu Leu Gln Val Lys Ala Ala Val His Gly Val Gln Asp Ala  
180 185 190  
Met Ala Glu Leu Asp Thr Phe Leu Pro Ile Ile Cys His Val Thr Val  
195 200 205  
Glu Thr Thr Gly Thr Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu  
210 215 220  
Thr Ala Leu Gln Pro Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala  
225 230 235 240  
Thr Gly Pro Asp Glu Met Ser Glu His Leu Arg Tyr Leu Ser Lys His  
245 250 255  
Ala Asp Ile Pro Val Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu  
260 265 270  
Gly Lys Asn Gly Ala Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln  
275 280 285  
Ala Leu Ala Gly Phe Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly  
290 295 300  
Cys Cys Gly Thr Thr Pro Glu His Ile Arg Ala Val Arg Asp Ala Val  
305 310 315 320

cag ctg gcc gct atg cct ttg ttt gag cgt ttg gca cag cgc atc atc  
 2131  
 Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu Ala Gln Arg Ile Ile  
 665 670 675

gac ggc gat aag aat ggc ctt gag gat gat ctg gaa gca ggc atg aag  
 2179  
 Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu Glu Ala Gly Met Lys  
 680 685 690

gag aag tct cct att gcg atc atc aac gag gac ctt ctc aac ggc atg  
 2227  
 Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp Leu Leu Asn Gly Met  
 695 700 705

aag acc gtg ggt gag ctg ttt ggt tcc gga cag atg cag ctg cca ttc  
 2275  
 Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln Met Gln Leu Pro Phe  
 710 715 720 725

gtg ctg caa tcg gca gaa acc atg aaa act gcg gtg gcc tat ttg gaa  
 2323  
 Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala Val Ala Tyr Leu Glu  
 730 735 740

ccg ttc atg gaa gag gaa gca gaa gct acc gga tct gcg cag gca gag  
 2371  
 Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly Ser Ala Gln Ala Glu  
 745 750 755

ggc aag ggc aaa atc gtc gtg gcc acc gtc aag ggt gac gtg cac gat  
 2419  
 Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys Gly Asp Val His Asp  
 760 765 770

atc ggc aag aac ttg gtg gac atc att ttg tcc aac aac ggt tac gac  
 2467  
 Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser Asn Asn Gly Tyr Asp  
 775 780 785

gtg gtg aac ttg ggc atc aag cag cca ctg tcc gcc atg ttg gaa gca  
 2515  
 Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser Ala Met Leu Glu Ala  
 790 795 800 805

gcg gaa gaa cac aaa gca gac gtc atc ggc atg tcg gga ctt ctt gtg  
 2563  
 Ala Glu Glu His Lys Ala Asp Val Ile Gly Met Ser Gly Leu Leu Val  
 810 815 820

aag tcc acc gtg gtg  
 2578  
 Lys Ser Thr Val Val  
 825

&lt;210&gt; 214

&lt;211&gt; 826

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

ggc gat ggc cct gag tcc cgc tac cag cgc atc atg aaa ctg gta aag  
 1555  
 Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile Met Lys Leu Val Lys  
 470 475 480 485  
 cag cac ggt gcg gcc gtg gtt gcg ctg acc att gat gag gaa ggc cag  
 1603  
 Gln His Gly Ala Ala Val Val Ala Leu Thr Ile Asp Glu Glu Gly Gln  
 490 495 500  
 gca cgt acc gct gag cac aag gtg cgc att gct aaa cga ctg att gac  
 1651  
 Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala Lys Arg Leu Ile Asp  
 505 510 515  
 gat atc acc ggc agc tac ggc ctg gat atc aaa gac atc gtt gtg gac  
 1699  
 Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys Asp Ile Val Val Asp  
 520 525 530  
 tgc ctg acc ttc ccg atc tct act ggc cag gaa gaa acc agg cga gat  
 1747  
 Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu Glu Thr Arg Arg Asp  
 535 540 545  
 ggc att gaa acc atc gaa gcc atc cgc gag ctg aag aag ctc tac cca  
 1795  
 Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu Lys Lys Leu Tyr Pro  
 550 555 560 565  
 gaa atc cac acc acc ctg ggt ctg tcc aat att tcc ttc ggc ctg aac  
 1843  
 Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile Ser Phe Gly Leu Asn  
 570 575 580  
 cct gct gca cgc cag gtt ctt aac tct gtg ttc ctc aat gag tgc att  
 1891  
 Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe Leu Asn Glu Cys Ile  
 585 590 595  
 gag gct ggt ctg gac tct gcg att gcg cac agc tcc aag att ttg ccg  
 1939  
 Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser Ser Lys Ile Leu Pro  
 600 605 610  
 atg aac cgc att gat gat cgc cag cgc gaa gtg gcg ttg gat atg gtc  
 1987  
 Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val Ala Leu Asp Met Val  
 615 620 625  
 tat gat cgc cgc acc gag gat tac gat ccg ctg cag gaa ttc atg cag  
 2035  
 Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu Gln Glu Phe Met Gln  
 630 635 640 645  
 ctg ttt gag ggc gtt tct gct gcc gat gcc aag gat gct cgc gct gaa  
 2083  
 Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys Asp Ala Arg Ala Glu  
 650 655 660

265										270										275										
gaa tac cca ctt gag gct gag gat ttg gcg cag gcg ctg gct gga ttc																														979
Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln Ala Leu Ala Gly Phe																														
280										285										290										
gtc tcc gaa tat ggc ctg tcc atg gtg ggt ggt tgt tgt ggc acc aca																														
1027																														
Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly Cys Cys Gly Thr Thr																														
295										300										305										
cct gag cac atc cgt gcg gtc cgc gat gcg gtg gtt ggt gtt cca gag																														
1075																														
Pro Glu His Ile Arg Ala Val Arg Asp Ala Val Val Gly Val Pro Glu																														
310										315										320										325
cag gaa acc tcc aca ctg acc aag atc cct gca ggc cct gtt gag cag																														
1123																														
Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala Gly Pro Val Glu Gln																														
										330										335										340
gcc tcc cgc gag gtg gag aaa gag gac tcc gtc gcg tcg ctg tac acc																														
1171																														
Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val Ala Ser Leu Tyr Thr																														
										345										350										355
tcg gtg cca ttg tcc cag gaa acc ggc att tcc atg atc ggt gag cgc																														
1219																														
Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser Met Ile Gly Glu Arg																														
										360										365										370
acc aac tcc aac ggt tcc aag gca ttc cgt gag gca atg ctg tct ggc																														
1267																														
Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu Ala Met Leu Ser Gly																														
										375										380										385
gat tgg gaa aag tgt gtg gat att gcc aag cag caa acc cgc gat ggt																														
1315																														
Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln Gln Thr Arg Asp Gly																														
390										395										400										405
gca cac atg ctg gat ctt tgt gtg gat tac gtg gga cga gac ggc acc																														
1363																														
Ala His Met Leu Asp Leu Cys Val Asp Tyr Val Gly Arg Asp Gly Thr																														
										410										415										420
gcc gat atg gcg acc ttg gca gca ctt ctt gct acc agc tcc act ttg																														
1411																														
Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala Thr Ser Ser Thr Leu																														
										425										430										435
cca atc atg att gac tcc acc gag cca gag gtt att cgc aca ggc ctt																														
1459																														
Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val Ile Arg Thr Gly Leu																														
										440										445										450
gag cac ttg ggt gga cga agc atc gtt aac tcc gtc aac ttt gaa gag																														
1507																														
Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser Val Asn Phe Glu Asp																														
										455										460										465

Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala Met Gly Thr Gln Leu	25	30	35	
caa ggc ttt gac ctg gac gtg gaa aag gat ttc ctt gat ctg gag ggg				259
Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe Leu Asp Leu Glu Gly	40	45	50	
tgt aat gag att ctc aac gac acc cgc cct gat gtg ttg agg cag att				307
Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp Val Leu Arg Gln Ile	55	60	65	
cac cgc gcc tac ttt gag gcg gga gct gac ttg gtt gag acc aat act				355
His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu Val Glu Thr Asn Thr	70	75	80	85
ttt ggt tgc aac ctg ccg aac ttg gcg gat tat gac atc gct gat cgt				403
Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr Asp Ile Ala Asp Arg	90	95	100	
tgc cgt gag ctt gcc tac aag ggc act gca gtg gct agg gaa gtg gct				451
Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val Ala Arg Glu Val Ala	105	110	115	
gat gag atg ggg ccg ggc cga aac ggc atg ccg cgt ttc gtg gtt ggt				499
Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg Arg Phe Val Val Gly	120	125	130	
tcc ctg gga cct gga acg aag ctt cca tgc ctg ggc cat gca ccg tat				547
Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu Gly His Ala Pro Tyr	135	140	145	
gca gat ttg cgt ggg cac tac aag gaa gca gcg ctt ggc atc atc gac				595
Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala Leu Gly Ile Ile Asp	150	155	160	165
ggt ggt ggc gat gcc ttt ttg att gag act gct cag gac ttg ctt cag				643
Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala Gln Asp Leu Leu Gln	170	175	180	
gtc aag gct gcg gtt cac ggc gtt caa gat gcc atg gct gaa ctt gat				691
Val Lys Ala Ala Val His Gly Val Gln Asp Ala Met Ala Glu Leu Asp	185	190	195	
aca ttc ttg ccc att att tgc cac gtc acc gta gag acc acc ggc acc				739
Thr Phe Leu Pro Ile Ile Cys His Val Thr Val Glu Thr Thr Gly Thr	200	205	210	
atg ctc atg ggt tct gag atc ggt gcc gcg ttg aca gcg ctg cag cca				787
Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu Thr Ala Leu Gln Pro	215	220	225	
ctg ggt atc gac atg att ggt ctg aac tgc gcc acc ggc cca gat gag				835
Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala Thr Gly Pro Asp Glu	230	235	240	245
atg agc gag cac ctg cgt tac ctg tcc aag cac gcc gat att cct gtg				883
Met Ser Glu His Leu Arg Tyr Leu Ser Lys His Ala Asp Ile Pro Val	250	255	260	
tcg gtg atg cct aac gca ggt ctt cct gtc ctg ggt aaa aac ggt gca				931
Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu Gly Lys Asn Gly Ala				

Asp

ttg gca aac cat gtg ttg atc ggc gac ggc gcc atg ggc acc cag ctc 211

Val Gly Val Pro Glu Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala  
 325 330 335  
 Gly Pro Val Glu Gln Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val  
 340 345 350  
 Ala Ser Leu Tyr Thr Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser  
 355 360 365  
 Met Ile Gly Glu Arg Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu  
 370 375 380  
 Ala Met Leu Ser Gly Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln  
 385 390 395 400  
 Gln Thr Arg Asp Gly Ala His Met Leu Asp Leu Cys Val Asp Tyr Val  
 405 410 415  
 Gly Arg Asp Gly Thr Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala  
 420 425 430  
 Thr Ser Ser Thr Leu Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val  
 435 440 445  
 Ile Arg Thr Gly Leu Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser  
 450 455 460  
 Val Asn Phe Glu Asp Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile  
 465 470 475 480  
 Met Lys Leu Val Lys Gln His Gly Ala Ala Val Val Ala Leu Thr Ile  
 485 490 495  
 Asp Glu Glu Gly Gln Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala  
 500 505 510  
 Lys Arg Leu Ile Asp Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys  
 515 520 525  
 Asp Ile Val Val Asp Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu  
 530 535 540  
 Glu Thr Arg Arg Asp Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu  
 545 550 555 560  
 Lys Lys Leu Tyr Pro Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile  
 565 570 575  
 Ser Phe Gly Leu Asn Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe  
 580 585 590  
 Leu Asn Glu Cys Ile Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser  
 595 600 605  
 Ser Lys Ile Leu Pro Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val  
 610 615 620  
 Ala Leu Asp Met Val Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu  
 625 630 635 640  
 Gln Glu Phe Met Gln Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys



&lt;400&gt; 212

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Met Ser Thr Ser Val Thr Ser Pro Ala His Asn Asn Ala His Ser Ser
 1              5              10              15

Glu Phe Leu Asp Ala Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala
      20              25              30

Met Gly Thr Gln Leu Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe
      35              40              45

Leu Asp Leu Glu Gly Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp
      50              55              60

Val Leu Arg Gln Ile His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu
      65              70              75              80

Val Glu Thr Asn Thr Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr
      85              90              95

Asp Ile Ala Asp Arg Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val
      100              105              110

Ala Arg Glu Val Ala Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg
      115              120              125

Arg Phe Val Val Gly Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu
      130              135              140

Gly His Ala Pro Tyr Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala
      145              150              155              160

Leu Gly Ile Ile Asp Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala
      165              170              175

Gln Asp Leu Leu Gln Val Lys Ala Ala Val His Gly Val Gln Asp Ala
      180              185              190

Met Ala Glu Leu Asp Thr Phe Leu Pro Ile Ile Cys His Val Thr Val
      195              200              205

Glu Thr Thr Gly Thr Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu
      210              215              220

Thr Ala Leu Gln Pro Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala
      225              230              235              240

Thr Gly Pro Asp Glu Met Ser Glu His Leu Arg Tyr Leu Ser Lys His
      245              250              255

Ala Asp Ile Pro Val Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu
      260              265              270

Gly Lys Asn Gly Ala Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln
      275              280              285

Ala Leu Ala Gly Phe Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly
      290              295              300

Cys Cys Gly Thr Thr Pro Glu His Ile Arg Ala Val Arg Asp Ala Val
      305              310              315              320

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cag ctg gcc gct atg cct ttg ttt gag cgt ttg gca cag cgc atc atc  
2131

Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu Ala Gln Arg Ile Ile  
665 670 675

gac ggc gat aag aat ggc ctt gag gat gat ctg gaa gca ggc atg aag  
2179

Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu Glu Ala Gly Met Lys  
680 685 690

gag aag tct cct att gcg atc atc aac gag gac ctt ctc aac ggc atg  
2227

Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp Leu Leu Asn Gly Met  
695 700 705

aag acc gtg ggt gag ctg ttt ggt tcc gga cag atg cag ctg cca ttc  
2275

Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln Met Gln Leu Pro Phe  
710 715 720 725

gtg ctg caa tcg gca gaa acc atg aaa act gcg gtg gcc tat ttg gaa  
2323

Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala Val Ala Tyr Leu Glu  
730 735 740

ccg ttc atg gaa gag gaa gca gaa gct acc gga tct gcg cag gca gag  
2371

Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly Ser Ala Gln Ala Glu  
745 750 755

ggc aag ggc aaa atc gtc gtg gcc acc gtc aag ggt gac gtg cac gat  
2419

Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys Gly Asp Val His Asp  
760 765 770

atc ggc aag aac ttg gtg gac atc att ttg tcc aac aac ggt tac gac  
2467

Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser Asn Asn Gly Tyr Asp  
775 780 785

gtg gtg aac ttg ggc atc aag cag cca ctg tcc gcc atg ttg gaa gca  
2515

Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser Ala Met Leu Glu Ala  
790 795 800 805

gcg gaa gaa cac aaa gca gac gtc atc ggc atg tcg gga ctt ctt gtg  
2563

Ala Glu Glu His Lys Ala Asp Val Ile Gly Met Ser Gly Leu Leu Val  
810 815 820

aag tcc acc gtg gtg atg aag caa acc atc agc gac  
2599

Lys Ser Thr Val Val Met Lys Gln Thr Ile Ser Asp  
825 830

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<211> 833

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<213> Corynebacterium glutamicum

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 1555

Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr Phe Ser Glu Leu Leu  
 470 475 480 485

gac ggt ttc ctc tca acc gcc aac ggc tgg gtc caa agc tac ggc tcc  
 1603

Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val Gln Ser Tyr Gly Ser  
 490 495 500

cgc tgt gtt cgt cct cca gtg ttg ttc gga aac gtt tcc cgc cca gcg  
 1651

Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn Val Ser Arg Pro Ala  
 505 510 515

cca atg act gtc aag tgg ttc cag tac gca cag agc ctg acc cag aag  
 1699

Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln Ser Leu Thr Gln Lys  
 520 525 530

cat gtc aag gga atg ctc acc ggt cca gtc acc atc ctt gca tgg tcc  
 1747

His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile Leu Ala Trp Ser  
 535 540 545

ttc gtt cgc gat gat cag ccg ctg gct acc act gct gac cag gtt gca  
 1795

Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr Ala Asp Gln Val Ala  
 550 555 560 565

ctg gca ctg cgc gat gaa att aac gat ctc atc gag gct ggc gcg aag  
 1843

Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile Glu Ala Gly Ala Lys  
 570 575 580

atc atc cag gtg gat gag cct gcg att cgt gaa ctg ttg ccc gct acg  
 1891

Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu Leu Leu Pro Ala Thr  
 585 590 595

aga cgt cga taagcctgcc tacctgcagt ggt  
 1923

Arg Arg Arg  
 600

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<211> 600

<212> PRT

<213> Corynebacterium glutamicum

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 20 25 30

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 Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly  
 265 270 275

gag gag ctg ctg gtt gcg ggc atc gtt gat ggt cgt aac att tgg cgc 979  
 Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg  
 280 285 290

acc gac ctg tgt gct gct ctt gct tcc ctg aag cgc ctg gca gct cgc  
 1027  
 Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys Arg Leu Ala Ala Arg  
 295 300 305

ggc cca atc gca gtg tct acc tct tgt tca ctg ctg cac gtt cct tac  
 1075  
 Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr  
 310 315 320 325

acc ctc gag gct gag aac att gag cct gag gtc cgc gac tgg ctt gcc  
 1123  
 Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val Arg Asp Trp Leu Ala  
 330 335 340

ttc ggc tcg gag aag atc acc gag gtc aag ctg ctt gcc gac gcc cta  
 1171  
 Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu Leu Ala Asp Ala Leu  
 345 350 355

gcc ggc aac atc gac gcg gct gcg ttc gat gcg gcg tcc gca gca att  
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 360 365 370

gct tct cga cgc acc tcc cca cgc acc gca cca atc acg cag gaa ctc  
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 Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro Ile Thr Gln Glu Leu  
 375 380 385

cct ggc cgt agc cgt gga tcc ttc gac act cgt gtt acg ctg cag gag  
 1315  
 Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg Val Thr Leu Gln Glu  
 390 395 400 405

aag tca ctg gag ctt cca gct ctg cca acc acc acc att ggt tct ttc  
 1363  
 Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr Thr Ile Gly Ser Phe  
 410 415 420

cca cag acc cca tcc att cgt tct gct cgc gct cgt ctg cgc aag gaa  
 1411  
 Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala Arg Leu Arg Lys Glu  
 425 430 435

tcc atc act ttg gag cag tac gaa gag gca atg cgc gaa gaa atc gat  
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 Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met Arg Glu Glu Ile Asp  
 440 445 450

ctg gtc atc gcc aag cag gaa gaa ctt ggt ctt gat gtg ttg gtt cac  
 1507

10						15						20						
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Lys	Phe	Ala	Leu	Glu	Gly	Tyr	Trp	Asn	Gly	Ser	Ile	Glu	Gly	Arg	Glu			
			25					30					35					
ctt	gcg	cag	acc	gcc	cgc	caa	ttg	gtc	aac	act	gca	tcg	gat	tct	ttg	259		
Leu	Ala	Gln	Thr	Ala	Arg	Gln	Leu	Val	Asn	Thr	Ala	Ser	Asp	Ser	Leu			
		40					45					50						
tct	gga	ttg	gat	tcc	gtt	ccg	ttt	gca	gga	cgt	tcc	tac	tac	gac	gca	307		
Ser	Gly	Leu	Asp	Ser	Val	Pro	Phe	Ala	Gly	Arg	Ser	Tyr	Tyr	Asp	Ala			
	55					60					65							
atg	ctc	gat	acc	gcc	gct	att	ttg	ggg	gtg	ctg	ccg	gag	cgt	ttt	gat	355		
Met	Leu	Asp	Thr	Ala	Ala	Ile	Leu	Gly	Val	Leu	Pro	Glu	Arg	Phe	Asp			
	70				75					80					85			
gac	atc	gct	gat	cat	gaa	aac	gat	ggg	ctc	cca	ctg	tgg	att	gac	cgc	403		
Asp	Ile	Ala	Asp	His	Glu	Asn	Asp	Gly	Leu	Pro	Leu	Trp	Ile	Asp	Arg			
				90				95						100				
tac	ttt	ggc	gct	gct	cgc	ggg	act	gag	acc	ctg	cct	gca	cag	gca	atg	451		
Tyr	Phe	Gly	Ala	Ala	Arg	Gly	Thr	Glu	Thr	Leu	Pro	Ala	Gln	Ala	Met			
		105				110							115					
acc	aag	tgg	ttt	gat	acc	aac	tac	cac	tac	ctc	gtg	ccg	gag	ttg	tct	499		
Thr	Lys	Trp	Phe	Asp	Thr	Asn	Tyr	His	Tyr	Leu	Val	Pro	Glu	Leu	Ser			
		120				125						130						
gcg	gat	aca	cgt	ttc	gtt	ttg	gat	gcg	tcc	gcg	ctg	att	gag	gat	ctc	547		
Ala	Asp	Thr	Arg	Phe	Val	Leu	Asp	Ala	Ser	Ala	Leu	Ile	Glu	Asp	Leu			
	135				140						145							
cgt	tgc	cag	cag	gtt	cgt	ggc	gtt	aat	gcc	cgc	cct	gtt	ctg	gtt	ggg	595		
Arg	Cys	Gln	Gln	Val	Arg	Gly	Val	Asn	Ala	Arg	Pro	Val	Leu	Val	Gly			
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cca	ctg	act	ttc	ctt	tcc	ctt	gct	cgc	acc	act	gat	ggg	tcc	aat	cct	643		
Pro	Leu	Thr	Phe	Leu	Ser	Leu	Ala	Arg	Thr	Thr	Asp	Gly	Ser	Asn	Pro			
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ttg	gat	cac	ctg	cct	gca	ctg	ttt	gag	gtc	tac	gag	cgc	ctc	atc	aag	691		
Leu	Asp	His	Leu	Pro	Ala	Leu	Phe	Glu	Val	Tyr	Glu	Arg	Leu	Ile	Lys			
		185				190							195					
tct	ttc	gat	act	gag	tgg	gtt	cag	atc	gat	gag	cct	gcg	ttg	gtc	acc	739		
Ser	Phe	Asp	Thr	Glu	Trp	Val	Gln	Ile	Asp	Glu	Pro	Ala	Leu	Val	Thr			
		200				205						210						
gat	gtt	gct	cct	gag	gtt	ttg	gag	cag	gtc	cgc	gct	ggg	tac	acc	act	787		
Asp	Val	Ala	Pro	Glu	Val	Leu	Glu	Gln	Val	Arg	Ala	Gly	Tyr	Thr	Thr			
	215				220						225							
ttg	gct	aag	cgc	gat	ggc	gtg	ttt	gtc	aat	act	tac	ttc	ggc	tct	ggc	835		
Leu	Ala	Lys	Arg	Asp	Gly	Val	Phe	Val	Asn	Thr	Tyr	Phe	Gly	Ser	Gly			
	230				235				240				245					
gat	cag	gcg	ctg	aac	act	ctt	gcg	ggc	atc	ggc	ctt	ggc	gcg	att	ggc	883		
Asp	Gln	Ala	Leu	Asn	Thr	Leu	Ala	Gly	Ile	Gly	Leu	Gly	Ala	Ile	Gly			
			250					255					260					

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Ile Leu Ala Trp Ser Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr			
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Ala Asp Gln Val Ala Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile			
	565	570	575
Glu Ala Gly Ala Lys Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu			
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Leu Leu Pro Leu Arg Asp Val Asp Lys Pro Ala Tyr Leu Gln Trp Ser			
	595	600	605
Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp Val Gln			
	610	615	620
Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu Val Ile Ser Ser			
625	630	635	640
Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu Ala Ala Arg Ser			
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Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly Phe Glu Leu Gly			
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Val Gly Pro Gly Val Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala			
	675	680	685
Gln Lys Val Asp Gly Leu Leu Glu Ala Ala Leu Gln Ser Val Asp Pro			
	690	695	700
Arg Gln Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Trp			
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Met Thr Ser Asn Phe			
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Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly Ala Lys Arg Glu Leu			

Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg  
 210 215 220  
 Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr  
 225 230 235 240  
 Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly  
 245 250 255  
 Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu  
 260 265 270  
 Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly  
 275 280 285  
 Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys  
 290 295 300  
 Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu  
 305 310 315 320  
 Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val  
 325 330 335  
 Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu  
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 Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala  
 355 360 365  
 Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro  
 370 375 380  
 Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg  
 385 390 395 400  
 Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr  
 405 410 415  
 Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala  
 420 425 430  
 Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met  
 435 440 445  
 Arg Glu Glu Ile Asp Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu  
 450 455 460  
 Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr  
 465 470 475 480  
 Phe Ser Glu Leu Leu Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val  
 485 490 495  
 Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn  
 500 505 510  
 Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln  
 515 520 525  
 Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr

aac cca gac tgt ggt ctg aag acc cgt gga tgg cca gaa gtg gaa gct  
2275

Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala  
710 715 720 725

tcc cta aag gtt ctc gtt gag tcc gct aag cag gct cgt gag aaa atc  
2323

Ser Leu Lys Val Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile  
730 735 740

gga gca act atc taaattgggt taccgctagg aac  
2358

Gly Ala Thr Ile  
745

<210> 226

<211> 745

<212> PRT

<213> Corynebacterium glutamicum

<400> 226

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20 25 30

Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr  
35 40 45

Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg  
50 55 60

Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu  
65 70 75 80

Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro  
85 90 95

Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu  
100 105 110

Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu  
115 120 125

Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala  
130 135 140

Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg  
145 150 155 160

Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr  
165 170 175

Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr  
180 185 190

Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu  
195 200 205



cca atg act gtc aag tgg ttc cag tac gca cag agc ctg acc cag aag  
1699  
Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln Ser Leu Thr Gln Lys  
520 525 530

cat gtc aag gga atg ctc acc ggt cca gtc acc atc ctt gca tgg tcc  
1747  
His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile Leu Ala Trp Ser  
535 540 545

ttc gtt cgc gat gat cag ccg ctg gct acc act gct gac cag gtt gca  
1795  
Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr Ala Asp Gln Val Ala  
550 555 560 565

ctg gca ctg cgc gat gaa att aac gat ctc atc gag gct ggc gcg aag  
1843  
Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile Glu Ala Gly Ala Lys  
570 575 580

atc atc cag gtg gat gag cct gcg att cgt gaa ctg ttg ccg cta cga  
1891  
Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu Leu Leu Pro Leu Arg  
585 590 595

gac gtc gat aag cct gcc tac ctg cag tgg tcc gtg gac tcc ttc cgc  
1939  
Asp Val Asp Lys Pro Ala Tyr Leu Gln Trp Ser Val Asp Ser Phe Arg  
600 605 610

ctg gcg act gcc ggc gca ccc gac gac gtc caa atc cac acc cac atg  
1987  
Leu Ala Thr Ala Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met  
615 620 625

tgc tac tcc gag ttc aac gaa gtg atc tcc tcg gtc atc gcg ttg gat  
2035  
Cys Tyr Ser Glu Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp  
630 635 640 645

gcc gat gtc acc acc atc gaa gca gca cgt tcc gac atg cag gtc ctc  
2083  
Ala Asp Val Thr Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu  
650 655 660

gct gct ctg aaa tct tcc ggc ttc gag ctc ggc gtc gga cct ggt gtg  
2131  
Ala Ala Leu Lys Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val  
665 670 675

tgg gat atc cac tcc ccg cgc gtt cct tcc gcg cag aaa gtg gac ggt  
2179  
Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly  
680 685 690

ctc ctc gag gct gca ctg cag tcc gtg gat cct cgc cag ctg tgg gtc  
2227  
Leu Leu Glu Ala Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val  
695 700 705

acc ctc gag gct gag aac att gag cct gag gtc cgc gac tgg ctt gcc  
1123

Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val Arg Asp Trp Leu Ala  
330 335 340

ttc ggc tcg gag aag atc acc gag gtc aag ctg ctt gcc gac gcc cta  
1171

Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu Leu Ala Asp Ala Leu  
345 350 355

gcc ggc aac atc gac gcg gct gcg ttc gat gcg gcg tcc gca gca att  
1219

Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala Ala Ser Ala Ala Ile  
360 365 370

gct tct cga cgc acc tcc cca cgc acc gca cca atc acg cag gaa ctc  
1267

Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro Ile Thr Gln Glu Leu  
375 380 385

cct ggc cgt agc cgt gga tcc ttc gac act cgt gtt acg ctg cag gag  
1315

Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg Val Thr Leu Gln Glu  
390 395 400 405

aag tca ctg gag ctt cca gct ctg cca acc acc acc att ggt tct ttc  
1363

Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr Thr Ile Gly Ser Phe  
410 415 420

cca cag acc cca tcc att cgt tct gct cgc gct cgt ctg cgc aag gaa  
1411

Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala Arg Leu Arg Lys Glu  
425 430 435

tcc atc act ttg gag cag tac gaa gag gca atg cgc gaa gaa atc gat  
1459

Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met Arg Glu Glu Ile Asp  
440 445 450

ctg gtc atc gcc aag cag gaa gaa ctt ggt ctt gat gtg ttg gtt cac  
1507

Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu Asp Val Leu Val His  
455 460 465

ggt gag cca gag cgc aac gac atg gtt cag tac ttc tct gaa ctt ctc  
1555

Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr Phe Ser Glu Leu Leu  
470 475 480 485

gac ggt ttc ctc tca acc gcc aac ggc tgg gtc caa agc tac ggc tcc  
1603

Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val Gln Ser Tyr Gly Ser  
490 495 500

cgc tgt gtt cgt cct cca gtg ttg ttc gga aac gtt tcc cgc cca gcg  
1651

Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn Val Ser Arg Pro Ala  
505 510 515

gac atc gct gat cat gaa aac gat ggt ctc cca ctg tgg att gac cgc	403
Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro Leu Trp Ile Asp Arg	
90 95 100	
tac ttt ggc gct gct cgc ggt act gag acc ctg cct gca cag gca atg	451
Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Gln Ala Met	
105 110 115	
acc aag tgg ttt gat acc aac tac cac tac ctc gtg ccg gag ttg tct	499
Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser	
120 125 130	
gcg gat aca cgt ttc gtt ttg gat gcg tcc gcg ctg att gag gat ctc	547
Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala Leu Ile Glu Asp Leu	
135 140 145	
cgt tgc cag cag gtt cgt ggc gtt aat gcc cgc cct gtt ctg gtt ggt	595
Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg Pro Val Leu Val Gly	
150 155 160 165	
cca ctg act ttc ctt tcc ctt gct cgc acc act gat ggt tcc aat cct	643
Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr Asp Gly Ser Asn Pro	
170 175 180	
ttg gat cac ctg cct gca ctg ttt gag gtc tac gag cgc ctc atc aag	691
Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys	
185 190 195	
tct ttc gat act gag tgg gtt cag atc gat gag cct gcg ttg gtc acc	739
Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr	
200 205 210	
gat gtt gct cct gag gtt ttg gag cag gtc cgc gct ggt tac acc act	787
Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr	
215 220 225	
ttg gct aag cgc gat ggc gtg ttt gtc aat act tac ttc ggc tct ggc	835
Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly	
230 235 240 245	
gat cag gcg ctg aac act ctt gcg ggc atc ggc ctt ggc gcg att ggc	883
Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly	
250 255 260	
gtt gac ttg gtc acc cat ggc gtc act gag ctt gct gcg tgg aag ggt	931
Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly	
265 270 275	
gag gag ctg ctg gtt gcg ggc atc gtt gat ggt cgt aac att tgg cgc	979
Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg	
280 285 290	
acc gac ctg tgt gct gct ctt gct tcc ctg aag cgc ctg gca gct cgc	
1027	
Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys Arg Leu Ala Ala Arg	
295 300 305	
ggc cca atc gca gtg tct acc tct tgt tca ctg ctg cac gtt cct tac	
1075	
Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr	
310 315 320 325	

				325					330					335					
Asp	His	Ala	Leu	Leu	Gly	Asn	Ile	Gly	His	Phe	Asp	Asn	Glu	Ile	Asp				
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Met	His	Ser	Leu	Leu	His	Arg	Asp	Asp	Val	Thr	Arg	Thr	Thr	Ile	Lys				
		355					360					365							
Pro	Gln	Val	Asp	Glu	Phe	Thr	Phe	Ser	Thr	Gly	Arg	Ser	Ile	Ile	Val				
	370					375					380								
Leu	Ser	Glu	Gly	Arg	Leu	Leu	Asn	Leu	Gly	Asn	Ala	Thr	Gly	His	Pro				
385					390					395					400				
Ser	Phe	Val	Met	Ser	Asn	Ser	Phe	Ala	Asp	Gln	Thr	Ile	Ala	Gln	Ile				
			405						410					415					
Glu	Leu	Phe	Gln	Asn	Glu	Gly	Gln	Tyr	Glu	Asn	Glu	Val	Tyr	Arg	Leu				
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<223> RXN02085
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										Met Thr Ser Asn Phe					
										1	5				
tct tcc act gtc gct ggt ctt cct cgc atc gga gcg aag cgt gaa ctg	163														
Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly Ala Lys Arg Glu Leu															
10	15	20													
aag ttc gcg ctc gaa ggc tac tgg aat gga tca att gaa ggt cgc gaa	211														
Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser Ile Glu Gly Arg Glu															
25	30	35													
ctt gcg cag acc gcc cgc caa ttg gtc aac act gca tcg gat tct ttg	259														
Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr Ala Ser Asp Ser Leu															
40	45	50													
tct gga ttg gat tcc gtt ccg ttt gca gga cgt tcc tac tac gac gca	307														
Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg Ser Tyr Tyr Asp Ala															
55	60	65													
atg ctc gat acc gcc gct att ttg ggt gtg ctg ccg gag cgt ttt gat	355														
Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu Pro Glu Arg Phe Asp															
70	75	80	85												

Met Ala Gln Val Met Asp Phe Lys Val Ala Asp Leu Ser Leu Ala Glu  
 1 5 10 15  
 Ala Gly Arg His Gln Ile Arg Leu Ala Glu Tyr Glu Met Pro Gly Leu  
 20 25 30  
 Met Gln Leu Arg Lys Glu Phe Ala Asp Glu Gln Pro Leu Lys Gly Ala  
 35 40 45  
 Arg Ile Ala Gly Ser Ile His Met Thr Val Gln Thr Ala Val Leu Ile  
 50 55 60  
 Glu Thr Leu Thr Ala Leu Gly Ala Glu Val Arg Trp Ala Ser Cys Asn  
 65 70 75 80  
 Ile Phe Ser Thr Gln Asp Glu Ala Ala Ala Ala Ile Val Val Gly Ser  
 85 90 95  
 Gly Thr Val Glu Glu Pro Ala Gly Val Pro Val Phe Ala Trp Lys Gly  
 100 105 110  
 Glu Ser Leu Glu Glu Tyr Trp Trp Cys Ile Asn Gln Ile Phe Ser Trp  
 115 120 125  
 Gly Asp Glu Leu Pro Asn Met Ile Leu Asp Asp Gly Gly Asp Ala Thr  
 130 135 140  
 Met Ala Val Ile Arg Gly Arg Glu Tyr Glu Gln Ala Gly Leu Val Pro  
 145 150 155 160  
 Pro Ala Glu Ala Asn Asp Ser Asp Glu Tyr Ile Ala Phe Leu Gly Met  
 165 170 175  
 Leu Arg Glu Val Leu Ala Ala Glu Pro Gly Lys Trp Gly Lys Ile Ala  
 180 185 190  
 Glu Ala Val Lys Gly Val Thr Glu Glu Thr Thr Thr Gly Val His Arg  
 195 200 205  
 Leu Tyr His Phe Ala Glu Glu Gly Val Leu Pro Phe Pro Ala Met Asn  
 210 215 220  
 Val Asn Asp Ala Val Thr Lys Ser Lys Phe Asp Asn Lys Tyr Gly Thr  
 225 230 235 240  
 Arg His Ser Leu Ile Asp Gly Ile Asn Arg Ala Thr Asp Met Leu Met  
 245 250 255  
 Gly Gly Lys Asn Val Leu Val Cys Gly Tyr Gly Asp Val Gly Lys Gly  
 260 265 270  
 Cys Ala Glu Ala Phe Asp Gly Gln Gly Ala Arg Val Lys Val Thr Glu  
 275 280 285  
 Ala Asp Pro Ile Asn Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser Val  
 290 295 300  
 Val Thr Val Asp Glu Ala Ile Glu Asp Ala Asp Ile Val Ile Thr Ala  
 305 310 315 320  
 Thr Gly Asn Lys Asp Ile Ile Ser Phe Glu Gln Met Leu Lys Met Lys

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ctt gtc tgc ggt tac ggc gat gtc ggc aag ggc tgc gct gag gct ttc 931
Leu Val Cys Gly Tyr Gly Asp Val Gly Lys Gly Cys Ala Glu Ala Phe
                265                      270                      275

gac ggc cag ggc gct cgc gtc aag gtc acc gaa gct gac cca atc aac 979
Asp Gly Gln Gly Ala Arg Val Lys Val Thr Glu Ala Asp Pro Ile Asn
                280                      285                      290

gct ctt cag gct ctg atg gat ggc tac tct gtg gtc acc gtt gat gag
1027
Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser Val Val Thr Val Asp Glu
                295                      300                      305

gcc atc gag gac gcc gac atc gtg atc acc gcg acc ggc aac aag gac
1075
Ala Ile Glu Asp Ala Asp Ile Val Ile Thr Ala Thr Gly Asn Lys Asp
310                      315                      320                      325

atc att tcc ttc gag cag atg ctc aag atg aag gat cac gct ctg ctg
1123
Ile Ile Ser Phe Glu Gln Met Leu Lys Met Lys Asp His Ala Leu Leu
                330                      335                      340

ggc aac atc ggt cac ttt gat aat gag atc gat atg cat tcc ctg ttg
1171
Gly Asn Ile Gly His Phe Asp Asn Glu Ile Asp Met His Ser Leu Leu
                345                      350                      355

cac cgc gac gac gtc acc cgc acc acg atc aag cca cag gtc gac gag
1219
His Arg Asp Asp Val Thr Arg Thr Thr Ile Lys Pro Gln Val Asp Glu
                360                      365                      370

ttc acc ttc tcc acc ggt cgc tcc atc atc gtc ctg tcc gaa ggt cgc
1267
Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile Val Leu Ser Glu Gly Arg
                375                      380                      385

ctg ttg aac ctt ggc aac gcc acc gga cac cca tca ttt gtc atg tcc
1315
Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro Ser Phe Val Met Ser
390                      395                      400                      405

aac tct ttc gcc gat cag acc att gcg cag atc gaa ctg ttc caa aac
1363
Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile Glu Leu Phe Gln Asn
                410                      415                      420

gaa gga cag tac gag aac gag gtc tac cgt ctg
1396
Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg Leu
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&lt;210&gt; 224

&lt;211&gt; 432

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 224

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Ile Arg Leu Ala Glu Tyr Glu Met Pro Gly Leu Met Gln Leu Arg Lys				
	25	30	35	
gaa ttc gca gac gag cag cct ttg aag ggc gcc cga att gct ggt tct				259
Glu Phe Ala Asp Glu Gln Pro Leu Lys Gly Ala Arg Ile Ala Gly Ser				
	40	45	50	
atc cac atg acg gtc cag acc gcc gtg ctt att gag acc ctc act gct				307
Ile His Met Thr Val Gln Thr Ala Val Leu Ile Glu Thr Leu Thr Ala				
	55	60	65	
ttg ggc gct gag gtt cgt tgg gct tcc tgc aac att ttc tcc acc cag				355
Leu Gly Ala Glu Val Arg Trp Ala Ser Cys Asn Ile Phe Ser Thr Gln				
	70	75	80	85
gat gag gct gca gcg gct atc gtt gtc ggc tcc ggc acc gtc gaa gag				403
Asp Glu Ala Ala Ala Ile Val Val Gly Ser Gly Thr Val Glu Glu				
	90	95	100	
cca gct ggt gtt cca gta ttc gcg tgg aag ggt gag tca ctg gag gag				451
Pro Ala Gly Val Pro Val Phe Ala Trp Lys Gly Glu Ser Leu Glu Glu				
	105	110	115	
tac tgg tgg tgc atc aac cag atc ttc agc tgg ggc gat gag ctg cca				499
Tyr Trp Trp Cys Ile Asn Gln Ile Phe Ser Trp Gly Asp Glu Leu Pro				
	120	125	130	
aac atg atc ctc gac gac ggc ggt gac gcc acc atg gct gtt att cgc				547
Asn Met Ile Leu Asp Asp Gly Gly Asp Ala Thr Met Ala Val Ile Arg				
	135	140	145	
ggt cgc gaa tac gag cag gct ggt ctg gtt cca cca gca gag gcc aac				595
Gly Arg Glu Tyr Glu Gln Ala Gly Leu Val Pro Pro Ala Glu Ala Asn				
	150	155	160	165
gat tcc gat gag tac atc gca ttc ttg ggc atg ctg cgt gag gtt ctt				643
Asp Ser Asp Glu Tyr Ile Ala Phe Leu Gly Met Leu Arg Glu Val Leu				
	170	175	180	
gct gca gag cct ggc aag tgg ggc aag atc gct gag gcc gtt aag ggt				691
Ala Ala Glu Pro Gly Lys Trp Gly Lys Ile Ala Glu Ala Val Lys Gly				
	185	190	195	
gtc acc gag gaa acc acc acc ggt gtg cac cgc ctg tac cac ttc gct				739
Val Thr Glu Glu Thr Thr Thr Gly Val His Arg Leu Tyr His Phe Ala				
	200	205	210	
gaa gaa ggc gtg ctg cct ttc cca gcg atg aac gtc aac gac gct gtc				787
Glu Glu Gly Val Leu Pro Phe Pro Ala Met Asn Val Asn Asp Ala Val				
	215	220	225	
acc aag tcc aag ttt gat aac aag tac ggc acc cgc cac tcc ctg atc				835
Thr Lys Ser Lys Phe Asp Asn Lys Tyr Gly Thr Arg His Ser Leu Ile				
	230	235	240	245
gac ggc atc aac cgc gcc act gac atg ctc atg ggc ggc aag aac gtg				883
Asp Gly Ile Asn Arg Ala Thr Asp Met Leu Met Gly Gly Lys Asn Val				
	250	255	260	

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 <213> Corynebacterium glutamicum

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 <223> FRXA00132

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 gct gag tac atc ggc gtt gac gtt gca ggc cca ttc aag ccg gag cac 96  
 Ala Glu Tyr Ile Gly Val Asp Val Ala Gly Pro Phe Lys Pro Glu His  
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 Tyr Arg Tyr  
 35

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 <212> PRT  
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<400> 222  
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 Ala Glu Tyr Ile Gly Val Asp Val Ala Gly Pro Phe Lys Pro Glu His  
 20 25 30  
 Tyr Arg Tyr  
 35

<210> 223  
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<220>  
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 <222> (101)..(1396)  
 <223> FRXA01371

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 Met Ala Gln Val Met  
 1 5  
 gac ttc aag gtt gcc gat ctt tca cta gca gag gca gga cgt cac cag 163  
 Asp Phe Lys Val Ala Asp Leu Ser Leu Ala Glu Ala Gly Arg His Gln



Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe Ala Ala Gln Ala Val  
 250 255 260

tgg acg ttg gcg cat gct gat gtc gca ggc ccc tac act ttg gtc gct 931  
 Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro Tyr Thr Leu Val Ala  
 265 270 275

gac ggc gcg ccg ttg ctg tcg gag ttc cca acg ctc acc acc gat gac 979  
 Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr Leu Thr Thr Asp Asp  
 280 285 290

ctc gcc gaa tac aac cca gag gct tac acc aac acg gtg tcc acg ttg  
 1027  
 Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn Thr Val Ser Thr Leu  
 295 300 305

ttt gcg ttg cag gat gga tcg ttg tcg agg gtc agt tcc ggc aat gtg  
 1075  
 Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val Ser Ser Gly Asn Val  
 310 315 320 325

agt cca cta cag ggc att tgg agc ggt gga gat atc gat tct gca gcg  
 1123  
 Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp Ile Asp Ser Ala Ala  
 330 335 340

att tcc tcc tcc gcc aat gtg gtg gca gcg gta cgc cac gaa aac aac  
 1171  
 Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val Arg His Glu Asn Asn  
 345 350 355

gag gca gtg ctt act gtt ggc tcc atg gaa ggc gtg act tca gat gcg  
 1219  
 Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly Val Thr Ser Asp Ala  
 360 365 370

ttg agg agt gaa acg atc act cgt ccc acc ttt gaa tac gcg tcg agt  
 1267  
 Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe Glu Tyr Ala Ser Ser  
 375 380 385

ggg ttg tgg gct gtg gtg gat ggg gag acg cct gtc cga gtc gca cga  
 1315  
 Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro Val Arg Val Ala Arg  
 390 395 400 405

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 1363  
 Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu Ala Glu Ile Val Leu  
 410 415 420

cca agg gat gtg acg ggt ccg atc tct gaa ttc caa ctg tca cga act  
 1411  
 Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe Gln Leu Ser Arg Thr  
 425 430 435

ggg gtc cgg gcc gcc atg atc att gaa ggc aag gtg tac gtg ggc gtc  
 1459  
 Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys Val Tyr Val Gly Val  
 440 445 450

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Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser Val Thr Thr Leu Val	
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gct ggg tgt tcc acg ctt ccg cag aac acg gat ccg caa gtg ctg cgc	211
Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp Pro Gln Val Leu Arg	
25 30 35	
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Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile Ala Gly Pro Thr Pro	
40 45 50	
aat caa gat ccg gat ttg ttg atc cgc ggc ttc ttc agc gca ggt gcg	307
Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe Phe Ser Ala Gly Ala	
55 60 65	
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Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala Tyr Leu Thr Glu Gly	
70 75 80 85	
acg cgc agc acg tgg aat ccg gct gcg tgc act cgt att ttg gat cgc	403
Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr Arg Ile Leu Asp Arg	
90 95 100	
att gat ctg aac act ctg cca ggt tgc acg aat gcg gaa cga acg att	451
Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn Ala Glu Arg Thr Ile	
105 110 115	
gcg atc cgt gga acg cag gtc gga acg ttg ctc agc ggt ggc gtg tat	499
Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu Ser Gly Gly Val Tyr	
120 125 130	
cag ccg gag aat gcg gag ttt gaa gct gag atc acg atg cgt cgg gaa	547
Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile Thr Met Arg Arg Glu	
135 140 145	
gat ggg gag tgg cgt atc gat gct ttg ccg gac ggg att tta tta gag	595
Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp Gly Ile Leu Leu Glu	
150 155 160 165	
aga aac gat ctg cgg aac cat tac act ccg cac gat gtg tat ttc ttt	643
Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His Asp Val Tyr Phe Phe	
170 175 180	
gat cct tct ggc cag gtg ttg gtg ggg gat ccg cgt tgg ttg ttc aat	691
Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg Arg Trp Leu Phe Asn	
185 190 195	
gag tgc cag tgc atg tcc acg gtg ctg atg gcc ctt ctg gtt aat ggt	739
Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala Leu Leu Val Asn Gly	
200 205 210	
cct tgc ccg gca att tct cct ggt gtg gtc aat cag ctg tcc acg gat	787
Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn Gln Leu Ser Thr Asp	
215 220 225	
gcg tgc ttc gtg ggg ttc aat gat ggg gag tat cag ttc act ggt ttg	835
Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr Gln Phe Thr Gly Leu	
230 235 240 245	
gga aat ttg gat gat gat gcg cgt ttg cgt ttc gcc gcc cag gcc gtg	883

gcc ctc gtg atc ttc gca gcc aag cgt gcg cgc cag atc aac agc ttc 259  
 Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg Gln Ile Asn Ser Phe  
                   40                                  45                                  50

tac cat cag gca gat gag gga gta ttc gag ttc atc gga cca ttg gtt 307  
 Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe Ile Gly Pro Leu Val  
                   55                                  60                                  65

act ccg cag cca ggc gaa aag cca ctt tct att gct ctg cgt gag atc 355  
 Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile Ala Leu Arg Glu Ile  
                   70                                  75                                  80                                  85

aat gca ggt ctg ttg gac cac gag gaa ggt taaaagacct tataacttca 405  
 Asn Ala Gly Leu Leu Asp His Glu Glu Gly  
                                   90                                  95

cac 408

<210> 238

<211> 95

<212> PRT

<213> Corynebacterium glutamicum

<400> 238

Val Thr Asn Val Ser Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp  
                   1                                  5                                  10                                  15

Pro Pro Val Gly Ile Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys  
                   20                                  25                                  30

Val Thr Ser Lys Tyr Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg  
                   35                                  40                                  45

Gln Ile Asn Ser Phe Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe  
                   50                                  55                                  60

Ile Gly Pro Leu Val Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile  
                   65                                  70                                  75                                  80

Ala Leu Arg Glu Ile Asn Ala Gly Leu Leu Asp His Glu Glu Gly  
                                   85                                  90                                  95

<210> 239

<211> 1827

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1804)

<223> RXC00128

<400> 239

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cgttgatcgc tccagagaca ccgtgggaag gggagcagca gtg agt aaa att tcg 115  
   Val Ser Lys Ile Ser  
   1  5

50                      55                      60

Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn  
65                      70                      75                      80

Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg  
                    85                      90                      95

Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu  
                    100                      105                      110

Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr  
                    115                      120                      125

Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn  
                    130                      135                      140

Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln  
145                      150                      155                      160

Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr  
                    165                      170                      175

Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr  
                    180                      185                      190

Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp  
                    195                      200                      205

Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val  
                    210                      215                      220

Gln Leu Asp Ala  
225

<210> 237  
<211> 408  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(385)  
<223> RXC02238

<400> 237  
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ctcttaaacac tactgtccat atacttttga aaagggtgtca gtg acc aac gtg agc 115  
Val Thr Asn Val Ser  
1 5  
aac gag acc aac gcc acc aag gcc gtc ttc gat ccg cca gtg ggc att 163  
Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp Pro Pro Val Gly Ile  
10 15 20  
acc gct cct ccg atc gat gaa ctg ctg gat aag gtc act tcc aag tac 211  
Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys Val Thr Ser Lys Tyr  
25 30 35

gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc 307  
 Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr  
 55 60 65  
 tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355  
 Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg  
 70 75 80 85  
 ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa 403  
 Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu  
 90 95 100  
 gca gtg cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat 451  
 Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp  
 105 110 115  
 cgt cgc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct 499  
 Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser  
 120 125 130  
 ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag ttc acc gga 547  
 Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly  
 135 140 145  
 cct att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg 595  
 Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu  
 150 155 160 165  
 ctg aag aag ggc atg aac gca gcg gga gct acc gac ggc ttc gtt gca 643  
 Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala  
 170 175 180  
 gca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac 691  
 Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp  
 185 190 195  
 act gat gaa gaa gtc gtc gca gca tgt gct gat gcg ctt tcc cag gaa 739  
 Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp Ala Leu Ser Gln Glu  
 200 205 210  
 tac aag atc atc acc gat gca ggt ctg acc gtt cag ctc gac gca 784  
 Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala  
 215 220 225

&lt;210&gt; 236

&lt;211&gt; 228

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 236

Met Ser Gln Asn Arg Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg  
 1 5 10 15

Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile  
 20 25 30

Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val  
 35 40 45

Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu

Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile  
 20 25 30

Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile  
 35 40 45

Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly  
 50 55 60

Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe  
 65 70 75 80

Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu  
 85 90 95

Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His  
 100 105 110

Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val  
 115 120 125

Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp  
 130 135 140

Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu  
 145 150 155 160

Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe  
 165 170 175

&lt;210&gt; 235

&lt;211&gt; 784

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(784)

&lt;223&gt; FRXA02658

&lt;400&gt; 235

atgaataaaa ttccgggtgc agtgaccgta ggtgaggtaa acgcgggttag agtcgaatga 60

gagtttgata ctttctttcg acttttagat tggattttca atg agc cag aac cgc 115  
 Met Ser Gln Asn Arg  
 1 5

atc agg acc act cac gtt ggt tcc ttg ccc cgt acc cca gag cta ctt 163  
 Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu  
 10 15 20

gat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc 211  
 Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe  
 25 30 35

ttc cag att ctg cag tct tct gta gat gac gtg atc aag cgc cag gtt 259  
 Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val  
 40 45 50

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(525)

&lt;223&gt; FRXA02648

&lt;400&gt; 233

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gac gca ccg gac ttg gca gaa gca tgg gat cag atc aac cca gag cca 48
Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro
  1             5             10             15

agc gtg aag gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc 96
Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile
             20             25             30

aac agt gca gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc 144
Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile
             35             40             45

tgc tgg ggc tct tgg cac gga cca cac gtc act gac atc cca ttc ggt 192
Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly
             50             55             60

gac atc att ggt gag atc ctg cgc gca gag gtc ggt ggc ttc tcc ttc 240
Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe
             65             70             75             80

gaa ggc gca tct cct cgt cac gca cac gag tgg cgt gta tgg gaa gaa 288
Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu
             85             90             95

aac aag ctt cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac 336
Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His
             100             105             110

tcc atc aac gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt 384
Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val
             115             120             125

cag ttc gcc aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac 432
Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp
             130             135             140

tgt ggt ctg ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg 480
Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu
             145             150             155             160

gag tcc cta gta gag ggc gct cgc att gca tca aag gaa ctg ttc 525
Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
             165             170             175

taagctagac aacgagggtt gct 548

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&lt;210&gt; 234

&lt;211&gt; 175

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 234

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Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro
  1             5             10             15

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Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn  
 130 135 140  
 Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln  
 145 150 155 160  
 Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr  
 165 170 175  
 Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr  
 180 185 190  
 Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp  
 195 200 205  
 Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val  
 210 215 220  
 Gln Leu Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro  
 225 230 235 240  
 Glu Pro Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp  
 245 250 255  
 Ala Ile Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu  
 260 265 270  
 His Ile Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro  
 275 280 285  
 Phe Gly Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe  
 290 295 300  
 Ser Phe Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp  
 305 310 315 320  
 Glu Glu Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val  
 325 330 335  
 Ser His Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg  
 340 345 350  
 Ile Val Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser  
 355 360 365  
 Thr Asp Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala  
 370 375 380  
 Lys Leu Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu  
 385 390 395 400  
 Phe

&lt;210&gt; 233

&lt;211&gt; 548

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum



Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu Asn Lys Leu  
310 315 320 325

cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac tcc atc aac  
1123

Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His Ser Ile Asn  
330 335 340

gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt cag ttc gcc  
1171

Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val Gln Phe Ala  
345 350 355

aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac tgt ggt ctg  
1219

Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp Cys Gly Leu  
360 365 370

ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg gag tcc cta  
1267

Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu Glu Ser Leu  
375 380 385

gta gag ggc gct cgc att gca tca aag gaa ctg ttc taagctagac  
1313

Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe  
390 395 400

aacgagggtt gct  
1326

<210> 232

<211> 401

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 232

Met Ser Gln Asn Arg Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg  
1 5 10 15

Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile  
20 25 30

Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val  
35 40 45

Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu  
50 55 60

Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn  
65 70 75 80

Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg  
85 90 95

Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu  
100 105 110

Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr  
115 120 125

70	75	80	85	
ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa	403			
Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu				
	90	95	100	
gca gtg cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat	451			
Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp				
	105	110	115	
cgt cgc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct	499			
Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser				
	120	125	130	
ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag ttc acc gga	547			
Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly				
	135	140	145	
cct att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg	595			
Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu				
	150	155	160	165
ctg aag aag ggc atg aac gca gcg gga gct acc gac ggc ttc gtt gca	643			
Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala				
	170	175	180	
gca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac	691			
Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp				
	185	190	195	
act gat gaa gaa gtc gtc gca gca tgt gct gat gcg ctt tcc cag gaa	739			
Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp Ala Leu Ser Gln Glu				
	200	205	210	
tac aag atc atc acc gat gca ggt ctg acc gtt cag ctc gac gca ccg	787			
Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala Pro				
	215	220	225	
gac ttg gca gaa gca tgg gat cag atc aac cca gag cca agc gtg aag	835			
Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro Ser Val Lys				
	230	235	240	245
gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc aac agt gca	883			
Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile Asn Ser Ala				
	250	255	260	
gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc tgc tgg ggc	931			
Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile Cys Trp Gly				
	265	270	275	
tct tgg cac gga cca cac gtc act gac atc cca ttc ggt gac atc att	979			
Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly Asp Ile Ile				
	280	285	290	
ggg gag atc ctg cgc gca gag gtc ggt ggc ttc tcc ttc gaa ggc gca				
1027				
Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe Glu Gly Ala				
	295	300	305	
tct cct cgt cac gca cac gag tgg cgt gta tgg gaa gaa aac aag ctt				
1075				

Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr  
 50 55 60  
 Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys  
 65 70 75 80  
 Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val Trp Asp Ile His  
 85 90 95  
 Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala  
 100 105 110  
 Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys  
 115 120 125  
 Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val  
 130 135 140  
 Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile Gly Ala Thr Ile  
 145 150 155 160

<210> 231  
 <211> 1326  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1303)  
 <223> RXN02648

<400> 231  
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 gagtttgata ctttctttcg acttttagat tggattttca atg agc cag aac cgc 115  
 Met Ser Gln Asn Arg  
 1 5  
 atc agg acc act cac gtt ggt tcc ttg ccc cgt acc cca gag cta ctt 163  
 Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu  
 10 15 20  
 gat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc 211  
 Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe  
 25 30 35  
 ttc cag att ctg cag tct tct gta gat gac gtg atc aag cgc cag gtt 259  
 Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val  
 40 45 50  
 gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc 307  
 Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr  
 55 60 65  
 tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355  
 Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg

aacgatctca	tcgaggctgg	cgcgaaagatc	atccagggtgg	atg	agc	ctg	cga	ttc	115
				Met	Ser	Leu	Arg	Phe	
				1				5	
gtg aac tgt tgc ccg cta cga gac gtc gat aag cct gcc tac ctg cag	163								
Val Asn Cys Cys Pro Leu Arg Asp Val Asp Lys Pro Ala Tyr Leu Gln									
10 15 20									
tgg tcc gtg gac tcc ttc cgc ctg gcg act gcc ggc gca ccc gac gac	211								
Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp									
25 30 35									
gtc caa atc cac acc cac atg tgc tac tcc gag ttc aac gaa gtg atc	259								
Val Gln Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu Val Ile									
40 45 50									
tcc tcg gtc atc gcg ttg gat gcc gat gtc acc acc atc gaa gca gca	307								
Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu Ala Ala									
55 60 65									
cgt tcc gac atg cag gtc ctc gct gct ctg aaa tct tcc ggc ttc gag	355								
Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly Phe Glu									
70 75 80 85									
ctc ggc gtc gga cct ggt gtg tgg gat atc cac tcc ccg cgc gtt cct	403								
Leu Gly Val Gly Pro Gly Val Trp Asp Ile His Ser Pro Arg Val Pro									
90 95 100									
tcc gcg cag aaa gtg gac ggt ctc ctc gag gct gca ctg cag tcc gtg	451								
Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala Ala Leu Gln Ser Val									
105 110 115									
gat cct cgc cag ctg tgg gtc aac cca gac tgt ggt ctg aag acc cgt	499								
Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg									
120 125 130									
gga tgg cca gaa gtg gaa gct tcc cta aag gtt ctc gtt gag tcc gct	547								
Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val Leu Val Glu Ser Ala									
135 140 145									
aag cag gct cgt gag aaa atc gga gca act atc taaattgggt taccgctagg	600								
Lys Gln Ala Arg Glu Lys Ile Gly Ala Thr Ile									
150 155 160									
aac	603								

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<210> 230
<211> 160
<212> PRT
<213> Corynebacterium glutamicum
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<400> 230
Met Ser Leu Arg Phe Val Asn Cys Cys Pro Leu Arg Asp Val Asp Lys
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Pro Ala Tyr Leu Gln Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala
          20             25             30
Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met Cys Tyr Ser Glu
      35             40             45

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355	360	365
Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro		
370	375	380
Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg		
385	390	395
Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr		
	405	410
Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala		
	420	425
Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met		
	435	440
Arg Glu Glu Ile Asp Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu		
	450	455
Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr		
	465	470
Phe Ser Glu Leu Leu Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val		
	485	490
Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn		
	500	505
Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln		
	515	520
Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr		
	530	535
Ile Leu Ala Trp Ser Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr		
	545	550
Ala Asp Gln Val Ala Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile		
	565	570
Glu Ala Gly Ala Lys Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu		
	580	585
Leu Leu Pro Ala Thr Arg Arg Arg		
	595	600

&lt;210&gt; 229

&lt;211&gt; 603

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(580)

&lt;223&gt; FRXA02086

&lt;400&gt; 229

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Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr  
                   35                                  40                                  45  
 Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg  
                   50                                  55                                  60  
 Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu  
                   65                                  70                                  75                                  80  
 Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro  
                                   85                                  90                                  95  
 Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu  
                                   100                                  105                                  110  
 Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu  
                                   115                                  120                                  125  
 Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala  
                                   130                                  135                                  140  
 Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg  
                                   145                                  150                                  155                                  160  
 Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr  
                                   165                                  170                                  175  
 Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr  
                                   180                                  185                                  190  
 Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu  
                                   195                                  200                                  205  
 Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg  
                                   210                                  215                                  220  
 Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr  
                                   225                                  230                                  235                                  240  
 Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly  
                                   245                                  250                                  255  
 Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu  
                                   260                                  265                                  270  
 Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly  
                                   275                                  280                                  285  
 Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys  
                                   290                                  295                                  300  
 Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu  
                                   305                                  310                                  315                                  320  
 Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val  
                                   325                                  330                                  335  
 Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu  
                                   340                                  345                                  350  
 Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala

ctg ctt atc gtg gct ggc ggc gtt gtt tcg agc ctg ggc acg tgg tgg	211
Leu Leu Ile Val Ala Gly Gly Val Val Ser Ser Leu Gly Thr Trp Trp	
25 30 35	
ggc agc gcg ctg atg gcg cgc gcg ttg gag ccg gcg atc gcg ggg ctg	259
Gly Ser Ala Leu Met Ala Arg Ala Leu Glu Pro Ala Ile Ala Gly Leu	
40 45 50	
cgc gag gat gtg ttg cgc gcg gcg gtg agt ttg gat gcg aac acg att	307
Arg Glu Asp Val Leu Arg Ala Ala Val Ser Leu Asp Ala Asn Thr Ile	
55 60 65	
gaa acg gcg ggg cgc ggc gac gtg att tcg cgt atc gcg gat gat tcg	355
Glu Thr Ala Gly Arg Gly Asp Val Ile Ser Arg Ile Ala Asp Asp Ser	
70 75 80 85	
cgg gag gtg tcc act gcg gcg agc acc gtg gtg ccg ctg atg gtg cag	403
Arg Glu Val Ser Thr Ala Ala Ser Thr Val Val Pro Leu Met Val Gln	
90 95 100	
gcg ggc ttt acc gtg gtg att tcc gcg ttt ggc atg gcg gcg gtt gat	451
Ala Gly Phe Thr Val Val Ile Ser Ala Phe Gly Met Ala Ala Val Asp	
105 110 115	
tgg cgc ctc ggc ctt gtc ggt ttg gtc gcg atc ccg ctg tat tgg acc	499
Trp Arg Leu Gly Leu Val Gly Leu Val Ala Ile Pro Leu Tyr Trp Thr	
120 125 130	
acg ttg cgc gtc tat tta ccc cgc tca ggt ccg ctt tat acg cgt gag	547
Thr Leu Arg Val Tyr Leu Pro Arg Ser Gly Pro Leu Tyr Thr Arg Glu	
135 140 145	
cgc gag gcc ttt ggg gtg cgc acg cag ccg ctt gtc ggc gca gtc gaa	595
Arg Glu Ala Phe Gly Val Arg Thr Gln Arg Leu Val Gly Ala Val Glu	
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ggc gcg gaa acc ttg cgc gct ttc cgc gca gaa gat aca gaa tta aag	643
Gly Ala Glu Thr Leu Arg Ala Phe Arg Ala Glu Asp Thr Glu Leu Lys	
170 175 180	
cgt atc gac gca gcc tcc ggc gaa gcc cgc gac att tcc att tct gtt	691
Arg Ile Asp Ala Ala Ser Gly Glu Ala Arg Asp Ile Ser Ile Ser Val	
185 190 195	
ttc agg ttc ctc aca tgg gca ttt tcc cgc aac aac cgc gcg gaa tgc	739
Phe Arg Phe Leu Thr Trp Ala Phe Ser Arg Asn Asn Arg Ala Glu Cys	
200 205 210	
atc acc ctc gtg ctc atc ttg ggc acc ggc ttt tac ctg gtc aac atc	787
Ile Thr Leu Val Leu Ile Leu Gly Thr Gly Phe Tyr Leu Val Asn Ile	
215 220 225	
gat ctg gtc acc gtc ggc gca gtc tca acc gcc gca ctg atc ttc cac	835
Asp Leu Val Thr Val Gly Ala Val Ser Thr Ala Ala Leu Ile Phe His	
230 235 240 245	
cga ctc ttc ggt cca atc ggc acg ctc gtg ggc atg ttc tcc gac atc	883
Arg Leu Phe Gly Pro Ile Gly Thr Leu Val Gly Met Phe Ser Asp Ile	
250 255 260	
caa tcc gcc agc gca tcg ctg atc cgc atg gtg ggc gtt att aac gcg	931

Leu Leu Ala Gly Leu Arg Val Pro Asp Gln Gly Gln Val Leu Val Asp  
 370 375 380  
 Asp Phe Pro Val Ser His Leu Ser Asp Arg Glu Arg Ile Ala Arg Leu  
 385 390 395 400  
 Ala Met Val Ser Gln Glu Val His Val Phe Ser Gly Thr Leu Arg Gln  
 405 410 415  
 Asp Leu Thr Leu Ala Lys Pro Asp Ala Ser Asp Glu Glu Leu Ala His  
 420 425 430  
 Ala Leu Gly Gln Val Asn Ala Leu Asp Trp Leu Glu Ser Leu Pro Glu  
 435 440 445  
 Gly Leu Asp Thr Val Val Gly Ala Arg Gly Ile Gln Leu Glu Pro Val  
 450 455 460  
 Val Ala Gln Gln Leu Ala Leu Ala Arg Val Leu Leu Leu Asn Pro Ala  
 465 470 475 480  
 Ile Val Ile Met Asp Glu Ala Thr Ala Glu Ala Gly Ser Ala Gly Ala  
 485 490 495  
 Ser Ala Leu Glu Glu Ala Ala Asp Ala Val Ser Lys Asn Arg Ser Ala  
 500 505 510  
 Leu Val Val Ala His Arg Leu Asp Gln Ala Ser Arg Ala Asp Gln Ile  
 515 520 525  
 Leu Val Met Asp Lys Gly Glu Val Val Glu Ser Gly Thr His Gln Glu  
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 <213> Corynebacterium glutamicum

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 <222> (101)..(1690)  
 <223> RXC01191

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 Val Gly Gly Leu Val  
 1 5  
 gat aag ctc ctt gca acc ccg agc atg cgc gac gtt gta gtg ttc gcg 163  
 Asp Lys Leu Leu Ala Thr Pro Ser Met Arg Asp Val Val Val Phe Ala  
 10 15 20



Val Glu Leu Ser Val Ile Leu Ile Ala Val Ala Ile Ala Gly Ala Val  
 50 55 60  
 Leu Ser Ala Cys Gly Phe Tyr Val Val Ser Arg Ile Ser Glu Lys Ile  
 65 70 75 80  
 Ile Ala Asn Leu Arg Glu Asp Met Val Gly Thr Ala Leu Gly Leu Pro  
 85 90 95  
 Thr His Gln Val Glu Asp Ala Gly Ser Gly Asp Leu Val Ser Arg Ser  
 100 105 110  
 Thr Asp Asp Val Ser Glu Leu Ser Ala Ala Val Thr Glu Thr Val Pro  
 115 120 125  
 Ile Leu Ser Ser Ser Leu Phe Thr Ile Ala Ala Thr Ile Ile Ala Leu  
 130 135 140  
 Phe Ser Leu Asp Trp Gln Phe Val Leu Ile Pro Val Val Val Ala Pro  
 145 150 155 160  
 Val Tyr Tyr Phe Ala Ser Lys His Tyr Leu Ser Lys Ala Pro Asp Arg  
 165 170 175  
 Tyr Ala Ala Glu Arg Ala Ala Met Ala Glu Arg Ala Arg Lys Val Leu  
 180 185 190  
 Glu Ala Ile Arg Gly Arg Ala Thr Val Arg Ala Tyr Ser Met Glu Asp  
 195 200 205  
 Ala Met His Asn Gln Ile Asp Gln Ala Ser Trp Ser Val Val Val Lys  
 210 215 220  
 Gly Ile Arg Ala Arg Thr Thr Met Leu Ile Leu Asn Met Trp Met Leu  
 225 230 235 240  
 Phe Ala Glu Phe Leu Met Leu Ala Val Ala Leu Val Ile Gly Tyr Lys  
 245 250 255  
 Leu Val Ile Asp Asn Ala Leu Thr Ile Gly Ala Val Thr Gly Ala Val  
 260 265 270  
 Leu Met Ile Ile Arg Leu Arg Gly Pro Met Asn Met Phe Met Arg Val  
 275 280 285  
 Leu Asp Thr Ile Gln Ser Gly Tyr Ala Ser Leu Ala Arg Ile Val Gly  
 290 295 300  
 Val Val Ala Asp Pro Pro Ile Pro Val Pro Asp Ser Gly Val Lys Ala  
 305 310 315 320  
 Pro Gln Gly Lys Val Glu Leu Arg Asn Val Ser Phe Ser Tyr Gly Asp  
 325 330 335  
 Ser Trp Ala Val Lys Asp Ile Asp Ile Thr Ile Asn Ser Gly Glu Thr  
 340 345 350  
 Val Ala Leu Val Gly Ala Ser Gly Ala Gly Lys Thr Thr Val Ala Ala  
 355 360 365

Lys Pro Asp Ala Ser Asp Glu Glu Leu Ala His Ala Leu Gly Gln Val  
 425 430 435  
 aat gcc ctt gac tgg ttg gag agt ctt cca gaa gga ctg gac acg gtc  
 1459  
 Asn Ala Leu Asp Trp Leu Glu Ser Leu Pro Glu Gly Leu Asp Thr Val  
 440 445 450  
 gtt ggt gcg cga gga atc cag cta gaa cca gtg gtg gct cag cag ttg  
 1507  
 Val Gly Ala Arg Gly Ile Gln Leu Glu Pro Val Val Ala Gln Gln Leu  
 455 460 465  
 gcg ttg gcc cgg gtg ttg ttg ctc aat ccg gcg atc gtc atc atg gat  
 1555  
 Ala Leu Ala Arg Val Leu Leu Asn Pro Ala Ile Val Ile Met Asp  
 470 475 480 485  
 gaa gcc acg gca gaa gca gga tcg gcg ggt gcc agc gca ctg gaa gag  
 1603  
 Glu Ala Thr Ala Glu Ala Gly Ser Ala Gly Ala Ser Ala Leu Glu Glu  
 490 495 500  
 gct gca gat gca gtg agc aag aac cgt tcc gca ttg gtg gtg gcg cac  
 1651  
 Ala Ala Asp Ala Val Ser Lys Asn Arg Ser Ala Leu Val Val Ala His  
 505 510 515  
 cgg ttg gat cag gca tcg cgg gct gat cag att ctg gtg atg gat aag  
 1699  
 Arg Leu Asp Gln Ala Ser Arg Ala Asp Gln Ile Leu Val Met Asp Lys  
 520 525 530  
 ggg gag gtt gtg gaa tcc ggt act cac cag gag tta ttg gat cac ggg  
 1747  
 Gly Glu Val Val Glu Ser Gly Thr His Gln Glu Leu Leu Asp His Gly  
 535 540 545  
 ggt att tat cag cgt ctg tgg act gcg tgg agt gtc gga aga  
 1789  
 Gly Ile Tyr Gln Arg Leu Trp Thr Ala Trp Ser Val Gly Arg  
 550 555 560  
 tagttgactg ttcaatgcgt tga  
 1812

&lt;210&gt; 254

&lt;211&gt; 563

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 254

Val Gly Arg Ile Pro Arg Ala Lys Trp Trp Phe Leu Gly Ala Leu Val  
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Leu Leu Ser Ala Gly Ala Tyr Ala Ser Val Leu Val Pro Gln Val Leu  
 20 25 30

Gly Arg Ile Val Asp Leu Val Ser Asp Gly Ala Gln Met Arg Asp Phe  
 35 40 45

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Ile Asp Gln Ala Ser Trp Ser Val Val Val Lys Gly Ile Arg Ala Arg
215                220                225

acc acc atg ttg att ttg aac atg tgg atg ctg ttt gcg gaa ttc ctc      835
Thr Thr Met Leu Ile Leu Asn Met Trp Met Leu Phe Ala Glu Phe Leu
230                235                240                245

atg ctc gcg gtc gcg ttg gtg atc ggc tac aag ctg gtc att gat aat      883
Met Leu Ala Val Ala Leu Val Ile Gly Tyr Lys Leu Val Ile Asp Asn
                250                255                260

gcg ctg acg atc ggc gcg gtt acc ggt gcc gtg ctg atg att att cgt      931
Ala Leu Thr Ile Gly Ala Val Thr Gly Ala Val Leu Met Ile Ile Arg
                265                270                275

ctg cgt ggc ccg atg aat atg ttc atg cgc gtg ctc gac acc att caa      979
Leu Arg Gly Pro Met Asn Met Phe Met Arg Val Leu Asp Thr Ile Gln
                280                285                290

tcc ggc tat gcg tcg ctg gcg cgc atc gtg gga gtt gtt gcg gat ccg
1027
Ser Gly Tyr Ala Ser Leu Ala Arg Ile Val Gly Val Val Ala Asp Pro
295                300                305

ccg att cct gtg ccc gac agc ggt gtg aaa gca cct cag ggc aaa gtg
1075
Pro Ile Pro Val Pro Asp Ser Gly Val Lys Ala Pro Gln Gly Lys Val
310                315                320                325

gaa ttg cgc aac gtc agc ttt agc tat ggc gat tcc tgg gcg gtg aaa
1123
Glu Leu Arg Asn Val Ser Phe Ser Tyr Gly Asp Ser Trp Ala Val Lys
330                335                340

gac atc gac atc acg atc aat tcc ggc gaa act gtc gcg ctc gtg ggc
1171
Asp Ile Asp Ile Thr Ile Asn Ser Gly Glu Thr Val Ala Leu Val Gly
345                350                355

gca tct ggc gca ggt aag acg acg gtc gcc gcc ttg ctg gcg ggc ttg
1219
Ala Ser Gly Ala Gly Lys Thr Thr Val Ala Ala Leu Leu Ala Gly Leu
360                365                370

cgg gtg cca gat caa ggg caa gtg ctt gtc gac gac ttc ccc gtc tct
1267
Arg Val Pro Asp Gln Gly Gln Val Leu Val Asp Asp Phe Pro Val Ser
375                380                385

cac ctc tct gac cgc gag cgt atc gcc cgc ttg gcc atg gtc agc cag
1315
His Leu Ser Asp Arg Glu Arg Ile Ala Arg Leu Ala Met Val Ser Gln
390                395                400                405

gag gtt cat gtt ttc tcc ggc acg ctg cgc cag gat ctc acc ttg gct
1363
Glu Val His Val Phe Ser Gly Thr Leu Arg Gln Asp Leu Thr Leu Ala
410                415                420

aaa cca gat gcc tcc gat gag gaa tta gcg cat gct ctt ggg caa gtt
1411

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ggccagcctg ccgcaagtgc ggcgcgaggt ggcccggcag gtg ggt cgt att ccg 115  
 Val Gly Arg Ile Pro  
 1 5

cgg gcg aag tgg tgg ttt tta ggc gcg ctg gtg ttg ctg agt gcg ggc 163  
 Arg Ala Lys Trp Trp Phe Leu Gly Ala Leu Val Leu Leu Ser Ala Gly  
 10 15 20

gct tat gcg tcg gtg ctg gtg ccg cag gtg ctg ggg cgg att gtg gat 211  
 Ala Tyr Ala Ser Val Leu Val Pro Gln Val Leu Gly Arg Ile Val Asp  
 25 30 35

ctg gtg tcc gat ggc gcg cag atg cgt gat ttt gtt gag ctc agt gtg 259  
 Leu Val Ser Asp Gly Ala Gln Met Arg Asp Phe Val Glu Leu Ser Val  
 40 45 50

att ctc att gcg gtg gca att gcc ggc gcg gtg ctc agt gcg tgc ggg 307  
 Ile Leu Ile Ala Val Ala Ile Ala Gly Ala Val Leu Ser Ala Cys Gly  
 55 60 65

ttc tat gtg gtg tcg cgg att tct gag aag att atc gcc aat ttg agg 355  
 Phe Tyr Val Val Ser Arg Ile Ser Glu Lys Ile Ile Ala Asn Leu Arg  
 70 75 80 85

gaa gat atg gtg ggc acc gcg ctt ggg ttg ccc acg cac cag gtg gaa 403  
 Glu Asp Met Val Gly Thr Ala Leu Gly Leu Pro Thr His Gln Val Glu  
 90 95 100

gat gcg ggc tct ggc gat ttg gtg agc cgc tcc acc gat gat gtc tcc 451  
 Asp Ala Gly Ser Gly Asp Leu Val Ser Arg Ser Thr Asp Asp Val Ser  
 105 110 115

gag cta tcc gca gcg gtg aca gag acc gtc ccg att tta agt tcc tca 499  
 Glu Leu Ser Ala Ala Val Thr Glu Thr Val Pro Ile Leu Ser Ser Ser  
 120 125 130

ctg ttt acc att gcc gcg acg atc att gcg ctg ttt tct ttg gac tgg 547  
 Leu Phe Thr Ile Ala Ala Thr Ile Ile Ala Leu Phe Ser Leu Asp Trp  
 135 140 145

caa ttt gtg ctc att cct gtc gtg gtg gcg ccg gtg tac tac ttc gcg 595  
 Gln Phe Val Leu Ile Pro Val Val Val Ala Pro Val Tyr Tyr Phe Ala  
 150 155 160 165

tcc aag cac tat ttg agc aag gcg ccg gat cgg tat gcg gca gaa cgc 643  
 Ser Lys His Tyr Leu Ser Lys Ala Pro Asp Arg Tyr Ala Ala Glu Arg  
 170 175 180

gcg gcg atg gcg gag cgt gcg cga aag gta ctt gag gct att cgc ggg 691  
 Ala Ala Met Ala Glu Arg Ala Arg Lys Val Leu Glu Ala Ile Arg Gly  
 185 190 195

cgt gca act gtg cgg gcg tat tcc atg gaa gat gcc atg cat aat cag 739  
 Arg Ala Thr Val Arg Ala Tyr Ser Met Glu Asp Ala Met His Asn Gln  
 200 205 210

att gat cag gcg tcg tgg tct gtg gtg gtc aag ggt att cgt gcg cgc 787

Ile Asp Val Ser Phe Val Glu Asn Pro Asp Asp Pro Glu Ser Trp Gln  
 135 140 145

gca gcc gtt cag cca aac acc aaa gca ttc ttc ggc gag act ttc gcc 595  
 Ala Ala Val Gln Pro Asn Thr Lys Ala Phe Phe Gly Glu Thr Phe Ala  
 150 155 160 165

aac cca cag gca gac gtc 613  
 Asn Pro Gln Ala Asp Val  
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<210> 252  
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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 252  
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Arg Ser Ile His Ala Gly Gln Ser Val Asp Ala Gln Thr Ser Ala Arg  
 20 25 30

Asn Leu Pro Ile Tyr Gln Ser Thr Ala Phe Val Phe Asp Ser Ala Glu  
 35 40 45

His Ala Lys Gln Arg Phe Ala Leu Glu Asp Leu Gly Pro Val Tyr Ser  
 50 55 60

Arg Leu Thr Asn Pro Thr Val Glu Ala Leu Glu Asn Arg Ile Ala Ser  
 65 70 75 80

Leu Glu Gly Gly Val His Ala Val Ala Phe Ser Ser Gly Gln Ala Ala  
 85 90 95

Thr Thr Asn Ala Ile Leu Asn Leu Ala Gly Ala Gly Asp His Ile Val  
 100 105 110

Thr Ser Pro Arg Leu Tyr Gly Gly Thr Glu Thr Leu Phe Leu Ile Thr  
 115 120 125

Leu Asn Arg Leu Gly Ile Asp Val Ser Phe Val Glu Asn Pro Asp Asp  
 130 135 140

Pro Glu Ser Trp Gln Ala Ala Val Gln Pro Asn Thr Lys Ala Phe Phe  
 145 150 155 160

Gly Glu Thr Phe Ala Asn Pro Gln Ala Asp Val  
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<220>  
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 <222> (101)..(1789)  
 <223> RXC00164

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 165 170 175

Thr Ile Asp Asp Ile Ile Ala Asp Leu Glu Gly Gly Phe Ala Ala Ile  
 180 185 190

<210> 251

<211> 613

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(613)

<223> RXS00405

<400> 251

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 ggagaagaat ttcctaataa aaactcttaa ggacctccaa atg cca aag tac gac 115  
 Met Pro Lys Tyr Asp  
 1 5  
 aat tcc aat gct gac cag tgg ggc ttt gaa acc cgc tcc att cac gca 163  
 Asn Ser Asn Ala Asp Gln Trp Gly Phe Glu Thr Arg Ser Ile His Ala  
 10 15 20  
 ggc cag tca gta gac gca cag acc agc gca cga aac ctt ccg atc tac 211  
 Gly Gln Ser Val Asp Ala Gln Thr Ser Ala Arg Asn Leu Pro Ile Tyr  
 25 30 35  
 caa tcc acc gct ttc gtg ttc gac tcc gct gag cac gcc aag cag cgt 259  
 Gln Ser Thr Ala Phe Val Phe Asp Ser Ala Glu His Ala Lys Gln Arg  
 40 45 50  
 ttc gca ctt gag gat cta ggc cct gtt tac tcc cgc ctc acc aac cca 307  
 Phe Ala Leu Glu Asp Leu Gly Pro Val Tyr Ser Arg Leu Thr Asn Pro  
 55 60 65  
 acc gtt gag gct ttg gaa aac cgc atc gct tcc ctc gaa ggt ggc gtc 355  
 Thr Val Glu Ala Leu Glu Asn Arg Ile Ala Ser Leu Glu Gly Gly Val  
 70 75 80 85  
 cac gct gta gcg ttc tcc tcc gga cag gcc gca acc acc aac gcc att 403  
 His Ala Val Ala Phe Ser Ser Gly Gln Ala Ala Thr Thr Asn Ala Ile  
 90 95 100  
 ttg aac ctg gca gga gcg ggc gac cac atc gtc acc tcc cca cgc ctc 451  
 Leu Asn Leu Ala Gly Ala Gly Asp His Ile Val Thr Ser Pro Arg Leu  
 105 110 115  
 tac ggt ggc acc gag act cta ttc ctt atc act ctt aac cgc ctg ggt 499  
 Tyr Gly Gly Thr Glu Thr Leu Phe Leu Ile Thr Leu Asn Arg Leu Gly  
 120 125 130  
 atc gat gtt tcc ttc gtg gaa aac ccc gac gac cct gag tcc tgg cag 547

Lys Glu Lys Leu Gly Leu Lys Tyr Thr Gly Ser Val Leu Thr Phe Glu  
 100 105 110  
 atc aag ggc ggc aag gat gag gct tgg gca ttt atc gac gcc ctg aag 384  
 Ile Lys Gly Gly Lys Asp Glu Ala Trp Ala Phe Ile Asp Ala Leu Lys  
 115 120 125  
 cta cac tcc aac ctt gca aac atc ggc gat gtt cgc tcc ctc gtt gtt 432  
 Leu His Ser Asn Leu Ala Asn Ile Gly Asp Val Arg Ser Leu Val Val  
 130 135 140  
 cac cca gca acc acc acc cat tca cag tcc gac gaa gct ggc ctg gca 480  
 His Pro Ala Thr Thr Thr His Ser Gln Ser Asp Glu Ala Gly Leu Ala  
 145 150 155 160  
 cgc gcg ggc gtt acc cag tcc acc gtc cgc ctg tcc gtt ggc atc gag 528  
 Arg Ala Gly Val Thr Gln Ser Thr Val Arg Leu Ser Val Gly Ile Glu  
 165 170 175  
 acc att gat gat atc atc gct gac ctc gaa ggc ggc ttt gct gca atc 576  
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 <212> PRT  
 <213> Corynebacterium glutamicum

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 35 40 45  
 Ala Val Gln Gly Ile Asp Thr Leu Ser Leu Arg Leu Glu Arg His Asn  
 50 55 60  
 Glu Asn Ala Ile Lys Val Ala Glu Phe Leu Asn Asn His Glu Lys Val  
 65 70 75 80  
 Glu Lys Val Asn Phe Ala Gly Leu Lys Asp Ser Pro Trp Tyr Ala Thr  
 85 90 95  
 Lys Glu Lys Leu Gly Leu Lys Tyr Thr Gly Ser Val Leu Thr Phe Glu  
 100 105 110  
 Ile Lys Gly Gly Lys Asp Glu Ala Trp Ala Phe Ile Asp Ala Leu Lys  
 115 120 125  
 Leu His Ser Asn Leu Ala Asn Ile Gly Asp Val Arg Ser Leu Val Val  
 130 135 140  
 His Pro Ala Thr Thr Thr His Ser Gln Ser Asp Glu Ala Gly Leu Ala  
 145 150 155 160

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Val	Leu	Pro	Tyr	Phe	Val	Thr	Pro	Asp	Ala	Ala	Tyr	His	Gly	Leu	Lys		48	
1				5					10					15				
tac	gca	gac	ctt	ggt	gca	cca	gcc	ttc	ggc	ctc	aag	gtt	cgc	gtt	ggc			
Tyr	Ala	Asp	Leu	Gly	Ala	Pro	Ala	Phe	Gly	Leu	Lys	Val	Arg	Val	Gly		96	
			20					25					30					
ctt	cta	cgc	gac	acc	ggc	tcc	acc	ctc	tcc	gca	ttc	aac	gca	tgg	gct			
Leu	Leu	Arg	Asp	Thr	Gly	Ser	Thr	Leu	Ser	Ala	Phe	Asn	Ala	Trp	Ala		144	
		35					40					45						
gca	gtc	cag	ggc	atc	gac	acc	ctt	tcc	ctg	cgc	ctg	gag	cgc	cac	aac			
Ala	Val	Gln	Gly	Ile	Asp	Thr	Leu	Ser	Leu	Arg	Leu	Glu	Arg	His	Asn		192	
	50					55					60							
gaa	aac	gcc	atc	aag	gtt	gca	gaa	ttc	ctc	aac	aac	cac	gag	aag	gtg			
Glu	Asn	Ala	Ile	Lys	Val	Ala	Glu	Phe	Leu	Asn	Asn	His	Glu	Lys	Val		240	
65				70						75				80				
gaa	aag	gtt	aac	ttc	gca	ggc	ctg	aag	gat	tcc	cct	tgg	tac	gca	acc			
Glu	Lys	Val	Asn	Phe	Ala	Gly	Leu	Lys	Asp	Ser	Pro	Trp	Tyr	Ala	Thr		288	
				85					90					95				
ag	gaa	aag	ctt	ggc	ctg	aag	tac	acc	ggc	tcc	gtt	ctc	acc	ttc	gag		336	



Leu Ser Ala Phe Asn Ala Trp Ala Ala Val Gln Gly Ile Asp Thr Leu  
 50 55 60

tcc ctg cgc ctg gag cgc cac aac gaa aac gcc atc aag gtt gca gaa 240  
 Ser Leu Arg Leu Glu Arg His Asn Glu Asn Ala Ile Lys Val Ala Glu  
 65 70 75 80

ttc ctc aac aac cac gag aag gtg gaa aag gtt aac ttc gca ggc ctg 288  
 Phe Leu Asn Asn His Glu Lys Val Glu Lys Val Asn Phe Ala Gly Leu  
 85 90 95

aag gat tcc cct tgg tac gca acc aag gaa aag ctt ggc ctg aag tac 336  
 Lys Asp Ser Pro Trp Tyr Ala Thr Lys Glu Lys Leu Gly Leu Lys Tyr  
 100 105 110

acc ggc tcc gtt ctc acc ttc gag atc aag ggc ggc aag gat gag gct 384  
 Thr Gly Ser Val Leu Thr Phe Glu Ile Lys Gly Gly Lys Asp Glu Ala  
 115 120 125

tgg gca ttt atc gac gcc ctg aag cta cac tcc aac ctt gca aac atc 432  
 Trp Ala Phe Ile Asp Ala Leu Lys Leu His Ser Asn Leu Ala Asn Ile  
 130 135 140

ggc gat gtt cgc tcc ctc gtt gtt cac cca gca acc acc acc cat tca 480  
 Gly Asp Val Arg Ser Leu Val Val His Pro Ala Thr Thr Thr His Ser  
 145 150 155 160

cag tcc gac gaa gct ggc ctg gca cgc gcg ggc gtt acc cag tcc acc 528  
 Gln Ser Asp Glu Ala Gly Leu Ala Arg Ala Gly Val Thr Gln Ser Thr  
 165 170 175

gtc cgc ctg tcc gtt ggc atc gag acc att gat gat atc atc gct gac 576  
 Val Arg Leu Ser Val Gly Ile Glu Thr Ile Asp Asp Ile Ile Ala Asp  
 180 185 190

ctc gaa ggc ggc ttt gct gca atc tagctttaaa tagactcacc cca 623  
 Leu Glu Gly Gly Phe Ala Ala Ile  
 195 200

<210> 248  
 <211> 200  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 248  
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 1 5 10 15

Asp Ala Ala Tyr His Gly Leu Lys Tyr Ala Asp Leu Gly Ala Pro Ala  
 20 25 30

Phe Gly Leu Lys Val Arg Val Gly Leu Leu Arg Asp Thr Gly Ser Thr  
 35 40 45

Leu Ser Ala Phe Asn Ala Trp Ala Ala Val Gln Gly Ile Asp Thr Leu  
 50 55 60

Ser Leu Arg Leu Glu Arg His Asn Glu Asn Ala Ile Lys Val Ala Glu  
 65 70 75 80

Lys Ala Asp Glu Ile Val Ala Glu Arg Glu Asn Ala Val Leu Ala Arg  
 130 135 140  
 Gln Phe Glu Asn Glu Ala Asn Pro Arg Val Asn Arg Asp Thr Thr Ala  
 145 150 155 160  
 Lys Glu Ile Leu Glu Asp Thr Asp Gly Thr Val Asp Ile Phe Val Ala  
 165 170 175  
 Ser Phe Gly Thr Gly Gly Thr Val Thr Gly Val Gly Gln Val Leu Lys  
 180 185 190  
 Glu Asn Asn Ala Asp Val Gln Val Tyr Thr Val Glu Pro Glu Ala Ser  
 195 200 205  
 Pro Leu Leu Thr Ala Gly Lys Ala Gly Pro His Lys Ile Gln Gly Ile  
 210 215 220  
 Gly Ala Asn Phe Ile Pro Glu Val Leu Asp Arg Lys Val Leu Asp Asp  
 225 230 235 240  
 Val Leu Thr Val Ser Asn Glu Asp Ala Ile Ala Phe Ser Arg Lys Leu  
 245 250 255  
 Ala Thr Glu Glu Gly Ile Leu Gly Gly Ile Ser Thr Gly Ala Asn Ile  
 260 265 270  
 Lys Ala Ala Leu Asp Leu Ala Ala Lys Pro Glu Asn Ala Gly Lys Thr  
 275 280 285  
 Ile Val Thr Val Val Thr Asp Phe Gly Glu Arg Tyr Val Ser Thr Val  
 290 295 300  
 Leu Tyr Glu Asp Ile Arg Asp  
 305 310

<210> 247  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (1)..(600)  
 <223> RXN00402

<400> 247  
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 Thr Asp Glu Lys Asp Gly Lys Pro Val Leu Pro Tyr Phe Val Thr Pro  
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 gat gct gct tac cac gga ttg aag tac gca gac ctt ggt gca cca gcc 96  
 Asp Ala Ala Tyr His Gly Leu Lys Tyr Ala Asp Leu Gly Ala Pro Ala  
 20 25 30  
 ttc ggc ctc aag gtt cgc gtt ggc ctt cta cgc gac acc ggc tcc acc 144  
 Phe Gly Leu Lys Val Arg Val Gly Leu Leu Arg Asp Thr Gly Ser Thr  
 35 40 45  
 ctc tcc gca ttc aac gca tgg gct gca gtc cag ggc atc gac acc ctt 192

ggc aag gct ggt cca cac aag atc cag ggc atc ggc gca aac ttc atc 787  
 Gly Lys Ala Gly Pro His Lys Ile Gln Gly Ile Gly Ala Asn Phe Ile  
 215 220 225

ccc gag gtc ctg gac cgc aag gtt ctc gac gac gtg ctg acc gtc tcc 835  
 Pro Glu Val Leu Asp Arg Lys Val Leu Asp Asp Val Leu Thr Val Ser  
 230 235 240 245

aac gaa gac gca atc gca ttc tcc cgc aag ctc gct acc gaa gag ggc 883  
 Asn Glu Asp Ala Ile Ala Phe Ser Arg Lys Leu Ala Thr Glu Glu Gly  
 250 255 260

atc ctc ggc ggt atc tcc acc ggc gca aac atc aag gca gct ctt gac 931  
 Ile Leu Gly Gly Ile Ser Thr Gly Ala Asn Ile Lys Ala Ala Leu Asp  
 265 270 275

ctt gca gca aag cca gag aac gct ggc aaa acc atc gtc acc gtt gtc 979  
 Leu Ala Ala Lys Pro Glu Asn Ala Gly Lys Thr Ile Val Thr Val Val  
 280 285 290

acc gac ttc ggc gag cgc tac gtc tcc acc gtt ctt tac gaa gac atc  
 1027  
 Thr Asp Phe Gly Glu Arg Tyr Val Ser Thr Val Leu Tyr Glu Asp Ile  
 295 300 305

cgc gac taattcttag cgactgttaa cca  
 1056  
 Arg Asp  
 310

<210> 246

<211> 311

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 246

Met Gly Asn Val Tyr Asn Asn Ile Thr Glu Thr Ile Gly His Thr Pro  
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Leu Val Lys Leu Asn Lys Leu Thr Glu Gly Leu Asp Ala Thr Val Leu  
 20 25 30

Val Lys Leu Glu Ser Phe Asn Pro Ala Asn Ser Val Lys Asp Arg Ile  
 35 40 45

Gly Leu Ala Ile Val Glu Asp Ala Glu Lys Ser Gly Ala Leu Lys Pro  
 50 55 60

Gly Gly Thr Ile Val Glu Ala Thr Ser Gly Asn Thr Gly Ile Ala Leu  
 65 70 75 80

Ala Met Val Gly Ala Ala Arg Gly Tyr Asn Val Val Leu Thr Met Pro  
 85 90 95

Glu Thr Met Ser Asn Glu Arg Arg Val Leu Leu Arg Ala Tyr Gly Ala  
 100 105 110

Glu Ile Val Leu Thr Pro Gly Ala Ala Gly Met Gln Gly Ala Lys Asp  
 115 120 125



cca cgt ggc aag aca gag aag atc aag ctc gtc gat ccg gac tat tac 643  
 Pro Arg Gly Lys Thr Glu Lys Ile Lys Leu Val Asp Pro Asp Tyr Tyr  
                   170                  175                  180

att taagaacagt tagcgcccta cct 669  
 Ile

<210> 244

<211> 182

<212> PRT

<213> Corynebacterium glutamicum

<400> 244

Met Ile Arg Glu Asp Leu Ala Asn Ala Arg Glu His Asp Pro Ala Ala  
       1                  5                  10                  15

Arg Gly Asp Leu Glu Asn Ala Val Val Tyr Ser Gly Leu His Ala Ile  
                   20                  25                  30

Trp Ala His Arg Val Ala Asn Ser Trp Trp Lys Ser Gly Phe Arg Gly  
                   35                  40                  45

Pro Ala Arg Val Leu Ala Gln Phe Thr Arg Phe Leu Thr Gly Ile Glu  
                   50                  55                  60

Ile His Pro Gly Ala Thr Ile Gly Arg Arg Phe Phe Ile Asp His Gly  
       65                  70                  75                  80

Met Gly Ile Val Ile Gly Glu Thr Ala Glu Ile Gly Glu Gly Val Met  
                   85                  90                  95

Leu Tyr His Gly Val Thr Leu Gly Gly Gln Val Leu Thr Gln Thr Lys  
                   100                  105                  110

Arg His Pro Thr Leu Cys Asp Asn Val Thr Val Gly Ala Gly Ala Lys  
                   115                  120                  125

Ile Leu Gly Pro Ile Thr Ile Gly Glu Gly Ser Ala Ile Gly Ala Asn  
                   130                  135                  140

Ala Val Val Thr Lys Asp Val Pro Ala Glu His Ile Ala Val Gly Ile  
       145                  150                  155                  160

Pro Ala Val Ala Arg Pro Arg Gly Lys Thr Glu Lys Ile Lys Leu Val  
                   165                  170                  175

Asp Pro Asp Tyr Tyr Ile  
                   180

<210> 245

<211> 1056

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1033)

Arg Ala Ala Leu Lys Leu Ala  
405

<210> 243  
<211> 669  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(646)  
<223> RXA00780

<400> 243  
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tcacgctgtt agacttgcct gcatgctctc gacaataaaa atg atc cgt gaa gat 115  
Met Ile Arg Glu Asp  
1 5  
ctc gca aac gct cgt gaa cac gat cca gca gcc cga ggc gat tta gaa 163  
Leu Ala Asn Ala Arg Glu His Asp Pro Ala Ala Arg Gly Asp Leu Glu  
10 15 20  
aac gca gtg gtt tac tcc gga ctc cac gcc atc tgg gca cat cga gtt 211  
Asn Ala Val Val Tyr Ser Gly Leu His Ala Ile Trp Ala His Arg Val  
25 30 35  
gcc aac agc tgg tgg aaa tcc ggt ttc cgc ggc ccc gcc cgc gta tta 259  
Ala Asn Ser Trp Trp Lys Ser Gly Phe Arg Gly Pro Ala Arg Val Leu  
40 45 50  
gcc caa ttc acc cga ttc ctc acc ggc att gaa att cac ccc ggt gcc 307  
Ala Gln Phe Thr Arg Phe Leu Thr Gly Ile Glu Ile His Pro Gly Ala  
55 60 65  
acc att ggt cgt cgc ttt ttt att gac cac gga atg gga atc gtc atc 355  
Thr Ile Gly Arg Arg Phe Phe Ile Asp His Gly Met Gly Ile Val Ile  
70 75 80 85  
ggc gaa acc gct gaa atc ggc gaa ggc gtc atg ctc tac cac ggc gtc 403  
Gly Glu Thr Ala Glu Ile Gly Glu Gly Val Met Leu Tyr His Gly Val  
90 95 100  
acc ctc ggc gga cag gtt ctc acc caa acc aag cgc cac ccc acg ctc 451  
Thr Leu Gly Gly Gln Val Leu Thr Gln Thr Lys Arg His Pro Thr Leu  
105 110 115  
tgc gac aac gtg aca gtc ggc gcg ggc gca aaa atc tta ggt ccc atc 499  
Cys Asp Asn Val Thr Val Gly Ala Gly Ala Lys Ile Leu Gly Pro Ile  
120 125 130  
acc atc ggc gaa ggc tcc gca att ggc gcc aat gca gtt gtc acc aaa 547  
Thr Ile Gly Glu Gly Ser Ala Ile Gly Ala Asn Ala Val Val Thr Lys  
135 140 145  
gac gtg ccg gca gaa cac atc gca gtc gga att cct gcg gta gca cgc 595  
Asp Val Pro Ala Glu His Ile Ala Val Gly Ile Pro Ala Val Ala Arg  
150 155 160 165

65				70				75				80			
Gly	Phe	Asn	Ser	Ser	Glu	Val	Gly	Phe	Asp	Gly	Arg	Thr	Cys	Gly	Val
				85					90					95	
Ser	Val	Ser	Ile	Gly	Glu	Gln	Ser	Gln	Glu	Ile	Ala	Asp	Gly	Val	Asp
			100					105					110		
Asn	Ser	Asp	Glu	Ala	Arg	Thr	Asn	Gly	Asp	Val	Glu	Glu	Asp	Asp	Arg
		115					120					125			
Ala	Gly	Ala	Gly	Asp	Gln	Gly	Leu	Met	Phe	Gly	Tyr	Ala	Thr	Asn	Glu
	130					135					140				
Thr	Glu	Glu	Tyr	Met	Pro	Leu	Pro	Ile	Ala	Leu	Ala	His	Arg	Leu	Ser
145					150					155					160
Arg	Arg	Leu	Thr	Gln	Val	Arg	Lys	Glu	Gly	Ile	Val	Pro	His	Leu	Arg
				165					170					175	
Pro	Asp	Gly	Lys	Thr	Gln	Val	Thr	Phe	Ala	Tyr	Asp	Ala	Gln	Asp	Arg
			180					185					190		
Pro	Ser	His	Leu	Asp	Thr	Val	Val	Ile	Ser	Thr	Gln	His	Asp	Pro	Glu
		195					200					205			
Val	Asp	Arg	Ala	Trp	Leu	Glu	Thr	Gln	Leu	Arg	Glu	His	Val	Ile	Asp
	210					215					220				
Trp	Val	Ile	Lys	Asp	Ala	Gly	Ile	Glu	Asp	Leu	Ala	Thr	Gly	Glu	Ile
225				230						235					240
Thr	Val	Leu	Ile	Asn	Pro	Ser	Gly	Ser	Phe	Ile	Leu	Gly	Gly	Pro	Met
				245					250					255	
Gly	Asp	Ala	Gly	Leu	Thr	Gly	Arg	Lys	Ile	Ile	Val	Asp	Thr	Tyr	Gly
			260					265					270		
Gly	Met	Ala	Arg	His	Gly	Gly	Gly	Ala	Phe	Ser	Gly	Lys	Asp	Pro	Ser
		275					280					285			
Lys	Val	Asp	Arg	Ser	Ala	Ala	Tyr	Ala	Met	Arg	Trp	Val	Ala	Lys	Asn
	290					295					300				
Ile	Val	Ala	Ala	Gly	Leu	Ala	Asp	Arg	Ala	Glu	Val	Gln	Val	Ala	Tyr
305					310					315					320
Ala	Ile	Gly	Arg	Ala	Lys	Pro	Val	Gly	Leu	Tyr	Val	Glu	Thr	Phe	Asp
				325					330					335	
Thr	Asn	Lys	Glu	Gly	Leu	Ser	Asp	Glu	Gln	Ile	Gln	Ala	Ala	Val	Leu
			340					345					350		
Glu	Val	Phe	Asp	Leu	Arg	Pro	Ala	Ala	Ile	Ile	Arg	Glu	Leu	Asp	Leu
		355					360					365			
Leu	Arg	Pro	Ile	Tyr	Ala	Asp	Thr	Ala	Ala	Tyr	Gly	His	Phe	Gly	Arg
						375					380				
Thr	Asp	Leu	Asp	Leu	Pro	Trp	Glu	Ala	Ile	Asp	Arg	Val	Asp	Glu	Leu
385				390						395					400

gct gca tac gcc atg cgt tgg gta gca aag aac atc gtg gca gca ggc  
 1027  
 Ala Ala Tyr Ala Met Arg Trp Val Ala Lys Asn Ile Val Ala Ala Gly  
 295 300 305  
 ctt gct gat cgc gct gaa gtt cag gtt gca tac gcc att gga cgc gca  
 1075  
 Leu Ala Asp Arg Ala Glu Val Gln Val Ala Tyr Ala Ile Gly Arg Ala  
 310 315 320 325  
 aag cca gtc gga ctt tac gtt gaa acc ttt gac acc aac aag gaa ggc  
 1123  
 Lys Pro Val Gly Leu Tyr Val Glu Thr Phe Asp Thr Asn Lys Glu Gly  
 330 335 340  
 ctg agc gac gag cag att cag gct gcc gtg ttg gag gtc ttt gac ctg  
 1171  
 Leu Ser Asp Glu Gln Ile Gln Ala Ala Val Leu Glu Val Phe Asp Leu  
 345 350 355  
 cgt cca gca gca att atc cgt gag ctt gat ctg ctt cgt ccg atc tac  
 1219  
 Arg Pro Ala Ala Ile Ile Arg Glu Leu Asp Leu Leu Arg Pro Ile Tyr  
 360 365 370  
 gct gac act gct gcc tac ggc cac ttt ggt cgc act gat ttg gac ctt  
 1267  
 Ala Asp Thr Ala Ala Tyr Gly His Phe Gly Arg Thr Asp Leu Asp Leu  
 375 380 385  
 cct tgg gag gct atc gac cgc gtt gat gaa ctt cgc gca gcc ctc aag  
 1315  
 Pro Trp Glu Ala Ile Asp Arg Val Asp Glu Leu Arg Ala Ala Leu Lys  
 390 395 400 405  
 ttg gcc taaaaatctg atgtagtattc ttc  
 1344  
 Leu Ala

&lt;210&gt; 242

&lt;211&gt; 407

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 242

Val Ala Gln Pro Thr Ala Val Arg Leu Phe Thr Ser Glu Ser Val Thr  
 1 5 10 15

Glu Gly His Pro Asp Lys Ile Cys Asp Ala Ile Ser Asp Thr Ile Leu  
 20 25 30

Asp Ala Leu Leu Glu Lys Asp Pro Gln Ser Arg Val Ala Val Glu Thr  
 35 40 45

Val Val Thr Thr Gly Ile Val His Val Val Gly Glu Val Arg Thr Ser  
 50 55 60

Ala Tyr Val Glu Ile Pro Gln Leu Val Arg Asn Lys Leu Ile Glu Ile



40	45	50	
atc gtc cat gtt gtt ggc gag gtc cgt acc agc gct tac gta gag atc Ile Val His Val Val Gly Glu Val Arg Thr Ser Ala Tyr Val Glu Ile 55 60 65			307
cct caa tta gtc cgc aac aag ctc atc gaa atc gga ttc aac tcc tct Pro Gln Leu Val Arg Asn Lys Leu Ile Glu Ile Gly Phe Asn Ser Ser 70 75 80 85			355
gag gtt gga ttc gac gga cgc acc tgt ggc gtc tca gta tcc atc ggt Glu Val Gly Phe Asp Gly Arg Thr Cys Gly Val Ser Val Ser Ile Gly 90 95 100			403
gag cag tcc cag gaa atc gct gac ggc gtg gat aac tcc gac gaa gcc Glu Gln Ser Gln Glu Ile Ala Asp Gly Val Asp Asn Ser Asp Glu Ala 105 110 115			451
cgc acc aac ggc gac gtt gaa gaa gac gac cgc gca ggt gct ggc gac Arg Thr Asn Gly Asp Val Glu Glu Asp Asp Arg Ala Gly Ala Gly Asp 120 125 130			499
cag ggc ctg atg ttc ggc tac gcc acc aac gaa acc gaa gag tac atg Gln Gly Leu Met Phe Gly Tyr Ala Thr Asn Glu Thr Glu Glu Tyr Met 135 140 145			547
cct ctt cct atc gcg ttg gcg cac cga ctg tca cgt cgt ctg acc cag Pro Leu Pro Ile Ala Leu Ala His Arg Leu Ser Arg Arg Leu Thr Gln 150 155 160 165			595
gtt cgt aaa gag ggc atc gtt cct cac ctg cgt cca gac gga aaa acc Val Arg Lys Glu Gly Ile Val Pro His Leu Arg Pro Asp Gly Lys Thr 170 175 180			643
cag gtc acc ttc gca tac gat gcg caa gac cgc cct agc cac ctg gat Gln Val Thr Phe Ala Tyr Asp Ala Gln Asp Arg Pro Ser His Leu Asp 185 190 195			691
acc gtt gtc atc tcc acc cag cac gac cca gaa gtt gac cgt gca tgg Thr Val Val Ile Ser Thr Gln His Asp Pro Glu Val Asp Arg Ala Trp 200 205 210			739
ttg gaa acc caa ctg cgc gaa cac gtc att gat tgg gta atc aaa gac Leu Glu Thr Gln Leu Arg Glu His Val Ile Asp Trp Val Ile Lys Asp 215 220 225			787
gca ggc att gag gat ctg gca acc ggt gag atc acc gtg ttg atc aac Ala Gly Ile Glu Asp Leu Ala Thr Gly Glu Ile Thr Val Leu Ile Asn 230 235 240 245			835
cct tca ggt tcc ttc att ctg ggt ggc ccc atg ggt gat gcg ggt ctg Pro Ser Gly Ser Phe Ile Leu Gly Gly Pro Met Gly Asp Ala Gly Leu 250 255 260			883
acc ggc cgc aag atc atc gtg gat acc tac ggt ggc atg gct cgc cat Thr Gly Arg Lys Ile Ile Val Asp Thr Tyr Gly Gly Met Ala Arg His 265 270 275			931
ggg ggt gga gca ttc tcc ggt aag gat cca agc aag gtg gac cgc tct Gly Gly Gly Ala Phe Ser Gly Lys Asp Pro Ser Lys Val Asp Arg Ser 280 285 290			979

Val Arg Val Ala Arg Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu  
 405 410 415  
 Ala Glu Ile Val Leu Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe  
 420 425 430  
 Gln Leu Ser Arg Thr Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys  
 435 440 445  
 Val Tyr Val Gly Val Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val  
 450 455 460  
 Thr Asn Ile Thr Glu Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser  
 465 470 475 480  
 Ile Asn Trp Arg Pro Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro  
 485 490 495  
 Glu Thr Pro Leu Trp Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser  
 500 505 510  
 Met Pro Ser Gly Asn Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser  
 515 520 525  
 Ala Thr Thr Val Tyr Val Thr Asp Ser His Ala Met Leu Gln Leu Pro  
 530 535 540  
 Thr Ala Asp Asn Asp Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr  
 545 550 555 560  
 Arg Ala Ala Pro Val Val Ala Tyr  
 565

<210> 241  
 <211> 1344  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1321)  
 <223> RXA02240

<400> 241  
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 aagactattt attctcaact tcttcgaaag aagggtattt gtg gct cag cca acc 115  
 Val Ala Gln Pro Thr  
 1 5  
 gcc gtc cgt ttg ttc acc agt gaa tct gta act gag gga cat cca gac 163  
 Ala Val Arg Leu Phe Thr Ser Glu Ser Val Thr Glu Gly His Pro Asp  
 10 15 20  
 aaa ata tgt gat gct att tcc gat acc att ttg gac gcg ctg ctc gaa 211  
 Lys Ile Cys Asp Ala Ile Ser Asp Thr Ile Leu Asp Ala Leu Leu Glu  
 25 30 35  
 aaa gat ccg cag tcg cgc gtc gca gtg gaa act gtg gtc acc acc gga 259  
 Lys Asp Pro Gln Ser Arg Val Ala Val Glu Thr Val Val Thr Thr Gly

Tyr Leu Thr Glu Gly Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr  
 85 90 95  
 Arg Ile Leu Asp Arg Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn  
 100 105 110  
 Ala Glu Arg Thr Ile Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu  
 115 120 125  
 Ser Gly Gly Val Tyr Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile  
 130 135 140  
 Thr Met Arg Arg Glu Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp  
 145 150 155 160  
 Gly Ile Leu Leu Glu Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His  
 165 170 175  
 Asp Val Tyr Phe Phe Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg  
 180 185 190  
 Arg Trp Leu Phe Asn Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala  
 195 200 205  
 Leu Leu Val Asn Gly Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn  
 210 215 220  
 Gln Leu Ser Thr Asp Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr  
 225 230 235 240  
 Gln Phe Thr Gly Leu Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe  
 245 250 255  
 Ala Ala Gln Ala Val Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro  
 260 265 270  
 Tyr Thr Leu Val Ala Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr  
 275 280 285  
 Leu Thr Thr Asp Asp Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn  
 290 295 300  
 Thr Val Ser Thr Leu Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val  
 305 310 315 320  
 Ser Ser Gly Asn Val Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp  
 325 330 335  
 Ile Asp Ser Ala Ala Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val  
 340 345 350  
 Arg His Glu Asn Asn Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly  
 355 360 365  
 Val Thr Ser Asp Ala Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe  
 370 375 380  
 Glu Tyr Ala Ser Ser Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro  
 385 390 395 400

gta acg cgt cct ggt ccg ggc gag cgg cgc gtg aca aat atc acg gag  
 1507  
 Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val Thr Asn Ile Thr Glu  
 455 460 465  
 gtg gcg ccg agc ttg ggc gag gcg gcg ctg tgc atc aac tgg cgc cca  
 1555  
 Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser Ile Asn Trp Arg Pro  
 470 475 480 485  
 gac ggc att ttg ctt gtg ggc acg tca att cca gag acg ccg ctg tgg  
 1603  
 Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro Glu Thr Pro Leu Trp  
 490 495 500  
 cgc gtc gag cag gac gga tgc gcg att tgc tgc atg ccg agc ggg aat  
 1651  
 Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser Met Pro Ser Gly Asn  
 505 510 515  
 ctc agc gcg ccg gtg gtg gcg gtg gca agt tcc gcg acg acg gtc tac  
 1699  
 Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser Ala Thr Thr Val Tyr  
 520 525 530  
 gtc act gat tgc cat gcg atg ctt cag ctg ccg act gcc gat aat gat  
 1747  
 Val Thr Asp Ser His Ala Met Leu Gln Leu Pro Thr Ala Asp Asn Asp  
 535 540 545  
 att tgg cgc gag gtg ccc ggt ttg ctg ggc acg cgt gcg gcg ccg gtg  
 1795  
 Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr Arg Ala Ala Pro Val  
 550 555 560 565  
 gtt gcg tac tgatggagct gttcttcccg cgc  
 1827  
 Val Ala Tyr

&lt;210&gt; 240

&lt;211&gt; 568

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 240

Val Ser Lys Ile Ser Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser  
 1 5 10 15  
 Val Thr Thr Leu Val Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp  
 20 25 30  
 Pro Gln Val Leu Arg Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile  
 35 40 45  
 Ala Gly Pro Thr Pro Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe  
 50 55 60  
 Phe Ser Ala Gly Ala Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala  
 65 70 75 80

65	70	75	80	
gcc gag cgt atg cag cgt tca gca gct cga atg gca atg cca cag ttg				288
Ala Glu Arg Met Gln Arg Ser Ala Ala Arg Met Ala Met Pro Gln Leu	85	90	95	
cca acc gag gac ttt att aaa gca ctt gaa ctg ctg gta gac gcg gat				336
Pro Thr Glu Asp Phe Ile Lys Ala Leu Glu Leu Leu Val Asp Ala Asp	100	105	110	
cag gat tgg gtt cct gag tac ggc gga gaa gct tcc ctc tac ctg cgc				384
Gln Asp Trp Val Pro Glu Tyr Gly Gly Glu Ala Ser Leu Tyr Leu Arg	115	120	125	
cca ttc atg atc tcc acc gaa att ggc ttg ggt gtc agc cca gct gat				432
Pro Phe Met Ile Ser Thr Glu Ile Gly Leu Gly Val Ser Pro Ala Asp	130	135	140	
gcc tac aag ttc ctg gtc atc gca tcc cca gtc ggc gct tac ttc acc				480
Ala Tyr Lys Phe Leu Val Ile Ala Ser Pro Val Gly Ala Tyr Phe Thr	145	150	155	160
ggg gga atc aag cct gtt tcc gtc tgg ctg agc gaa gat tac gtc cgc				528
Gly Gly Ile Lys Pro Val Ser Val Trp Leu Ser Glu Asp Tyr Val Arg	165	170	175	
gct gca ccc ggc gga act ggt gac gcc aaa ttt gct ggc aac tac gcg				576
Ala Ala Pro Gly Gly Thr Gly Asp Ala Lys Phe Ala Gly Asn Tyr Ala	180	185	190	
gct tct ttg ctt gcc cag tcc cag gct gcg gaa aag ggc tgt gac cag				624
Ala Ser Leu Leu Ala Gln Ser Gln Ala Ala Glu Lys Gly Cys Asp Gln	195	200	205	
gtc gta tgg ttg gat gcc atc gag cac aag tac atc gaa gaa atg ggt				672
Val Val Trp Leu Asp Ala Ile Glu His Lys Tyr Ile Glu Glu Met Gly	210	215	220	
ggc atg aac ctt ggg ttc atc tac cgc aac ggc gac caa gtc aag cta				720
Gly Met Asn Leu Gly Phe Ile Tyr Arg Asn Gly Asp Gln Val Lys Leu	225	230	235	240
gtc acc cct gaa ctt tcc ggc tca cta ctt cca ggc atc acc cgc aag				768
Val Thr Pro Glu Leu Ser Gly Ser Leu Leu Pro Gly Ile Thr Arg Lys	245	250	255	
tca ctt cta caa gta gca cgc gac ttg gga tac gaa gta gaa gag cga				816
Ser Leu Leu Gln Val Ala Arg Asp Leu Gly Tyr Glu Val Glu Glu Arg	260	265	270	
aag atc acc acc acc gag tgg gaa gaa gac gca aag tct ggc gcc atg				864
Lys Ile Thr Thr Thr Glu Trp Glu Glu Asp Ala Lys Ser Gly Ala Met	275	280	285	
acc gag gca ttt gct tgc ggt act gca gct gtt atc acc cct gtt ggc				912
Thr Glu Ala Phe Ala Cys Gly Thr Ala Ala Val Ile Thr Pro Val Gly	290	295	300	
acc gtg aaa tca gct cac ggc acc ttc gaa gtg aac aac aat gaa gtc				960
Thr Val Lys Ser Ala His Gly Thr Phe Glu Val Asn Asn Asn Glu Val	305	310	315	320

Ala Ser Leu Leu Ala Gln Ser Gln Ala Ala Glu Lys Gly Cys Asp Gln  
 210 215 220  
 Val Val Trp Leu Asp Ala Ile Glu His Lys Tyr Ile Glu Glu Met Gly  
 225 230 235 240  
 Gly Met Asn Leu Gly Phe Ile Tyr Arg Asn Gly Asp Gln Val Lys Leu  
 245 250 255  
 Val Thr Pro Glu Leu Ser Gly Ser Leu Leu Pro Gly Ile Thr Arg Lys  
 260 265 270  
 Ser Leu Leu Gln Val Ala Arg Asp Leu Gly Tyr Glu Val Glu Glu Arg  
 275 280 285  
 Lys Ile Thr Thr Thr Glu Trp Glu Glu Asp Ala Lys Ser Gly Ala Met  
 290 295 300  
 Thr Glu Ala Phe Ala Cys Gly Thr Ala Ala Val Ile Thr Pro Val Gly  
 305 310 315 320  
 Thr Val Lys Ser Ala His Gly Thr Phe Glu Val Asn Asn Asn Glu Val  
 325 330 335  
 Gly Glu Ile Thr Met Lys Leu Arg Glu Thr Leu Thr Gly Ile Gln Gln  
 340 345 350  
 Gly Asn Val Glu Asp Gln Asn Gly Trp Leu Tyr Pro Leu Val Gly  
 355 360 365

<210> 263  
 <211> 1076  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(1053)  
 <223> FRXA01690

<400> 263  
 ccc gat cgt ctg aag gaa att ctt gcc gca ccg aag ttc ggt aag ttc 48  
 Pro Asp Arg Leu Lys Glu Ile Leu Ala Ala Pro Lys Phe Gly Lys Phe  
 1 5 10 15  
 ttc acc gac cac atg gtg acc att gac tgg aac gag tcg gaa ggc tgg 96  
 Phe Thr Asp His Met Val Thr Ile Asp Trp Asn Glu Ser Glu Gly Trp  
 20 25 30  
 cac aac gcc caa tta gtg cca tac gcg ccg att cct atg gat cct gcc 144  
 His Asn Ala Gln Leu Val Pro Tyr Ala Pro Ile Pro Met Asp Pro Ala  
 35 40 45  
 acc acc gta ttc cac tac gga cag gca att ttt gag gga att aag gcc 192  
 Thr Thr Val Phe His Tyr Gly Gln Ala Ile Phe Glu Gly Ile Lys Ala  
 50 55 60  
 tac cgc cat tcg gac gaa acc atc aag act ttc cgt cct gat gaa aac 240  
 Tyr Arg His Ser Asp Glu Thr Ile Lys Thr Phe Arg Pro Asp Glu Asn

His Gly Thr Phe Glu Val Asn Asn Asn Glu Val Gly Glu Ile Thr Met  
 330 335 340

aag ctt cgt gaa acc ctc acc gga att cag caa gga aac gtt gaa gac  
 1171

Lys Leu Arg Glu Thr Leu Thr Gly Ile Gln Gln Gly Asn Val Glu Asp  
 345 350 355

caa aac gga tgg ctt tac cca ctg gtt ggc taaatcaacc gggtttaaga  
 1221

Gln Asn Gly Trp Leu Tyr Pro Leu Val Gly  
 360 365

ccc  
 1224

<210> 262

<211> 367

<212> PRT

<213> Corynebacterium glutamicum

<400> 262

Met Thr Ser Leu Glu Phe Thr Val Thr Arg Thr Glu Asn Pro Thr Ser  
 1 5 10 15

Pro Asp Arg Leu Lys Glu Ile Leu Ala Ala Pro Lys Phe Gly Lys Phe  
 20 25 30

Phe Thr Asp His Met Val Thr Ile Asp Trp Asn Glu Ser Glu Gly Trp  
 35 40 45

His Asn Ala Gln Leu Val Pro Tyr Ala Pro Ile Pro Met Asp Pro Ala  
 50 55 60

Thr Thr Val Phe His Tyr Gly Gln Ala Ile Phe Glu Gly Ile Lys Ala  
 65 70 75 80

Tyr Arg His Ser Asp Glu Thr Ile Lys Thr Phe Arg Pro Asp Glu Asn  
 85 90 95

Ala Glu Arg Met Gln Arg Ser Ala Ala Arg Met Ala Met Pro Gln Leu  
 100 105 110

Pro Thr Glu Asp Phe Ile Lys Ala Leu Glu Leu Leu Val Asp Ala Asp  
 115 120 125

Gln Asp Trp Val Pro Glu Tyr Gly Gly Glu Ala Ser Leu Tyr Leu Arg  
 130 135 140

Pro Phe Met Ile Ser Thr Glu Ile Gly Leu Gly Val Ser Pro Ala Asp  
 145 150 155 160

Ala Tyr Lys Phe Leu Val Ile Ala Ser Pro Val Gly Ala Tyr Phe Thr  
 165 170 175

Gly Gly Ile Lys Pro Val Ser Val Trp Leu Ser Glu Asp Tyr Val Arg  
 180 185 190

Ala Ala Pro Gly Gly Thr Gly Asp Ala Lys Phe Ala Gly Asn Tyr Ala  
 195 200 205

cgt tca gca gct cga atg gca atg cca cag ttg cca acc gag gac ttt 451  
 Arg Ser Ala Ala Arg Met Ala Met Pro Gln Leu Pro Thr Glu Asp Phe  
 105 110 115  
 att aaa gca ctt gaa ctg ctg gta gac gcg gat cag gat tgg gtt cct 499  
 Ile Lys Ala Leu Glu Leu Leu Val Asp Ala Asp Gln Asp Trp Val Pro  
 120 125 130  
 gag tac ggc gga gaa gct tcc ctc tac ctg cgc cca ttc atg atc tcc 547  
 Glu Tyr Gly Gly Glu Ala Ser Leu Tyr Leu Arg Pro Phe Met Ile Ser  
 135 140 145  
 acc gaa att ggc ttg ggt gtc agc cca gct gat gcc tac aag ttc ctg 595  
 Thr Glu Ile Gly Leu Gly Val Ser Pro Ala Asp Ala Tyr Lys Phe Leu  
 150 155 160 165  
 gtc atc gca tcc cca gtc ggc gct tac ttc acc ggt gga atc aag cct 643  
 Val Ile Ala Ser Pro Val Gly Ala Tyr Phe Thr Gly Gly Ile Lys Pro  
 170 175 180  
 gtt tcc gtc tgg ctg agc gaa gat tac gtc cgc gct gca ccc ggc gga 691  
 Val Ser Val Trp Leu Ser Glu Asp Tyr Val Arg Ala Ala Pro Gly Gly  
 185 190 195  
 act ggt gac gcc aaa ttt gct ggc aac tac gcg gct tct ttg ctt gcc 739  
 Thr Gly Asp Ala Lys Phe Ala Gly Asn Tyr Ala Ala Ser Leu Leu Ala  
 200 205 210  
 cag tcc cag gct gcg gaa aag ggc tgt gac cag gtc gta tgg ttg gat 787  
 Gln Ser Gln Ala Ala Glu Lys Gly Cys Asp Gln Val Val Trp Leu Asp  
 215 220 225  
 gcc atc gag cac aag tac atc gaa gaa atg ggt ggc atg aac ctt ggg 835  
 Ala Ile Glu His Lys Tyr Ile Glu Glu Met Gly Gly Met Asn Leu Gly  
 230 235 240 245  
 ttc atc tac cgc aac ggc gac caa gtc aag cta gtc acc cct gaa ctt 883  
 Phe Ile Tyr Arg Asn Gly Asp Gln Val Lys Leu Val Thr Pro Glu Leu  
 250 255 260  
 tcc ggc tca cta ctt cca ggc atc acc cgc aag tca ctt cta caa gta 931  
 Ser Gly Ser Leu Leu Pro Gly Ile Thr Arg Lys Ser Leu Leu Gln Val  
 265 270 275  
 gca cgc gac ttg gga tac gaa gta gaa gag cga aag atc acc acc acc 979  
 Ala Arg Asp Leu Gly Tyr Glu Val Glu Glu Arg Lys Ile Thr Thr Thr  
 280 285 290  
 gag tgg gaa gaa gac gca aag tct ggc gcc atg acc gag gca ttt gct 1027  
 Glu Trp Glu Glu Asp Ala Lys Ser Gly Ala Met Thr Glu Ala Phe Ala  
 295 300 305  
 tgc ggt act gca gct gtt atc acc cct gtt ggc acc gtg aaa tca gct 1075  
 Cys Gly Thr Ala Ala Val Ile Thr Pro Val Gly Thr Val Lys Ser Ala  
 310 315 320 325  
 cac ggc acc ttc gaa gtg aac aac aat gaa gtc gga gaa atc acg atg 1123



180	185	190
Phe Lys Gly Asp Lys Ile Arg Thr Pro Ser Pro Gly Gly Asp Ile Leu		
195	200	205
Pro Gly Thr Thr Gln Ala Ala Leu Phe Ala His Ala Thr Glu Lys Gly		
210	215	220
Trp Arg Cys Lys Glu Lys Asp Leu Ser Ile Asp Asp Leu Phe Gly Ala		
225	230	235
240		
Asp Ser Val Trp Leu Val Ser Ser Val Arg Gly Pro Val Arg Val Thr		
245	250	255
Arg Leu Asp Gly His Lys Leu Arg Lys Pro Asp Asn Glu Lys Glu Ile		
260	265	270
Lys Ala Leu Ile Thr Lys Ala Leu Gly		
275	280	

<210> 261  
 <211> 1224  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1201)  
 <223> RXN01690

<400> 261  
 cctagccatt cctcaaaacc gtgagacgaa attggctatt catcccataa aatggggctg 60  
 actagtgtat ctgtcaggta gcagggtgtac cttaaaatcc atg acg tca tta gag 115  
 Met Thr Ser Leu Glu  
 1 5  
 ttc aca gta acc cgt acc gaa aat ccg acg tca ccc gat cgt ctg aag 163  
 Phe Thr Val Thr Arg Thr Glu Asn Pro Thr Ser Pro Asp Arg Leu Lys  
 10 15 20  
 gaa att ctt gcc gca ccg aag ttc ggt aag ttc ttc acc gac cac atg 211  
 Glu Ile Leu Ala Ala Pro Lys Phe Gly Lys Phe Phe Thr Asp His Met  
 25 30 35  
 gtg acc att gac tgg aac gag tcg gaa ggc tgg cac aac gcc caa tta 259  
 Val Thr Ile Asp Trp Asn Glu Ser Glu Gly Trp His Asn Ala Gln Leu  
 40 45 50  
 gtg cca tac gcg ccg att cct atg gat cct gcc acc acc gta ttc cac 307  
 Val Pro Tyr Ala Pro Ile Pro Met Asp Pro Ala Thr Thr Val Phe His  
 55 60 65  
 tac gga cag gca att ttt gag gga att aag gcc tac cgc cat tcg gac 355  
 Tyr Gly Gln Ala Ile Phe Glu Gly Ile Lys Ala Tyr Arg His Ser Asp  
 70 75 80 85  
 gaa acc atc aag act ttc cgt cct gat gaa aac gcc gag cgt atg cag 403  
 Glu Thr Ile Lys Thr Phe Arg Pro Asp Glu Asn Ala Glu Arg Met Gln  
 90 95 100

gca gca ctc ttt gca cac gca acc gaa aaa gga tgg cga tgt aaa gaa 787  
 Ala Ala Leu Phe Ala His Ala Thr Glu Lys Gly Trp Arg Cys Lys Glu  
           215                                  220                                  225

aaa gac tta agc att gac gat ctt ttc gga gcc gac agc gtg tgg cta 835  
 Lys Asp Leu Ser Ile Asp Asp Leu Phe Gly Ala Asp Ser Val Trp Leu  
           230                                  235                                  240                                  245

gtg tcc tcc gtc cgc gga cca gtt cgg gtg acc agg ctc gat gga cac 883  
 Val Ser Ser Val Arg Gly Pro Val Arg Val Thr Arg Leu Asp Gly His  
                                   250                                  255                                  260

aaa tta cgg aaa cca gac aat gaa aaa gaa atc aag gcg ctg att acc 931  
 Lys Leu Arg Lys Pro Asp Asn Glu Lys Glu Ile Lys Ala Leu Ile Thr  
                                   265                                  270                                  275

aaa gct ctg ggg tagaggctgg cgctgggact tgc 966  
 Lys Ala Leu Gly  
                   280

&lt;210&gt; 260

&lt;211&gt; 281

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 260

Met Val Phe Trp Asp Asp Ala Ala Leu Thr Arg Gly Asp Gly Ile Phe  
       1                                  5                                  10                                  15

Glu Thr Leu Leu Ile Arg Asp Gly His Ala Cys Asn Val Arg Arg His  
                   20                                  25                                  30

Gly Glu Arg Phe Lys Ala Ser Ala Ala Leu Leu Gly Leu Pro Glu Pro  
                   35                                  40                                  45

Ile Leu Glu Asp Trp Glu Lys Ala Thr Gln Met Gly Ile Glu Ser Trp  
           50                                  55                                  60

Tyr Ser His Pro Asn Ala Gly Glu Ala Ser Cys Thr Trp Thr Leu Ser  
       65                                  70                                  75                                  80

Arg Gly Arg Ser Ser Thr Gly Leu Ala Ser Gly Trp Leu Thr Ile Thr  
                                   85                                  90                                  95

Pro Val Ser Ser Asp Lys Leu Ala Gln Arg Glu His Gly Val Ser Val  
                   100                                  105                                  110

Met Thr Ser Ser Arg Gly Tyr Ser Ile Asp Thr Gly Leu Pro Gly Ile  
           115                                  120                                  125

Gly Lys Ala Thr Arg Gly Glu Leu Ser Lys Val Glu Arg Thr Pro Ala  
       130                                  135                                  140

Pro Trp Leu Thr Val Gly Ala Lys Thr Leu Ala Tyr Ala Ala Asn Met  
       145                                  150                                  155                                  160

Ala Ala Leu Arg Tyr Ala Lys Ser Asn Gly Phe Asp Asp Val Ile Phe  
                   165                                  170                                  175

Thr Asp Gly Asp Arg Val Leu Glu Gly Ala Thr Ser Thr Val Val Ser

&lt;223&gt; RXA00766

&lt;400&gt; 259

tatggcgctt gaaccacaaa taaagtctgc accgacgccg gtgatcttaa ttgtcgaacc 60

ctacggcggg tccatccggc aacaaaaccc caacctacca atg gtt ttt tgg gac 115  
 Met Val Phe Trp Asp  
 1 5

gat gca gcc tta acc cga ggc gat ggc atc ttt gaa aca ctc ctc atc 163  
 Asp Ala Ala Leu Thr Arg Gly Asp Gly Ile Phe Glu Thr Leu Leu Ile  
 10 15 20

cgc gac gga cat gcc tgc aac gtg cgc cga cac gga gaa cgc ttc aaa 211  
 Arg Asp Gly His Ala Cys Asn Val Arg Arg His Gly Glu Arg Phe Lys  
 25 30 35

gca tcg gca gca cta ttg gga ctg cca gag ccg atc ctg gaa gac tgg 259  
 Ala Ser Ala Ala Leu Leu Gly Leu Pro Glu Pro Ile Leu Glu Asp Trp  
 40 45 50

gaa aaa gcc acc caa atg ggc atc gaa tcc tgg tac tcc cac ccc aac 307  
 Glu Lys Ala Thr Gln Met Gly Ile Glu Ser Trp Tyr Ser His Pro Asn  
 55 60 65

gca ggc gag gcc tca tgc acc tgg acg ctc agc cga ggt cgt tcc tcc 355  
 Ala Gly Glu Ala Ser Cys Thr Trp Thr Leu Ser Arg Gly Arg Ser Ser  
 70 75 80 85

acg ggg ctg gcc tca gga tgg tta acc atc acc cca gtc tcc tcc gac 403  
 Thr Gly Leu Ala Ser Gly Trp Leu Thr Ile Thr Pro Val Ser Ser Asp  
 90 95 100

aaa ctg gcg caa cgt gaa cac ggt gta tcg gtc atg acc agt tca aga 451  
 Lys Leu Ala Gln Arg Glu His Gly Val Ser Val Met Thr Ser Ser Arg  
 105 110 115

gga tat tcc atc gac acc ggc ctc ccc gga atc gga aaa gcc acc cga 499  
 Gly Tyr Ser Ile Asp Thr Gly Leu Pro Gly Ile Gly Lys Ala Thr Arg  
 120 125 130

ggc gag cta tct aaa gtg gaa cga acc ccc gca cca tgg ctg aca gtc 547  
 Gly Glu Leu Ser Lys Val Glu Arg Thr Pro Ala Pro Trp Leu Thr Val  
 135 140 145

ggc gcc aaa aca cta gcc tac gca gca aac atg gca gcc ctg cgc tac 595  
 Gly Ala Lys Thr Leu Ala Tyr Ala Ala Asn Met Ala Ala Leu Arg Tyr  
 150 155 160 165

gcc aaa tca aac gga ttc gac gat gtg atc ttc acc gat ggc gac cgc 643  
 Ala Lys Ser Asn Gly Phe Asp Asp Val Ile Phe Thr Asp Gly Asp Arg  
 170 175 180

gtt cta gaa ggc gcc acc tcc acc gta gtg agt ttc aaa ggc gac aaa 691  
 Val Leu Glu Gly Ala Thr Ser Thr Val Val Ser Phe Lys Gly Asp Lys  
 185 190 195

atc cgc acc cct tca ccc ggt ggc gac att ctc ccc gga acc acc caa 739  
 Ile Arg Thr Pro Ser Pro Gly Gly Asp Ile Leu Pro Gly Thr Thr Gln  
 200 205 210

Val Ile Gly Gln Gly Thr Val Ala Ala Glu Ile Leu Ser Gln Leu Thr  
 165 170 175  
 Ser Met Gly Lys Ser Ala Asp His Val Met Val Pro Val Gly Gly Gly  
 180 185 190  
 Gly Leu Leu Ala Gly Val Val Ser Tyr Met Ala Asp Met Ala Pro Arg  
 195 200 205  
 Thr Ala Ile Val Gly Ile Glu Pro Ala Gly Ala Ala Ser Met Gln Ala  
 210 215 220  
 Ala Leu His Asn Gly Gly Pro Ile Thr Leu Glu Thr Val Asp Pro Phe  
 225 230 235 240  
 Val Asp Gly Ala Ala Val Lys Arg Val Gly Asp Leu Asn Tyr Thr Ile  
 245 250 255  
 Val Glu Lys Asn Gln Gly Arg Val His Met Met Ser Ala Thr Glu Gly  
 260 265 270  
 Ala Val Cys Thr Glu Met Leu Asp Leu Tyr Gln Asn Glu Gly Ile Ile  
 275 280 285  
 Ala Glu Pro Ala Gly Ala Leu Ser Ile Ala Gly Leu Lys Glu Met Ser  
 290 295 300  
 Phe Ala Ala Arg Ser Val Val Val Cys Ile Ile Ser Gly Gly Asn Asn  
 305 310 315 320  
 Asp Val Leu Arg Tyr Ala Glu Ile Ala Glu Arg Ser Leu Val Arg Arg  
 325 330 335  
 Gly Leu Lys His Tyr Phe Leu Val Asn Phe Pro Gln Lys Pro Gly Gln  
 340 345 350  
 Leu Arg His Phe Leu Glu Asp Ile Leu Gly Pro Asp Asp Asp Ile Thr  
 355 360 365  
 Leu Phe Glu Tyr Leu Lys Arg Asn Asn Arg Glu Thr Gly Thr Ala Leu  
 370 375 380  
 Val Gly Ile His Leu Ser Glu Ala Ser Gly Leu Asp Ser Leu Leu Glu  
 385 390 395 400  
 Arg Met Glu Glu Ser Ala Ile Asp Ser Arg Arg Leu Glu Pro Gly Thr  
 405 410 415  
 Pro Glu Tyr Glu Tyr Leu Thr  
 420

&lt;210&gt; 259

&lt;211&gt; 966

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(943)

gaa gat atc ctg gga ccg gat gat gac atc acg ctg ttt gag tac ctc  
 1219  
 Glu Asp Ile Leu Gly Pro Asp Asp Asp Ile Thr Leu Phe Glu Tyr Leu  
           360                                  365                                  370

aag cgc aac aac cgt gag acc ggt act gcg ttg gtg ggt att cac ttg  
 1267  
 Lys Arg Asn Asn Arg Glu Thr Gly Thr Ala Leu Val Gly Ile His Leu  
           375                                  380                                  385

agt gaa gca tca gga ttg gat tct ttg ctg gaa cgt atg gag gaa tcg  
 1315  
 Ser Glu Ala Ser Gly Leu Asp Ser Leu Leu Glu Arg Met Glu Glu Ser  
           390                                  395                                  400                                  405

gca att gat tcc cgt cgc ctc gag ccg ggc acc cct gag tac gaa tac  
 1363  
 Ala Ile Asp Ser Arg Arg Leu Glu Pro Gly Thr Pro Glu Tyr Glu Tyr  
                                   410                                  415                                  420

ttg acc taaacatagc tgaaggccac ctc  
 1392  
 Leu Thr

<210> 258  
 <211> 423  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 258  
 Met Ala Ser Gly Ala Glu Leu Ile Arg Ala Ala Asp Ile Gln Thr Ala  
       1                                  5                                  10                                  15  
 Gln Ala Arg Ile Ser Ser Val Ile Ala Pro Thr Pro Leu Gln Tyr Cys  
           20                                  25                                  30  
 Pro Arg Leu Ser Glu Glu Thr Gly Ala Glu Ile Tyr Leu Lys Arg Glu  
           35                                  40                                  45  
 Asp Leu Gln Asp Val Arg Ser Tyr Lys Ile Arg Gly Ala Leu Asn Ser  
       50                                  55                                  60  
 Gly Ala Gln Leu Thr Gln Glu Gln Arg Asp Ala Gly Ile Val Ala Ala  
       65                                  70                                  75                                  80  
 Ser Ala Gly Asn His Ala Gln Gly Val Ala Tyr Val Cys Lys Ser Leu  
           85                                  90                                  95  
 Gly Val Gln Gly Arg Ile Tyr Val Pro Val Gln Thr Pro Lys Gln Lys  
           100                                  105                                  110  
 Arg Asp Arg Ile Met Val His Gly Gly Glu Phe Val Ser Leu Val Val  
           115                                  120                                  125  
 Thr Gly Asn Asn Phe Asp Glu Ala Ser Ala Ala Ala His Glu Asp Ala  
           130                                  135                                  140  
 Glu Arg Thr Gly Ala Thr Leu Ile Glu Pro Phe Asp Ala Arg Asn Thr  
       145                                  150                                  155                                  160

gac gaa gca tcg gct gca gcg cat gaa gat gca gag cgc acc ggc gca 547  
 Asp Glu Ala Ser Ala Ala Ala His Glu Asp Ala Glu Arg Thr Gly Ala  
 135 140 145

acg ctg atc gag cct ttc gat gct cgc aac acc gtc atc ggt cag ggc 595  
 Thr Leu Ile Glu Pro Phe Asp Ala Arg Asn Thr Val Ile Gly Gln Gly  
 150 155 160 165

acc gtg gct gct gag atc ttg tcg cag ctg act tcc atg ggc aag agt 643  
 Thr Val Ala Ala Glu Ile Leu Ser Gln Leu Thr Ser Met Gly Lys Ser  
 170 175 180

gca gat cac gtg atg gtt cca gtc ggc ggt ggc gga ctt ctt gca ggt 691  
 Ala Asp His Val Met Val Pro Val Gly Gly Gly Gly Leu Leu Ala Gly  
 185 190 195

gtg gtc agc tac atg gct gat atg gca cct cgc act gcg atc gtt ggt. 739  
 Val Val Ser Tyr Met Ala Asp Met Ala Pro Arg Thr Ala Ile Val Gly  
 200 205 210

atc gaa cca gcg gga gca gca tcc atg cag gct gca ttg cac aat ggt 787  
 Ile Glu Pro Ala Gly Ala Ala Ser Met Gln Ala Ala Leu His Asn Gly  
 215 220 225

gga cca atc act ttg gag act gtt gat ccc ttt gtg gac ggc gca gca 835  
 Gly Pro Ile Thr Leu Glu Thr Val Asp Pro Phe Val Asp Gly Ala Ala  
 230 235 240 245

gtc aaa cgt gtc gga gat ctc aac tac acc atc gtg gag aag aac cag 883  
 Val Lys Arg Val Gly Asp Leu Asn Tyr Thr Ile Val Glu Lys Asn Gln  
 250 255 260

ggt cgc gtg cac atg atg agc gcg acc gag ggc gct gtg tgt act gag 931  
 Gly Arg Val His Met Met Ser Ala Thr Glu Gly Ala Val Cys Thr Glu  
 265 270 275

atg ctc gat ctt tac caa aac gaa ggc atc atc gcg gag cct gct ggc 979  
 Met Leu Asp Leu Tyr Gln Asn Glu Gly Ile Ile Ala Glu Pro Ala Gly  
 280 285 290

gcg ctg tct atc gct ggg ttg aag gaa atg tcc ttt gca gct cgc tct  
 1027  
 Ala Leu Ser Ile Ala Gly Leu Lys Glu Met Ser Phe Ala Ala Arg Ser  
 295 300 305

gtc gtg gtg tgc atc atc tct ggt ggc aac aac gat gtg ctg cgt tat  
 1075  
 Val Val Val Cys Ile Ile Ser Gly Gly Asn Asn Asp Val Leu Arg Tyr  
 310 315 320 325

gcg gaa atc gct gag cgc tcc ttg gtg cgc cgc ggt tta aag cac tac  
 1123  
 Ala Glu Ile Ala Glu Arg Ser Leu Val Arg Arg Gly Leu Lys His Tyr  
 330 335 340

ttc ttg gtg aac ttc ccg caa aag cct ggt cag ttg cgt cac ttc ctg  
 1171  
 Phe Leu Val Asn Phe Pro Gln Lys Pro Gly Gln Leu Arg His Phe Leu  
 345 350 355

	485	490	495	
Ile Val Met Asp Ser Gly Glu Ile Ile Glu Ser Gly Thr His Glu Glu				
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Leu Arg Ala Ile Gly Gly Arg Tyr Glu Gln Leu Trp Thr Ala Trp Ser				
	515	520	525	
Ala Arg				
530				
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<223> RXA02646				
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		Met Ala Ser Gly Ala		
		1 5		
gag ctg att cgt gcc gcc gac att caa acg gcg cag gca cga att tcc	163			
Glu Leu Ile Arg Ala Ala Asp Ile Gln Thr Ala Gln Ala Arg Ile Ser				
	10 15 20			
tcc gtc att gca cca act cca ttg cag tat tgc cct cgt ctt tct gag	211			
Ser Val Ile Ala Pro Thr Pro Leu Gln Tyr Cys Pro Arg Leu Ser Glu				
	25 30 35			
gaa acc gga gcg gaa atc tac ctt aag cgt gag gat ctg cag gat gtt	259			
Glu Thr Gly Ala Glu Ile Tyr Leu Lys Arg Glu Asp Leu Gln Asp Val				
	40 45 50			
cgt tcc tac aag atc cgc ggt gcg ctg aac tct gga gcg cag ctc acc	307			
Arg Ser Tyr Lys Ile Arg Gly Ala Leu Asn Ser Gly Ala Gln Leu Thr				
	55 60 65			
caa gag cag cgc gat gca ggt atc gtt gcc gca tct gca ggt aac cat	355			
Gln Glu Gln Arg Asp Ala Gly Ile Val Ala Ala Ser Ala Gly Asn His				
	70 75 80 85			
gcc cag ggc gtg gcc tat gtg tgc aag tcc ttg ggc gtt cag gga cgc	403			
Ala Gln Gly Val Ala Tyr Val Cys Lys Ser Leu Gly Val Gln Gly Arg				
	90 95 100			
atc tat gtt cct gtg cag act cca aag caa aag cgt gac cgc atc atg	451			
Ile Tyr Val Pro Val Gln Thr Pro Lys Gln Lys Arg Asp Arg Ile Met				
	105 110 115			
gtt cac ggc gga gag ttt gtc tcc ttg gtg gtc act ggc aat aac ttc	499			
Val His Gly Gly Glu Phe Val Ser Leu Val Val Thr Gly Asn Asn Phe				
	120 125 130			

Val Gly Ala Val Glu Gly Ala Glu Thr Leu Arg Ala Phe Arg Ala Glu  
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 Asp Thr Glu Leu Lys Arg Ile Asp Ala Ala Ser Gly Glu Ala Arg Asp  
 180 185 190  
 Ile Ser Ile Ser Val Phe Arg Phe Leu Thr Trp Ala Phe Ser Arg Asn  
 195 200 205  
 Asn Arg Ala Glu Cys Ile Thr Leu Val Leu Ile Leu Gly Thr Gly Phe  
 210 215 220  
 Tyr Leu Val Asn Ile Asp Leu Val Thr Val Gly Ala Val Ser Thr Ala  
 225 230 235 240  
 Ala Leu Ile Phe His Arg Leu Phe Gly Pro Ile Gly Thr Leu Val Gly  
 245 250 255  
 Met Phe Ser Asp Ile Gln Ser Ala Ser Ala Ser Leu Ile Arg Met Val  
 260 265 270  
 Gly Val Ile Asn Ala Ala Ser Asn Gln Val Ser Gly Thr Ser Pro Ala  
 275 280 285  
 Ser Ala Ser Thr Ala Leu Thr Leu Phe Asp Val Ser His His Tyr His  
 290 295 300  
 Thr Ala Pro Val Ile Lys Asn Ala Ser Val Gln Leu Glu Pro Gly Glu  
 305 310 315 320  
 His Ile Ala Ile Val Gly Ala Thr Gly Ala Gly Lys Ser Thr Leu Ala  
 325 330 335  
 Leu Ile Ala Ala Gly Leu Leu Ser Pro Thr Ser Gly Gln Val Ala Leu  
 340 345 350  
 Gly Gly Ser Ser Phe Ser Asn Val Glu Pro Glu Ala Leu Arg Gln Lys  
 355 360 365  
 Ile Ala Met Val Ser Gln Glu Ile His Cys Phe Arg Gly Ser Val Leu  
 370 375 380  
 Asp Asn Leu Arg Ile Ala Arg Pro Glu Ala Thr Asp Ala Asp Ile His  
 385 390 395 400  
 Ala Val Leu Ala Asp Ile Gly Asp Ser Trp Leu Glu Arg Leu Pro Gln  
 405 410 415  
 Gly Ile Asp Thr Ile Val Gly Asp Gly Ala Phe Arg Leu Thr Ser Val  
 420 425 430  
 Glu Asn Gln Ile Met Ala Leu Ala Arg Val His Leu Ala Asp Leu Ala  
 435 440 445  
 Ile Val Ile Leu Asp Glu Ala Thr Ala Glu Ser Gly Ser Asp His Ala  
 450 455 460  
 Lys Gln Leu Glu Asp Ala Ala Leu Lys Val Thr Glu Asn Arg Ser Ala  
 465 470 475 480  
 Ile Ile Val Ala His Arg Leu Asn Gln Ala Lys Thr Ala Asp Arg Ile



gca gcc ctt aaa gtc act gaa aac aga tca gcc atc atc gtg gct cac  
1555

Ala Ala Leu Lys Val Thr Glu Asn Arg Ser Ala Ile Ile Val Ala His  
470 475 480 485

cgc ctc aac caa gcg aaa acc gcc gat cgc atc atc gtc atg gac tcc  
1603

Arg Leu Asn Gln Ala Lys Thr Ala Asp Arg Ile Ile Val Met Asp Ser  
490 495 500

gga gaa atc ata gaa tct gga acc cat gaa gag ctt cga gcg atc ggc  
1651

Gly Glu Ile Ile Glu Ser Gly Thr His Glu Glu Leu Arg Ala Ile Gly  
505 510 515

ggc cga tat gaa caa ctg tgg act gcg tgg tct gcg cgc taattagcca  
1700

Gly Arg Tyr Glu Gln Leu Trp Thr Ala Trp Ser Ala Arg  
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<211> 530

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 256

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20 25 30

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35 40 45

Ala Ile Ala Gly Leu Arg Glu Asp Val Leu Arg Ala Ala Val Ser Leu  
50 55 60

Asp Ala Asn Thr Ile Glu Thr Ala Gly Arg Gly Asp Val Ile Ser Arg  
65 70 75 80

Ile Ala Asp Asp Ser Arg Glu Val Ser Thr Ala Ala Ser Thr Val Val  
85 90 95

Pro Leu Met Val Gln Ala Gly Phe Thr Val Val Ile Ser Ala Phe Gly  
100 105 110

Met Ala Ala Val Asp Trp Arg Leu Gly Leu Val Gly Leu Val Ala Ile  
115 120 125

Pro Leu Tyr Trp Thr Thr Leu Arg Val Tyr Leu Pro Arg Ser Gly Pro  
130 135 140

Leu Tyr Thr Arg Glu Arg Glu Ala Phe Gly Val Arg Thr Gln Arg Leu  
145 150 155 160

Gln Ser Ala Ser Ala Ser Leu Ile Arg Met Val Gly Val Ile Asn Ala  
 265 270 275

gca tcg aac cag gtc agc ggc acc tcg ccg gcg tct gcc agc acc gct 979  
 Ala Ser Asn Gln Val Ser Gly Thr Ser Pro Ala Ser Ala Ser Thr Ala  
 280 285 290

tta acg ctt ttc gac gtc tcc cac cac tat cac act gca ccc gtc atc  
 1027

Leu Thr Leu Phe Asp Val Ser His His Tyr His Thr Ala Pro Val Ile  
 295 300 305

aag aat gca tcc gtg cag ctg gaa cca ggg gaa cac atc gcc att gtg  
 1075

Lys Asn Ala Ser Val Gln Leu Glu Pro Gly Glu His Ile Ala Ile Val  
 310 315 320 325

ggt gcg acc ggc gct ggt aaa agc acg ctc gcc ctc att gcg gca ggc  
 1123

Gly Ala Thr Gly Ala Gly Lys Ser Thr Leu Ala Leu Ile Ala Ala Gly  
 330 335 340

ctg ctc agc cca act tcc ggg cag gtg gct ctc ggc gga tcg agt ttt  
 1171

Leu Leu Ser Pro Thr Ser Gly Gln Val Ala Leu Gly Gly Ser Ser Phe  
 345 350 355

tct aac gtc gaa ccg gaa gca ttg cgc cag aag atc gcg atg gtc agc  
 1219

Ser Asn Val Glu Pro Glu Ala Leu Arg Gln Lys Ile Ala Met Val Ser  
 360 365 370

caa gaa atc cac tgc ttc cga gga tct gtt tta gat aat ctt cgt atc  
 1267

Gln Glu Ile His Cys Phe Arg Gly Ser Val Leu Asp Asn Leu Arg Ile  
 375 380 385

gca cgc ccc gaa gcc acc gat gcg gac atc cac gcc gtt ctc gcc gat  
 1315

Ala Arg Pro Glu Ala Thr Asp Ala Asp Ile His Ala Val Leu Ala Asp  
 390 395 400 405

att ggt gat tcc tgg ttg gag cgc tta ccg caa ggc ata gac acc atc  
 1363

Ile Gly Asp Ser Trp Leu Glu Arg Leu Pro Gln Gly Ile Asp Thr Ile  
 410 415 420

gtg ggt gat ggc gct ttc cgt tta acc tct gtg gaa aac cag atc atg  
 1411

Val Gly Asp Gly Ala Phe Arg Leu Thr Ser Val Glu Asn Gln Ile Met  
 425 430 435

gcg ctt gct cgc gta cat ttg gcc gac cta gca atc gtc atc ctt gat  
 1459

Ala Leu Ala Arg Val His Leu Ala Asp Leu Ala Ile Val Ile Leu Asp  
 440 445 450

gaa gca acg gct gaa tca ggc tct gat cat gca aaa cag ctt gaa gat  
 1507

Glu Ala Thr Ala Glu Ser Gly Ser Asp His Ala Lys Gln Leu Glu Asp  
 455 460 465

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ctg	gca	tcc	ctg	cgc	gag	cat	gac	gcg	atc	ctt	ctt	ggc	gct	atc	ggt	307				
Leu	Ala	Ser	Leu	Arg	Glu	His	Asp	Ala	Ile	Leu	Leu	Gly	Ala	Ile	Gly					
55			60				65													
gca	cca	ggt	tcc	gtc	cct	cca	gga	att	ctc	gag	cgt	ggt	ttg	ctg	ctg	355				
Ala	Pro	Gly	Ser	Val	Pro	Pro	Gly	Ile	Leu	Glu	Arg	Gly	Leu	Leu	Leu					
70		75				80				85										
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Lys	Met	Arg	Phe	Ala	Leu	Asp	His	His	Val	Asn	Leu	Arg	Pro	Ser	Lys					
90				95				100												
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Leu	Tyr	Asp	Gly	Val	Glu	Ser	Pro	Leu	Arg	Asn	Pro	Gly	Lys	Ile	Asp					
105			110				115													
ttc	gtt	gtg	gtc	cgc	gaa	ggt	acc	gaa	ggc	gcc	tac	act	ggc	aac	ggt	499				
Phe	Val	Val	Val	Arg	Glu	Gly	Thr	Glu	Gly	Ala	Tyr	Thr	Gly	Asn	Gly					
120			125				130													
gga	gca	atc	cgc	gtg	gga	acc	cct	cac	gag	att	gcc	aat	gaa	acc	tcc	547				
Gly	Ala	Ile	Arg	Val	Gly	Thr	Pro	His	Glu	Ile	Ala	Asn	Glu	Thr	Ser					
135		140				145														
gtg	aac	act	cgc	tac	ggc	gct	gag	cgc	gtt	att	cgc	tac	gca	ttc	gag	595				
Val	Asn	Thr	Arg	Tyr	Gly	Ala	Glu	Arg	Val	Ile	Arg	Tyr	Ala	Phe	Glu					
150		155				160				165										
ctg	gca	cag	agc	cgc	cgc	aag	aag	ctc	acc	ctc	gtg	cac	aag	acc	aac	643				
Leu	Ala	Gln	Ser	Arg	Arg	Lys	Lys	Leu	Thr	Leu	Val	His	Lys	Thr	Asn					
170				175				180												
gtc	ctg	gtt	cac	ggt	ggt	ggc	ctg	tgg	cag	cgc	acc	gta	gat	gag	gtt	691				
Val	Leu	Val	His	Gly	Gly	Gly	Leu	Trp	Gln	Arg	Thr	Val	Asp	Glu	Val					
185			190				195													
gca	aag	gaa	tac	cca	gag	gta	gcc	gtc	gat	tac	aac	cac	atc	gat	gca	739				
Ala	Lys	Glu	Tyr	Pro	Glu	Val	Ala	Val	Asp	Tyr	Asn	His	Ile	Asp	Ala					
200			205				210													
gca	acc	atc	tat	ctg	gtc	act	gat	cct	tcc	cgc	ttc	gat	gtg	att	gtt	787				
Ala	Thr	Ile	Tyr	Leu	Val	Thr	Asp	Pro	Ser	Arg	Phe	Asp	Val	Ile	Val					
215		220				225														
acc	gat	aac	ctc	ttc	ggc	gac	atc	ctc	acc	gat	gag	gca	ggc	gca	gtc	835				
Thr	Asp	Asn	Leu	Phe	Gly	Asp	Ile	Leu	Thr	Asp	Glu	Ala	Gly	Ala	Val					
230		235				240				245										
tct	ggc	gga	att	ggc	ctc	gca	gca	tcc	ggc	aac	atc	gat	gcc	acg	ggc	883				
Ser	Gly	Gly	Ile	Gly	Leu	Ala	Ala	Ser	Gly	Asn	Ile	Asp	Ala	Thr	Gly					
250			255				260													
acc	aac	cct	tcc	atg	ttc	gag	cca	gtc	cac	ggc	tct	gca	cca	gat	atc	931				
Thr	Asn	Pro	Ser	Met	Phe	Glu	Pro	Val	His	Gly	Ser	Ala	Pro	Asp	Ile					
265			270				275													

Gln Ile Ala Ala Asp Ile Leu Lys Gly His Lys Ile Ala Asp Gly Met .  
 355 360 365  
 Arg Met Met Val Val Pro Ser Ser Thr Trp Ile Lys Gln Glu Ala Glu  
 370 375 380  
 Ala Leu Gly Leu Asp Lys Ile Phe Thr Asp Ala Gly Ala Glu Trp Arg  
 385 390 395 400  
 Thr Ala Gly Cys Ser Met Cys Leu Gly Met Asn Pro Asp Gln Leu Lys  
 405 410 415  
 Pro Gly Glu Arg Ser Ala Phe Thr Ser Asn Arg Asn Phe Glu Gly Arg  
 420 425 430  
 Gln Gly Pro Gly Gly Arg Thr His Leu Val Ser Pro Ala Val Ala Ala  
 435 440 445  
 Ala Thr Glu Ser Ala Asp Pro Val Leu Thr Cys Arg Tyr Leu Arg Lys  
 450 455 460  
 Ala Arg Lys Gln Trp Lys Asn Leu Pro Pro Thr Pro Ala Leu Ala Phe  
 465 470 475 480  
 His Cys Ser Asp Pro Thr Trp Thr Pro Thr Arg Ser Ser Gln Pro Ser  
 485 490 495  
 Thr Ser Ser Ala Ser Pro Gly Pro Ala Ser Lys Thr Asp Cys Phe Pro  
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 515 520 525  
 Arg Thr Ala Pro Phe Ser  
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 <211> 1143  
 <212> DNA  
 <213> Corynebacterium glutamicum

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 <222> (101)..(1120)  
 <223> RXN01127

<400> 269  
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 Met Lys Leu Ala Val  
 1 5  
 att ggt gga gat ggt atc ggc cca gag gtt act gca gaa gcc ctc aag 163  
 Ile Gly Gly Asp Gly Ile Gly Pro Glu Val Thr Ala Glu Ala Leu Lys  
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 gtt cta aac gct gtc cgc gac gac atc gag acc acc gat tat gac ctt 211  
 Val Leu Asn Ala Val Arg Asp Asp Ile Glu Thr Thr Asp Tyr Asp Leu

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Ala	Phe	Asp	Gly	Leu	Arg	Met	Thr	Gly	Arg	Lys	Leu	Arg	His	Pro	Glu
		35					40					45			
Leu	His	Leu	Ala	Thr	Glu	Asp	His	Asn	Val	Pro	Thr	Glu	Gly	Ile	Lys
		50					55					60			
Thr	Gly	Ser	Leu	Leu	Glu	Ile	Asn	Asp	Lys	Ile	Ser	Arg	Leu	Gln	Val
		65					70					75			80
Ser	Thr	Leu	Arg	Asp	Asn	Cys	Glu	Glu	Phe	Gly	Val	Arg	Leu	His	Pro
				85					90					95	
Met	Gly	Asp	Val	Arg	Gln	Gly	Ile	Val	His	Thr	Val	Gly	Pro	Gln	Leu
			100						105				110		
Gly	Ala	Thr	Gln	Pro	Gly	Met	Thr	Ile	Val	Cys	Gly	Asp	Ser	His	Thr
			115						120				125		
Ser	Thr	His	Gly	Ala	Phe	Gly	Ser	Met	Ala	Phe	Gly	Ile	Gly	Thr	Ser
			130						135				140		
Glu	Val	Glu	His	Val	Met	Ala	Thr	Gln	Thr	Leu	Pro	Leu	Lys	Pro	Phe
				145					150						160
Lys	Thr	Met	Ala	Ile	Glu	Val	Thr	Gly	Glu	Leu	Gln	Pro	Gly	Val	Ser
				165					170						175
Ser	Lys	Asp	Leu	Ile	Leu	Ala	Ile	Ile	Ala	Lys	Ile	Gly	Thr	Gly	Gly
			180						185					190	
Gly	Gln	Gly	Tyr	Val	Leu	Glu	Tyr	Arg	Gly	Glu	Ala	Ile	Arg	Lys	Met
			195						200					205	
Ser	Met	Asp	Ala	Arg	Met	Thr	Met	Cys	Asn	Met	Ser	Ile	Glu	Ala	Gly
				210					215					220	
Ala	Arg	Ala	Gly	Met	Ile	Ala	Pro	Asp	Gln	Thr	Thr	Phe	Asp	Tyr	Val
				225					230					235	240
Glu	Gly	Arg	Glu	Met	Ala	Pro	Lys	Gly	Ala	Asp	Trp	Asp	Glu	Ala	Val
				245					250					255	
Ala	Tyr	Trp	Lys	Thr	Leu	Pro	Thr	Asp	Glu	Gly	Ala	Thr	Phe	Asp	Lys
				260					265					270	
Val	Val	Glu	Ile	Asp	Gly	Ser	Ala	Leu	Thr	Pro	Phe	Ile	Thr	Trp	Gly
			275						280					285	
Thr	Asn	Pro	Gly	Gln	Gly	Leu	Pro	Leu	Gly	Glu	Ser	Val	Pro	Ser	Pro
				290					295					300	
Glu	Asp	Phe	Thr	Asn	Asp	Asn	Asp	Lys	Ala	Ala	Ala	Glu	Lys	Ala	Leu
				305					310					315	320
Gln	Tyr	Met	Asp	Leu	Val	Pro	Gly	Thr	Pro	Leu	Arg	Asp	Ile	Lys	Ile
				325					330					335	
Asp	Thr	Val	Phe	Leu	Gly	Ser	Cys	Thr	Asn	Ala	Arg	Ile	Glu	Asp	Leu
				340					345					350	

gcg ctc gga ctg gac aaa atc ttc acc gac gct ggc gct gaa tgg cgt  
1200  
Ala Leu Gly Leu Asp Lys Ile Phe Thr Asp Ala Gly Ala Glu Trp Arg  
385 390 395 400

acc gca ggc tgc tcc atg tgc ctg ggc atg aac cca gac caa ctg aag  
1248  
Thr Ala Gly Cys Ser Met Cys Leu Gly Met Asn Pro Asp Gln Leu Lys  
405 410 415

cca ggc gag cgc tcc gca ttc acc tcc aac cga aac ttc gaa gga cgc  
1296  
Pro Gly Glu Arg Ser Ala Phe Thr Ser Asn Arg Asn Phe Glu Gly Arg  
420 425 430

caa gga cca gga ggc cgc acc cac ctg gta tcc cca gca gtc gca gcc  
1344  
Gln Gly Pro Gly Gly Arg Thr His Leu Val Ser Pro Ala Val Ala Ala  
435 440 445

gcc acc gaa tcc gcg gac cct gtc ctc acc tgc aga tat cta agg aag  
1392  
Ala Thr Glu Ser Ala Asp Pro Val Leu Thr Cys Arg Tyr Leu Arg Lys  
450 455 460

gct aga aaa caa tgg aaa aat tta cca cct aca ccg gcg ttg gcg ttc  
1440  
Ala Arg Lys Gln Trp Lys Asn Leu Pro Pro Thr Pro Ala Leu Ala Phe  
465 470 475 480

cac tgc agc gat cca acg tgg aca ccg acc aga tca tcc cag ccg tct  
1488  
His Cys Ser Asp Pro Thr Trp Thr Pro Thr Arg Ser Ser Gln Pro Ser  
485 490 495

acc tca agc gcg tca ccc gga ccg gct tcg aag acg gac tgt ttt cca  
1536  
Thr Ser Ser Ala Ser Pro Gly Pro Ala Ser Lys Thr Asp Cys Phe Pro  
500 505 510

act ggc gcc aaa acg acc cca act ttg tcc tca aca ccg aca cct aca  
1584  
Thr Gly Ala Lys Thr Thr Pro Thr Leu Ser Ser Thr Pro Thr Pro Thr  
515 520 525

aga acg gct ccg ttc tcg tagcaggccc tgactttggc acc  
1625  
Arg Thr Ala Pro Phe Ser  
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<210> 268

<211> 534

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 268

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Leu Leu Tyr Ile Asp Leu Gln Leu Leu His Glu Val Thr Ser Pro Gln

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Lys Thr Met Ala Ile Glu Val Thr Gly Glu Leu Gln Pro Gly Val Ser	
165 170 175	
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Ser Lys Asp Leu Ile Leu Ala Ile Ile Ala Lys Ile Gly Thr Gly Gly	
180 185 190	
gga cag ggc tac gtt ctg gaa tac cgc ggc gaa gca atc cgt aag atg	624
Gly Gln Gly Tyr Val Leu Glu Tyr Arg Gly Glu Ala Ile Arg Lys Met	
195 200 205	
tcc atg gat gca cgc atg acc atg tgc aac atg tcc atc gaa gct ggc	672
Ser Met Asp Ala Arg Met Thr Met Cys Asn Met Ser Ile Glu Ala Gly	
210 215 220	
gca cgt gcc ggc atg atc gcc cca gac caa acc acc ttc gac tac gtt	720
Ala Arg Ala Gly Met Ile Ala Pro Asp Gln Thr Thr Phe Asp Tyr Val	
225 230 235 240	
gaa ggc cgc gaa atg gca cca aag ggc gcc gac tgg gac gaa gca gtt	768
Glu Gly Arg Glu Met Ala Pro Lys Gly Ala Asp Trp Asp Glu Ala Val	
245 250 255	
gct tac tgg aag acc ctg cca acc gac gaa ggc gca acc ttt gac aag	816
Ala Tyr Trp Lys Thr Leu Pro Thr Asp Glu Gly Ala Thr Phe Asp Lys	
260 265 270	
gtc gta gaa atc gat ggc tcg gca ctg acc cca ttc atc acc tgg ggc	864
Val Val Glu Ile Asp Gly Ser Ala Leu Thr Pro Phe Ile Thr Trp Gly	
275 280 285	
acc aac cca ggc cag ggc ctg cca ctg ggc gaa tcc gta cca agc cca	912
Thr Asn Pro Gly Gln Gly Leu Pro Leu Gly Glu Ser Val Pro Ser Pro	
290 295 300	
gaa gac ttc acc aac gac aac gac aag gca gca gcc gaa aag gca ctg	960
Glu Asp Phe Thr Asn Asp Asn Asp Lys Ala Ala Ala Glu Lys Ala Leu	
305 310 315 320	
cag tac atg gac ctg gta cca gga acc cca ctg cgc gac atc aag atc	
1008	
Gln Tyr Met Asp Leu Val Pro Gly Thr Pro Leu Arg Asp Ile Lys Ile	
325 330 335	
gac acc gtc ttc ctg gga tcc tgc acc aac gcc cgc atc gaa gac ctg	
1056	
Asp Thr Val Phe Leu Gly Ser Cys Thr Asn Ala Arg Ile Glu Asp Leu	
340 345 350	
cag atc gcc gct gac atc ctc aag ggc cac aaa atc gcc gac ggc atg	
1104	
Gln Ile Ala Ala Asp Ile Leu Lys Gly His Lys Ile Ala Asp Gly Met	
355 360 365	
cgc atg atg gtc gtg cct tcc tcc acc tgg atc aag caa gag gca gaa	
1152	
Arg Met Met Val Val Pro Ser Ser Thr Trp Ile Lys Gln Glu Ala Glu	
370 375 380	

Gln Pro Ser Thr Ser Ser Ala Ser Pro Gly Pro Ala Ser Lys Thr Asp  
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Cys Phe Pro Thr Gly Ala Lys Thr Thr Pro Thr Leu Ser Ser Thr Pro  
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Thr Pro Thr Arg Thr Ala Pro Phe Ser  
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<211> 1625

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1602)

<223> FRXA01026

<400> 267

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ctc ctc tac atc gac ctg cag ctg ctg cat gaa gtg acc tca cca cag 96  
 Leu Leu Tyr Ile Asp Leu Gln Leu Leu His Glu Val Thr Ser Pro Gln  
 20 25 30

gca ttt gac ggc ctg cgc atg acc ggc cgt aaa ctg cgc cac cca gaa 144  
 Ala Phe Asp Gly Leu Arg Met Thr Gly Arg Lys Leu Arg His Pro Glu  
 35 40 45

ctg cac ctg gcc acc gaa gac cac aac gtg cca acc gaa ggc atc aag 192  
 Leu His Leu Ala Thr Glu Asp His Asn Val Pro Thr Glu Gly Ile Lys  
 50 55 60

act ggc tca ctg ctg gaa atc aac gac aag att tcc cgc ctg cag gta 240  
 Thr Gly Ser Leu Leu Glu Ile Asn Asp Lys Ile Ser Arg Leu Gln Val  
 65 70 75 80

tct act ctg cgc gac aac tgt gaa gaa ttc ggc gtg cgc ctg cac cca 288  
 Ser Thr Leu Arg Asp Asn Cys Glu Glu Phe Gly Val Arg Leu His Pro  
 85 90 95

atg ggt gat gtc cga cag ggc atc gtg cac acc gtc ggc cca cag ctc 336  
 Met Gly Asp Val Arg Gln Gly Ile Val His Thr Val Gly Pro Gln Leu  
 100 105 110

ggc gca acc cag cca ggc atg acc att gtg tgc ggt gac tcc cac acc 384  
 Gly Ala Thr Gln Pro Gly Met Thr Ile Val Cys Gly Asp Ser His Thr  
 115 120 125

tcc acc cac ggt gct ttt ggc tcc atg gca ttc ggc atc ggt acc tca 432  
 Ser Thr His Gly Ala Phe Gly Ser Met Ala Phe Gly Ile Gly Thr Ser  
 130 135 140

gag gtt gag cac gtc atg gct act caa acc ctg cca ctg aag cct ttc 480  
 Glu Val Glu His Val Met Ala Thr Gln Thr Leu Pro Leu Lys Pro Phe  
 145 150 155 160



180					185					190					
Gly	Val	Ser	Ser	Lys	Asp	Leu	Ile	Leu	Ala	Ile	Ile	Ala	Lys	Ile	Gly
	195						200					205			
Thr	Gly	Gly	Gly	Gln	Gly	Tyr	Val	Leu	Glu	Tyr	Arg	Gly	Glu	Ala	Ile
	210					215					220				
Arg	Lys	Met	Ser	Met	Asp	Ala	Arg	Met	Thr	Met	Cys	Asn	Met	Ser	Ile
225					230					235					240
Glu	Ala	Gly	Ala	Arg	Ala	Gly	Met	Ile	Ala	Pro	Asp	Gln	Thr	Thr	Phe
				245					250						255
Asp	Tyr	Val	Glu	Gly	Arg	Glu	Met	Ala	Pro	Lys	Gly	Ala	Asp	Trp	Asp
			260					265						270	
Glu	Ala	Val	Ala	Tyr	Trp	Lys	Thr	Leu	Pro	Thr	Asp	Glu	Gly	Ala	Thr
		275					280					285			
Phe	Asp	Lys	Val	Val	Glu	Ile	Asp	Gly	Ser	Ala	Leu	Thr	Pro	Phe	Ile
	290					295					300				
Thr	Trp	Gly	Thr	Asn	Pro	Gly	Gln	Gly	Leu	Pro	Leu	Gly	Glu	Ser	Val
305					310					315					320
Pro	Ser	Pro	Glu	Asp	Phe	Thr	Asn	Asp	Asn	Asp	Lys	Ala	Ala	Ala	Glu
				325					330					335	
Lys	Ala	Leu	Gln	Tyr	Met	Asp	Leu	Val	Pro	Gly	Thr	Pro	Leu	Arg	Asp
			340					345					350		
Ile	Lys	Ile	Asp	Thr	Val	Phe	Leu	Gly	Ser	Cys	Thr	Asn	Ala	Arg	Ile
		355					360					365			
Glu	Asp	Leu	Gln	Ile	Ala	Ala	Asp	Ile	Leu	Lys	Gly	His	Lys	Ile	Ala
	370					375					380				
Asp	Gly	Met	Arg	Met	Met	Val	Val	Pro	Ser	Ser	Thr	Trp	Ile	Lys	Gln
385					390					395					400
Glu	Ala	Glu	Ala	Leu	Gly	Leu	Asp	Lys	Ile	Phe	Thr	Asp	Ala	Gly	Ala
				405					410					415	
Glu	Trp	Arg	Thr	Ala	Gly	Cys	Ser	Met	Cys	Leu	Gly	Met	Asn	Pro	Asp
			420					425					430		
Gln	Leu	Lys	Pro	Gly	Glu	Arg	Ser	Ala	Phe	Thr	Ser	Asn	Arg	Asn	Phe
		435					440					445			
Glu	Gly	Arg	Gln	Gly	Pro	Gly	Gly	Arg	Thr	His	Leu	Val	Ser	Pro	Ala
	450					455					460				
Val	Ala	Ala	Ala	Thr	Glu	Ser	Ala	Asp	Pro	Val	Leu	Thr	Cys	Arg	Tyr
465					470					475					480
Leu	Arg	Lys	Ala	Arg	Lys	Gln	Trp	Lys	Asn	Leu	Pro	Pro	Thr	Pro	Ala
				485					490					495	
Leu	Ala	Phe	His	Cys	Ser	Asp	Pro	Thr	Trp	Thr	Pro	Thr	Arg	Ser	Ser
			500					505					510		

agc gat cca acg tgg aca ccg acc aga tca tcc cag ccg tct acc tca  
1651

Ser Asp Pro Thr Trp Thr Pro Thr Arg Ser Ser Gln Pro Ser Thr Ser  
505 510 515

agc gcg tca ccc gga ccg gct tcg aag acg gac tgt ttt cca act ggc  
1699

Ser Ala Ser Pro Gly Pro Ala Ser Lys Thr Asp Cys Phe Pro Thr Gly  
520 525 530

gcc aaa acg acc cca act ttg tcc tca aca ccg aca cct aca aga acg  
1747

Ala Lys Thr Thr Pro Thr Leu Ser Ser Thr Pro Thr Pro Thr Arg Thr  
535 540 545

gct ccg ttc tcg tagcaggccc tgactttggc acc  
1782

Ala Pro Phe Ser  
550

<210> 266

<211> 553

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 266

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20 25 30

Glu Pro Asp Leu Leu Tyr Ile Asp Leu Gln Leu Leu His Glu Val Thr  
35 40 45

Ser Pro Gln Ala Phe Asp Gly Leu Arg Met Thr Gly Arg Lys Leu Arg  
50 55 60

His Pro Glu Leu His Leu Ala Thr Glu Asp His Asn Val Pro Thr Glu  
65 70 75 80

Gly Ile Lys Thr Gly Ser Leu Leu Glu Ile Asn Asp Lys Ile Ser Arg  
85 90 95

Leu Gln Val Ser Thr Leu Arg Asp Asn Cys Glu Glu Phe Gly Val Arg  
100 105 110

Leu His Pro Met Gly Asp Val Arg Gln Gly Ile Val His Thr Val Gly  
115 120 125

Pro Gln Leu Gly Ala Thr Gln Pro Gly Met Thr Ile Val Cys Gly Asp  
130 135 140

Ser His Thr Ser Thr His Gly Ala Phe Gly Ser Met Ala Phe Gly Ile  
145 150 155 160

Gly Thr Ser Glu Val Glu His Val Met Ala Thr Gln Thr Leu Pro Leu  
165 170 175

Lys Pro Phe Lys Thr Met Ala Ile Glu Val Thr Gly Glu Leu Gln Pro

cca ggc cag ggc ctg cca ctg ggc gaa tcc gta cca agc cca gaa gac  
 1075  
 Pro Gly Gln Gly Leu Pro Leu Gly Glu Ser Val Pro Ser Pro Glu Asp  
 310 315 320 325

ttc acc aac gac aac gac aag gca gca gcc gaa aag gca ctg cag tac  
 1123  
 Phe Thr Asn Asp Asn Asp Lys Ala Ala Ala Glu Lys Ala Leu Gln Tyr  
 330 335 340

atg gac ctg gta cca gga acc cca ctg cgc gac atc aag atc gac acc  
 1171  
 Met Asp Leu Val Pro Gly Thr Pro Leu Arg Asp Ile Lys Ile Asp Thr  
 345 350 355

gtc ttc ctg gga tcc tgc acc aac gcc cgc atc gaa gac ctg cag atc  
 1219  
 Val Phe Leu Gly Ser Cys Thr Asn Ala Arg Ile Glu Asp Leu Gln Ile  
 360 365 370

gcc gct gac atc ctc aag ggc cac aaa atc gcc gac ggc atg cgc atg  
 1267  
 Ala Ala Asp Ile Leu Lys Gly His Lys Ile Ala Asp Gly Met Arg Met  
 375 380 385

atg gtc gtg cct tcc tcc acc tgg atc aag caa gag gca gaa gcg ctc  
 1315  
 Met Val Val Pro Ser Ser Thr Trp Ile Lys Gln Glu Ala Glu Ala Leu  
 390 395 400 405

gga ctg gac aaa atc ttc acc gac gct ggc gct gaa tgg cgt acc gca  
 1363  
 Gly Leu Asp Lys Ile Phe Thr Asp Ala Gly Ala Glu Trp Arg Thr Ala  
 410 415 420

ggc tgc tcc atg tgc ctg ggc atg aac cca gac caa ctg aag cca ggc  
 1411  
 Gly Cys Ser Met Cys Leu Gly Met Asn Pro Asp Gln Leu Lys Pro Gly  
 425 430 435

gag cgc tcc gca ttc acc tcc aac cga aac ttc gaa gga cgc caa gga  
 1459  
 Glu Arg Ser Ala Phe Thr Ser Asn Arg Asn Phe Glu Gly Arg Gln Gly  
 440 445 450

cca gga ggc cgc acc cac ctg gta tcc cca gca gtc gca gcc gcc acc  
 1507  
 Pro Gly Gly Arg Thr His Leu Val Ser Pro Ala Val Ala Ala Ala Thr  
 455 460 465

gaa tcc gcg gac cct gtc ctc acc tgc aga tat cta agg aag gct aga  
 1555  
 Glu Ser Ala Asp Pro Val Leu Thr Cys Arg Tyr Leu Arg Lys Ala Arg  
 470 475 480 485

aaa caa tgg aaa aat tta cca cct aca ccg gcg ttg gcg ttc cac tgc  
 1603  
 Lys Gln Trp Lys Asn Leu Pro Pro Thr Pro Ala Leu Ala Phe His Cys  
 490 495 500

Leu	Ala	Thr	Glu	Asp	His	Asn	Val	Pro	Thr	Glu	Gly	Ile	Lys	Thr	Gly	
70						75				80					85	
tca	ctg	ctg	gaa	atc	aac	gac	aag	att	tcc	cgc	ctg	cag	gta	tct	act	403
Ser	Leu	Leu	Glu	Ile	Asn	Asp	Lys	Ile	Ser	Arg	Leu	Gln	Val	Ser	Thr	
			90					95						100		
ctg	cgc	gac	aac	tgt	gaa	gaa	ttc	ggc	gtg	cgc	ctg	cac	cca	atg	ggc	451
Leu	Arg	Asp	Asn	Cys	Glu	Glu	Phe	Gly	Val	Arg	Leu	His	Pro	Met	Gly	
			105					110					115			
gat	gtc	cga	cag	ggc	atc	gtg	cac	acc	gtc	ggc	cca	cag	ctc	ggc	gca	499
Asp	Val	Arg	Gln	Gly	Ile	Val	His	Thr	Val	Gly	Pro	Gln	Leu	Gly	Ala	
			120				125					130				
acc	cag	cca	ggc	atg	acc	att	gtg	tgc	ggc	gac	tcc	cac	acc	tcc	acc	547
Thr	Gln	Pro	Gly	Met	Thr	Ile	Val	Cys	Gly	Asp	Ser	His	Thr	Ser	Thr	
			135				140				145					
cac	ggc	gct	ttt	ggc	tcc	atg	gca	ttc	ggc	atc	ggc	acc	tca	gag	gtt	595
His	Gly	Ala	Phe	Gly	Ser	Met	Ala	Phe	Gly	Ile	Gly	Thr	Ser	Glu	Val	
150					155					160					165	
gag	cac	gtc	atg	gct	act	caa	acc	ctg	cca	ctg	aag	cct	ttc	aag	acc	643
Glu	His	Val	Met	Ala	Thr	Gln	Thr	Leu	Pro	Leu	Lys	Pro	Phe	Lys	Thr	
				170					175					180		
atg	gcc	att	gaa	gtt	act	ggc	gaa	ctg	cag	cca	ggc	gtt	tcc	tcc	aag	691
Met	Ala	Ile	Glu	Val	Thr	Gly	Glu	Leu	Gln	Pro	Gly	Val	Ser	Ser	Lys	
			185					190					195			
gac	ctg	att	ctg	gcg	att	atc	gcc	aag	atc	ggc	acc	ggc	ggc	gga	cag	739
Asp	Leu	Ile	Leu	Ala	Ile	Ile	Ala	Lys	Ile	Gly	Thr	Gly	Gly	Gly	Gln	
			200				205					210				
ggc	tac	gtt	ctg	gaa	tac	cgc	ggc	gaa	gca	atc	cgt	aag	atg	tcc	atg	787
Gly	Tyr	Val	Leu	Glu	Tyr	Arg	Gly	Glu	Ala	Ile	Arg	Lys	Met	Ser	Met	
			215			220					225					
gat	gca	cgc	atg	acc	atg	tgc	aac	atg	tcc	atc	gaa	gct	ggc	gca	cgt	835
Asp	Ala	Arg	Met	Thr	Met	Cys	Asn	Met	Ser	Ile	Glu	Ala	Gly	Ala	Arg	
230					235					240					245	
gcc	ggc	atg	atc	gcc	cca	gac	caa	acc	acc	ttc	gac	tac	gtt	gaa	ggc	883
Ala	Gly	Met	Ile	Ala	Pro	Asp	Gln	Thr	Thr	Phe	Asp	Tyr	Val	Glu	Gly	
				250					255					260		
cgc	gaa	atg	gca	cca	aag	ggc	gcc	gac	tgg	gac	gaa	gca	gtt	gct	tac	931
Arg	Glu	Met	Ala	Pro	Lys	Gly	Ala	Asp	Trp	Asp	Glu	Ala	Val	Ala	Tyr	
			265				270						275			
tgg	aag	acc	ctg	cca	acc											

210	215	220
Gly Met Asn Leu Gly Phe Ile Tyr Arg Asn Gly Asp Gln Val Lys Leu		
225	230	235 240
Val Thr Pro Glu Leu Ser Gly Ser Leu Leu Pro Gly Ile Thr Arg Lys		
	245	250 255
Ser Leu Leu Gln Val Ala Arg Asp Leu Gly Tyr Glu Val Glu Glu Arg		
	260	265 270
Lys Ile Thr Thr Thr Glu Trp Glu Glu Asp Ala Lys Ser Gly Ala Met		
	275	280 285
Thr Glu Ala Phe Ala Cys Gly Thr Ala Ala Val Ile Thr Pro Val Gly		
	290	295 300
Thr Val Lys Ser Ala His Gly Thr Phe Glu Val Asn Asn Asn Glu Val		
	305	310 315 320
Gly Glu Ile Thr Met Lys Leu Arg Glu Thr Leu Thr Gly Ile Gln Gln		
	325	330 335
Gly Asn Val Glu Asp Gln Asn Gly Trp Leu Tyr Pro Leu Val Gly		
	340	345 350

&lt;210&gt; 265

&lt;211&gt; 1782

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1759)

&lt;223&gt; RXN01026

&lt;400&gt; 265

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				Met Thr Ser Pro Val	
				1 5	

gag aac agc acc tca act gag aag ctg acc ctg gca gag aag gtg tgg	163
Glu Asn Ser Thr Ser Thr Glu Lys Leu Thr Leu Ala Glu Lys Val Trp	
10 15 20	

cgc gac cat gtc gtg tcc aag gga gaa aac ggc gag ccc gac ctc ctc	211
Arg Asp His Val Val Ser Lys Gly Glu Asn Gly Glu Pro Asp Leu Leu	
25 30 35	

tac atc gac ctg cag ctg ctg cat gaa gtg acc tca cca cag gca ttt	259
Tyr Ile Asp Leu Gln Leu Leu His Glu Val Thr Ser Pro Gln Ala Phe	
40 45 50	

gac ggc ctg cgc atg acc ggc cgt aaa ctg cgc cac cca gaa ctg cac	307
Asp Gly Leu Arg Met Thr Gly Arg Lys Leu Arg His Pro Glu Leu His	
55 60 65	

ctg gcc acc gaa gac cac aac gtg cca acc gaa ggc atc aag act ggc	355
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gga gaa atc acg atg aag ctt cgt gaa acc ctc acc gga att cag caa  
1008

Gly Glu Ile Thr Met Lys Leu Arg Glu Thr Leu Thr Gly Ile Gln Gln  
325 330 335

gga aac gtt gaa gac caa aac gga tgg ctt tac cca ctg gtt ggc  
1053

Gly Asn Val Glu Asp Gln Asn Gly Trp Leu Tyr Pro Leu Val Gly  
340 345 350

taaatacaacc ggttttaaga ccc  
1076

<210> 264

<211> 351

<212> PRT

<213> Corynebacterium glutamicum

<400> 264

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Phe Thr Asp His Met Val Thr Ile Asp Trp Asn Glu Ser Glu Gly Trp  
20 25 30

His Asn Ala Gln Leu Val Pro Tyr Ala Pro Ile Pro Met Asp Pro Ala  
35 40 45

Thr Thr Val Phe His Tyr Gly Gln Ala Ile Phe Glu Gly Ile Lys Ala  
50 55 60

Tyr Arg His Ser Asp Glu Thr Ile Lys Thr Phe Arg Pro Asp Glu Asn  
65 70 75 80

Ala Glu Arg Met Gln Arg Ser Ala Ala Arg Met Ala Met Pro Gln Leu  
85 90 95

Pro Thr Glu Asp Phe Ile Lys Ala Leu Glu Leu Leu Val Asp Ala Asp  
100 105 110

Gln Asp Trp Val Pro Glu Tyr Gly Gly Glu Ala Ser Leu Tyr Leu Arg  
115 120 125

Pro Phe Met Ile Ser Thr Glu Ile Gly Leu Gly Val Ser Pro Ala Asp  
130 135 140

Ala Tyr Lys Phe Leu Val Ile Ala Ser Pro Val Gly Ala Tyr Phe Thr  
145 150 155 160

Gly Gly Ile Lys Pro Val Ser Val Trp Leu Ser Glu Asp Tyr Val Arg  
165 170 175

Ala Ala Pro Gly Gly Thr Gly Asp Ala Lys Phe Ala Gly Asn Tyr Ala  
180 185 190

Ala Ser Leu Leu Ala Gln Ser Gln Ala Ala Glu Lys Gly Cys Asp Gln  
195 200 205

Val Val Trp Leu Asp Ala Ile Glu His Lys Tyr Ile Glu Glu Met Gly

Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu Glu Gln Ala  
 170 175 180

ggt gcg ttt gcg gtt gtg ttg gag atg gtt cca gca gag gca gcg cgc 691  
 Gly Ala Phe Ala Val Val Leu Glu Met Val Pro Ala Glu Ala Ala Arg  
 185 190 195

gag gtt acc gag gat ctt tcc atc acc act atc gga atc ggt gcc ggc 739  
 Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile Gly Ala Gly  
 200 205 210

aat ggc aca gat ggg cag gtt ttg gtg tgg cag gat gcc ttc ggc ctc 787  
 Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala Phe Gly Leu  
 215 220 225

aac cgc ggc aag aag cca cgc ttc gtc cgc gag tac gcc acc ttg ggc 835  
 Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala Thr Leu Gly  
 230 235 240 245

gat tcc ttg cac gac gcc gcg cag gcc tac atc gcc gat atc cac gcg 883  
 Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp Ile His Ala  
 250 255 260

ggt acc ttc cca ggc gaa gcg gag tcc ttt taatgcaggt agcaaccaca 933  
 Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe  
 265 270

aag 936

&lt;210&gt; 280

&lt;211&gt; 271

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 280

Met Pro Met Ser Gly Ile Asp Ala Lys Lys Ile Arg Thr Arg His Phe  
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Arg Glu Ala Lys Val Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr  
 20 25 30

Asp Ala Leu Ser Ala Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu  
 35 40 45

Leu Val Gly Asp Ser Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr  
 50 55 60

Leu Ser Ile Thr Leu Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr  
 65 70 75 80

Ile Ala Thr Lys Arg Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr  
 85 90 95

Tyr Glu Val Ser Pro Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met  
 100 105 110

Arg Glu Thr Gly Ala Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile  
 115 120 125

Ala Gln Thr Ile Arg Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly

195

<210> 279  
 <211> 936  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(913)  
 <223> RXN01929

&lt;400&gt; 279

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                                         Met Pro Met Ser Gly
                                         1         5
att gat gca aag aaa atc cgc acc cgt cat ttc cgc gaa gct aaa gta 163
Ile Asp Ala Lys Lys Ile Arg Thr Arg His Phe Arg Glu Ala Lys Val
              10              15              20
aac ggc cag aaa gtt tcg gtt ctc acc agc tat gat gcg ctt tcg gcg 211
Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala Leu Ser Ala
              25              30              35
cgc att ttt gat gag gct ggc gtc gat atg ctc ctt gtt ggt gat tcc 259
Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val Gly Asp Ser
              40              45              50
gct gcc aac gtt gtg ctg ggt cgc gat acc acc ttg tcg atc acc ttg 307
Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser Ile Thr Leu
              55              60              65
gat gag atg att gtg ctg gcc aag gcg gtg acg atc gct acg aag cgt 355
Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala Thr Lys Arg
              70              75              80              85
gcg ctt gtg gtg gtt gat ctg ccg ttt ggt acc tat gag gtg agc cca 403
Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr Tyr Glu Val Ser Pro
              90              95              100
aat cag gcg gtg gag tcc gcg atc cgg gtc atg cgt gaa acg ggt gcg 451
Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met Arg Glu Thr Gly Ala
              105              110              115
gct gcg gtg aag atc gag ggt ggc gtg gag atc gcg cag acg att cga 499
Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile Ala Gln Thr Ile Arg
              120              125              130
cgc att gtt gat gct gga att ccg gtt gtc ggc cac atc ggg tac acc 547
Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly His Ile Gly Tyr Thr
              135              140              145
ccg cag tcc gag cat tcc ttg ggc ggc cac gtg gtt cag ggt cgt ggc 595
Pro Gln Ser Glu His Ser Leu Gly Gly His Val Val Gln Gly Arg Gly
              150              155              160              165
gcg agt tct gga aag ctc atc gcc gat gcc cgc gcg ttg gag cag gcg 643

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Leu Glu Leu Thr Val Asn Leu Glu Lys Gln Ile Val Thr Ala Gly Asp  
 135 140 145  
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 Val Val Ile Ser Phe Glu Val Asp Pro Tyr Ile Arg Trp Arg Leu Met  
 150 155 160 165  
 gaa ggc ctc gac gac gct ggc ctg acc ctg cgc aag ctc gat gaa att 643  
 Glu Gly Leu Asp Asp Ala Gly Leu Thr Leu Arg Lys Leu Asp Glu Ile  
 170 175 180  
 gaa gac tac gag gct aag cgc cct gcg ttt aag cca cgc act aac gct 691  
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 185 190 195  
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 <210> 278  
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 <212> PRT  
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 Ser Asn Val Asp Thr Asp Gln Ile Ile Pro Ala Val Tyr Leu Lys Arg  
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 Val Thr Arg Thr Gly Phe Glu Asp Gly Leu Phe Ser Asn Trp Arg Gln  
 35 40 45  
 Asn Asp Pro Asn Phe Val Leu Asn Thr Asp Thr Tyr Lys Asn Gly Ser  
 50 55 60  
 Val Leu Val Ala Gly Pro Asp Phe Gly Thr Gly Ser Ser Arg Glu His  
 65 70 75 80  
 Ala Val Trp Ala Leu Met Asp Tyr Gly Phe Arg Ala Val Phe Ser Ser  
 85 90 95  
 Arg Phe Ala Asp Ile Phe Arg Gly Asn Ser Gly Lys Ala Gly Met Leu  
 100 105 110  
 Thr Gly Ile Met Glu Gln Ser Asp Ile Glu Leu Leu Trp Lys Leu Met  
 115 120 125  
 Glu Gln Thr Pro Gly Leu Glu Leu Thr Val Asn Leu Glu Lys Gln Ile  
 130 135 140  
 Val Thr Ala Gly Asp Val Val Ile Ser Phe Glu Val Asp Pro Tyr Ile  
 145 150 155 160  
 Arg Trp Arg Leu Met Glu Gly Leu Asp Asp Ala Gly Leu Thr Leu Arg  
 165 170 175  
 Lys Leu Asp Glu Ile Glu Asp Tyr Glu Ala Lys Arg Pro Ala Phe Lys  
 180 185 190  
 Pro Arg Thr Asn Ala

Ala Phe Ser Gly Ser His Gln Asp Ala Val Asn Lys Gly Leu Asp Ala  
 370 375 380

Met Ala Ala Lys Val Gln Pro Gly Ala Ser Ser Thr Glu Val Ser Trp  
 385 390 395 400

Glu Gln Leu Arg Asp Thr Glu Trp Glu Val Pro  
 405 410

<210> 277

<211> 714

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(691)

<223> RXN02965

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 Met Glu Lys Phe Thr  
 1 5

acc tac acc ggc gtt ggc gtt cca ctg cag cga tcc aac gtg gac acc 163  
 Thr Tyr Thr Gly Val Gly Val Pro Leu Gln Arg Ser Asn Val Asp Thr  
 10 15 20

gac cag atc atc cca gcc gtc tac ctc aag cgc gtc acc cgg acc ggc 211  
 Asp Gln Ile Pro Ala Val Tyr Leu Lys Arg Val Thr Arg Thr Gly  
 25 30 35

ttc gaa gac gga ctg ttt tcc aac tgg cgc caa aac gac ccc aac ttt 259  
 Phe Glu Asp Gly Leu Phe Ser Asn Trp Arg Gln Asn Asp Pro Asn Phe  
 40 45 50

gtc ctc aac acc gac acc tac aag aac ggc tcc gtt ctc gta gca ggc 307  
 Val Leu Asn Thr Asp Thr Tyr Lys Asn Gly Ser Val Leu Val Ala Gly  
 55 60 65

cct gac ttt ggc acc ggc tcc tcc cgc gag cac gcc gtc tgg gca ctc 355  
 Pro Asp Phe Gly Thr Gly Ser Ser Arg Glu His Ala Val Trp Ala Leu  
 70 75 80 85

atg gac tac ggc ttc cgc gct gtc ttc tcc tca cga ttc gcc gac atc 403  
 Met Asp Tyr Gly Phe Arg Ala Val Phe Ser Ser Arg Phe Ala Asp Ile  
 90 95 100

ttc cgc ggc aac tcc gga aaa gcg ggc atg ctc acc ggc atc atg gaa 451  
 Phe Arg Gly Asn Ser Gly Lys Ala Gly Met Leu Thr Gly Ile Met Glu  
 105 110 115

cag tcc gac atc gaa ctt ctg tgg aag ctc atg gaa caa acc cca ggc 499  
 Gln Ser Asp Ile Glu Leu Leu Trp Lys Leu Met Glu Gln Thr Pro Gly  
 120 125 130

ctc gaa ctg acc gtg aac ctg gaa aag cag atc gtc acc gca ggc gac 547

35					40					45						
Glu	Asp	Ile	Ser	Leu	Pro	Asp	Arg	Thr	Trp	Pro	Asp	Lys	Lys	Ile	Thr	
50					55					60						
Val	Ala	Pro	Gln	Trp	Cys	Ala	Val	Asp	Leu	Arg	Asp	Gly	Asn	Gln	Ala	
65					70					75					80	
Leu	Ile	Asp	Pro	Met	Ser	Pro	Glu	Arg	Lys	Arg	Arg	Met	Phe	Glu	Leu	
					85					90					95	
Leu	Val	Gln	Met	Gly	Phe	Lys	Glu	Ile	Glu	Val	Gly	Phe	Pro	Ser	Ala	
					100					105					110	
Ser	Gln	Thr	Asp	Phe	Asp	Phe	Val	Arg	Glu	Ile	Ile	Glu	Lys	Gly	Met	
					115					120					125	
Ile	Pro	Asp	Asp	Val	Thr	Ile	Gln	Val	Leu	Val	Gln	Ala	Arg	Glu	His	
					130					135					140	
Leu	Ile	Arg	Arg	Thr	Phe	Glu	Ala	Cys	Glu	Gly	Ala	Lys	Asn	Val	Ile	
145					150					155					160	
Val	His	Phe	Tyr	Asn	Ser	Thr	Ser	Ile	Leu	Gln	Arg	Asn	Val	Val	Phe	
					165					170					175	
Arg	Met	Asp	Lys	Val	Gln	Val	Lys	Lys	Leu	Ala	Thr	Asp	Ala	Ala	Glu	
					180					185					190	
Leu	Ile	Lys	Thr	Ile	Ala	Gln	Asp	Tyr	Pro	Asp	Thr	Asn	Trp	Arg	Trp	
195					200					205						
Gln	Tyr	Ser	Pro	Glu	Ser	Phe	Thr	Gly	Thr	Glu	Val	Glu	Tyr	Ala	Lys	
210					215					220						
Glu	Val	Val	Asp	Ala	Val	Val	Glu	Val	Met	Asp	Pro	Thr	Pro	Glu	Asn	
225					230					235					240	
Pro	Met	Ile	Ile	Asn	Leu	Pro	Ser	Thr	Val	Glu	Met	Ile	Thr	Pro	Asn	
					245					250					255	
Val	Tyr	Ala	Asp	Ser	Ile	Glu	Trp	Met	His	Arg	Asn	Leu	Asn	Arg	Arg	
260					265					270						
Asp	Ser	Ile	Ile	Leu	Ser	Leu	His	Pro	His	Asn	Asp	Arg	Gly	Thr	Gly	
275					280					285						
Val	Gly	Ala	Ala	Glu	Leu	Gly	Tyr	Met	Ala	Gly	Ala	Asp	Arg	Ile	Glu	
290					295					300						
Gly	Cys	Leu	Phe	Gly	Asn	Gly	Glu	Arg	Thr	Gly	Asn	Val	Cys	Leu	Val	
305					310					315					320	
Thr	Leu	Ala	Leu	Asn	Met	Leu	Thr	Gln	Gly	Val	Asp	Pro	Gln	Leu	Asp	
					325					330					335	
Phe	Thr	Asp	Ile	Arg	Gln	Ile	Arg	Ser	Thr	Val	Glu	Tyr	Cys	Asn	Gln	
340					345					350						
Leu	Arg	Val	Pro	Glu	Arg	His	Pro	Tyr	Gly	Gly	Asp	Leu	Val	Phe	Thr	
355					360					365						

Ile Glu Trp Met His Arg Asn Leu Asn Arg Arg Asp Ser Ile Ile Leu  
 265 270 275

tcc ctg cac ccg cac aat gac cgt ggc acc ggc gtt ggc gca gct gag 979  
 Ser Leu His Pro His Asn Asp Arg Gly Thr Gly Val Gly Ala Ala Glu  
 280 285 290

ctg ggc tac atg gct ggc gct gac cgc atc gaa ggc tgc ctg ttc ggc  
 1027

Leu Gly Tyr Met Ala Gly Ala Asp Arg Ile Glu Gly Cys Leu Phe Gly  
 295 300 305

aac ggc gag cgc acc ggc aac gtc tgc ctg gtc acc ctg gca ctg aac  
 1075

Asn Gly Glu Arg Thr Gly Asn Val Cys Leu Val Thr Leu Ala Leu Asn  
 310 315 320 325

atg ctg acc cag ggc gtt gac cct cag ctg gac ttc acc gat ata cgc  
 1123

Met Leu Thr Gln Gly Val Asp Pro Gln Leu Asp Phe Thr Asp Ile Arg  
 330 335 340

cag atc cgc agc acc gtt gaa tac tgc aac cag ctg cgc gtt cct gag  
 1171

Gln Ile Arg Ser Thr Val Glu Tyr Cys Asn Gln Leu Arg Val Pro Glu  
 345 350 355

cgc cac cca tac ggc ggt gac ctg gtc ttc acc gct ttc tcc ggt tcc  
 1219

Arg His Pro Tyr Gly Gly Asp Leu Val Phe Thr Ala Phe Ser Gly Ser  
 360 365 370

cac cag gac gct gtg aac aag ggt ctg gac gcc atg gct gcc aag gtt  
 1267

His Gln Asp Ala Val Asn Lys Gly Leu Asp Ala Met Ala Ala Lys Val  
 375 380 385

cag cca ggt gct agc tcc act gaa gtt tct tgg gag cag ctg cgc gac  
 1315

Gln Pro Gly Ala Ser Ser Thr Glu Val Ser Trp Glu Gln Leu Arg Asp  
 390 395 400 405

acc gaa tgg gag gtt cct  
 1333

Thr Glu Trp Glu Val Pro  
 410

&lt;210&gt; 276

&lt;211&gt; 411

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 276

Met Ser Pro Asn Asp Ala Phe Ile Ser Ala Pro Ala Lys Ile Glu Thr  
 1 5 10 15

Pro Val Gly Pro Arg Asn Glu Gly Gln Pro Ala Trp Asn Lys Gln Arg  
 20 25 30

Gly Ser Ser Met Pro Val Asn Arg Tyr Met Pro Phe Glu Val Glu Val

aac gaa ggc cag cca gca tgg aat aag cag cgt ggc tcc tca atg cca	211
Asn Glu Gly Gln Pro Ala Trp Asn Lys Gln Arg Gly Ser Ser Met Pro	
25 30 35	
ggt aac cgc tac atg cct ttc gag gtt gag gta gaa gat att tct ctg	259
Val Asn Arg Tyr Met Pro Phe Glu Val Glu Val Glu Asp Ile Ser Leu	
40 45 50	
ccg gac cgc act tgg cca gat aaa aaa atc acc gtt gca cct cag tgg	307
Pro Asp Arg Thr Trp Pro Asp Lys Lys Ile Thr Val Ala Pro Gln Trp	
55 60 65	
tgt gct gtt gac ctg cgt gac ggc aac cag gct ctg att gat ccg atg	355
Cys Ala Val Asp Leu Arg Asp Gly Asn Gln Ala Leu Ile Asp Pro Met	
70 75 80 85	
tct cct gag cgt aag cgc cgc atg ttt gag ctg ctg gtt cag atg ggc	403
Ser Pro Glu Arg Lys Arg Arg Met Phe Glu Leu Leu Val Gln Met Gly	
90 95 100	
ttc aaa gaa atc gag gtc ggt ttc cct tca gct tcc cag act gat ttt	451
Phe Lys Glu Ile Glu Val Gly Phe Pro Ser Ala Ser Gln Thr Asp Phe	
105 110 115	
gat ttc gtt cgt gag atc atc gaa aag ggc atg atc cct gac gat gtc	499
Asp Phe Val Arg Glu Ile Ile Glu Lys Gly Met Ile Pro Asp Asp Val	
120 125 130	
acc att cag gtt ctg gtt cag gct cgt gag cac ctg att cgc cgt act	547
Thr Ile Gln Val Leu Val Gln Ala Arg Glu His Leu Ile Arg Arg Thr	
135 140 145	
ttt gaa gct tgc gaa ggc gca aaa aac gtt atc gtg cac ttc tac aac	595
Phe Glu Ala Cys Glu Gly Ala Lys Asn Val Ile Val His Phe Tyr Asn	
150 155 160 165	
tcc acc tcc atc ctg cag cgc aac gtg gtg ttc cgc atg gac aag gtg	643
Ser Thr Ser Ile Leu Gln Arg Asn Val Val Phe Arg Met Asp Lys Val	
170 175 180	
cag gtg aag aag ctg gct acc gat gcc gct gaa cta atc aag acc atc	691
Gln Val Lys Lys Leu Ala Thr Asp Ala Ala Glu Leu Ile Lys Thr Ile	
185 190 195	
gct cag gat tac cca gac acc aac tgg cgc tgg cag tac tcc cct gag	739
Ala Gln Asp Tyr Pro Asp Thr Asn Trp Arg Trp Gln Tyr Ser Pro Glu	
200 205 210	
tcc ttc acc ggc act gag gtt gag tac gcc aag gaa gtt gtg gac gca	787
Ser Phe Thr Gly Thr Glu Val Glu Tyr Ala Lys Glu Val Val Asp Ala	
215 220 225	
ggt gtt gag gtc atg gat cca act cct gag aac cca atg atc atc aac	835
Val Val Glu Val Met Asp Pro Thr Pro Glu Asn Pro Met Ile Ile Asn	
230 235 240 245	
ctg cct tcc acc gtt gag atg atc acc cct aac gtt tac gca gac tcc	883
Leu Pro Ser Thr Val Glu Met Ile Thr Pro Asn Val Tyr Ala Asp Ser	
250 255 260	
att gaa tgg atg cac cgc aat cta aac cgt cgt gat tcc att atc ctg	931

Val Tyr Ala Asp Ser Ile Glu Trp Met His Arg Asn Leu Asn Arg Arg  
 260 265 270  
 Asp Ser Ile Ile Leu Ser Leu His Pro His Asn Asp Arg Gly Thr Gly  
 275 280 285  
 Val Gly Ala Ala Glu Leu Gly Tyr Met Ala Gly Ala Asp Arg Ile Glu  
 290 295 300  
 Gly Cys Leu Phe Gly Asn Gly Glu Arg Thr Gly Asn Val Cys Leu Val  
 305 310 315 320  
 Thr Leu Ala Leu Asn Met Leu Thr Gln Gly Val Asp Pro Gln Leu Asp  
 325 330 335  
 Phe Thr Asp Ile Arg Gln Ile Arg Ser Thr Val Glu Tyr Cys Asn Gln  
 340 345 350  
 Leu Arg Val Pro Glu Arg His Pro Tyr Gly Gly Asp Leu Val Phe Thr  
 355 360 365  
 Ala Phe Ser Gly Ser His Gln Asp Ala Val Asn Lys Gly Leu Asp Ala  
 370 375 380  
 Met Ala Ala Lys Val Gln Pro Gly Ala Ser Ser Thr Glu Val Ser Trp  
 385 390 395 400  
 Glu Gln Leu Arg Asp Thr Arg Met Gly Gly Ser Leu Pro Ala Tyr Arg  
 405 410 415  
 Ser Lys Gly Cys Arg Ser Arg Leu Arg Gly Cys Tyr Pro Arg Glu Leu  
 420 425 430  
 Pro Val Arg Gln Gly Arg Arg Cys Leu His His Glu Asp Arg Ser Arg  
 435 440 445  
 Ser Ala Asp Pro Ser Leu His Ala Gly  
 450 455  
  
 <210> 275  
 <211> 1333  
 <212> DNA  
 <213> Corynebacterium glutamicum  
  
 <220>  
 <221> CDS  
 <222> (101)..(1333)  
 <223> FRXA00536  
  
 <400> 275  
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 tcgtggaccc acccaaaact ttttaagaag gttgaacaca atg tct cct aac gat 115  
 Met Ser Pro Asn Asp  
 1 5  
 gca ttc atc tcc gca cct gcc aag atc gaa acc cca gtt ggg cct cgc 163  
 Ala Phe Ile Ser Ala Pro Ala Lys Ile Glu Thr Pro Val Gly Pro Arg  
 10 15 20

ctc cat gca ggt tgagttctcc accgttggtcc aga

1494

Leu His Ala Gly

455

<210> 274

<211> 457

<212> PRT

<213> Corynebacterium glutamicum

<400> 274

Met Ser Pro Asn Asp Ala Phe Ile Ser Ala Pro Ala Lys Ile Glu Thr  
1 5 10 15

Pro Val Gly Pro Arg Asn Glu Gly Gln Pro Ala Trp Asn Lys Gln Arg  
20 25 30

Gly Ser Ser Met Pro Val Asn Arg Tyr Met Pro Phe Glu Val Glu Val  
35 40 45

Glu Asp Ile Ser Leu Pro Asp Arg Thr Trp Pro Asp Lys Lys Ile Thr  
50 55 60

Val Ala Pro Gln Trp Cys Ala Val Asp Leu Arg Asp Gly Asn Gln Ala  
65 70 75 80

Leu Ile Asp Pro Met Ser Pro Glu Arg Lys Arg Arg Met Phe Glu Leu  
85 90 95

Leu Val Gln Met Gly Phe Lys Glu Ile Glu Val Gly Phe Pro Ser Ala  
100 105 110

Ser Gln Thr Asp Phe Asp Phe Val Arg Glu Ile Ile Glu Lys Gly Met  
115 120 125

Ile Pro Asp Asp Val Thr Ile Gln Val Leu Val Gln Ala Arg Glu His  
130 135 140

Leu Ile Arg Arg Thr Phe Glu Ala Cys Glu Gly Ala Lys Asn Val Ile  
145 150 155 160

Val His Phe Tyr Asn Ser Thr Ser Ile Leu Gln Arg Asn Val Val Phe  
165 170 175

Arg Met Asp Lys Val Gln Val Lys Lys Leu Ala Thr Asp Ala Ala Glu  
180 185 190

Leu Ile Lys Thr Ile Ala Gln Asp Tyr Pro Asp Thr Asn Trp Arg Trp  
195 200 205

Gln Tyr Ser Pro Glu Ser Phe Thr Gly Thr Glu Val Glu Tyr Ala Lys  
210 215 220

Glu Val Val Asp Ala Val Val Glu Val Met Asp Pro Thr Pro Glu Asn  
225 230 235 240

Pro Met Ile Ile Asn Leu Pro Ser Thr Val Glu Met Ile Thr Pro Asn  
245 250 255

ctg cct tcc acc gtt gag atg atc acc cct aac gtt tac gca gac tcc 883  
 Leu Pro Ser Thr Val Glu Met Ile Thr Pro Asn Val Tyr Ala Asp Ser  
 250 255 260

att gaa tgg atg cac cgc aat cta aac cgt cgt gat tcc att atc ctg 931  
 Ile Glu Trp Met His Arg Asn Leu Asn Arg Arg Asp Ser Ile Ile Leu  
 265 270 275

tcc ctg cac ccg cac aat gac cgt ggc acc ggc gtt ggc gca gct gag 979  
 Ser Leu His Pro His Asn Asp Arg Gly Thr Gly Val Gly Ala Ala Glu  
 280 285 290

ctg ggc tac atg gct ggc gct gac cgc atc gaa ggc tgc ctg ttc ggc  
 1027  
 Leu Gly Tyr Met Ala Gly Ala Asp Arg Ile Glu Gly Cys Leu Phe Gly  
 295 300 305

aac ggc gag cgc acc ggc aac gtc tgc ctg gtc acc ctg gca ctg aac  
 1075  
 Asn Gly Glu Arg Thr Gly Asn Val Cys Leu Val Thr Leu Ala Leu Asn  
 310 315 320 325

atg ctg acc cag ggc gtt gac cct cag ctg gac ttc acc gat ata cgc  
 1123  
 Met Leu Thr Gln Gly Val Asp Pro Gln Leu Asp Phe Thr Asp Ile Arg  
 330 335 340

cag atc cgc agc acc gtt gaa tac tgc aac cag ctg cgc gtt cct gag  
 1171  
 Gln Ile Arg Ser Thr Val Glu Tyr Cys Asn Gln Leu Arg Val Pro Glu  
 345 350 355

cgc cac cca tac ggc ggt gac ctg gtc ttc acc gct ttc tcc ggt tcc  
 1219  
 Arg His Pro Tyr Gly Gly Asp Leu Val Phe Thr Ala Phe Ser Gly Ser  
 360 365 370

cac cag gac gct gtg aac aag ggt ctg gac gcc atg gct gcc aag gtt  
 1267  
 His Gln Asp Ala Val Asn Lys Gly Leu Asp Ala Met Ala Ala Lys Val  
 375 380 385

cag cca ggt gct agc tcc act gaa gtt tct tgg gag cag ctg cgc gac  
 1315  
 Gln Pro Gly Ala Ser Ser Thr Glu Val Ser Trp Glu Gln Leu Arg Asp  
 390 395 400 405

acc cga atg gga ggt tcc tta cct gcc tat cga tcc aaa gga tgt cgg  
 1363  
 Thr Arg Met Gly Gly Ser Leu Pro Ala Tyr Arg Ser Lys Gly Cys Arg  
 410 415 420

tcg cga cta cga ggc tgt tat ccg cgt gaa ctc cca gtc cgg caa ggg  
 1411  
 Ser Arg Leu Arg Gly Cys Tyr Pro Arg Glu Leu Pro Val Arg Gln Gly  
 425 430 435

cgg cgt tgc tta cat cat gaa gac cga tca cgg tct gca gat ccc tcg  
 1459  
 Arg Arg Cys Leu His His Glu Asp Arg Ser Arg Ser Ala Asp Pro Ser  
 440 445 450



gca ttc atc tcc gca cct gcc aag atc gaa acc cca gtt ggg cct cgc	163
Ala Phe Ile Ser Ala Pro Ala Lys Ile Glu Thr Pro Val Gly Pro Arg	
10 15 20	
aac gaa ggc cag cca gca tgg aat aag cag cgt ggc tcc tca atg cca	211
Asn Glu Gly Gln Pro Ala Trp Asn Lys Gln Arg Gly Ser Ser Met Pro	
25 30 35	
gtt aac cgc tac atg cct ttc gag gtt gag gta gaa gat att tct ctg	259
Val Asn Arg Tyr Met Pro Phe Glu Val Glu Val Glu Asp Ile Ser Leu	
40 45 50	
ccg gac cgc act tgg cca gat aaa aaa atc acc gtt gca cct cag tgg	307
Pro Asp Arg Thr Trp Pro Asp Lys Lys Ile Thr Val Ala Pro Gln Trp	
55 60 65	
tgt gct gtt gac ctg cgt gac ggc aac cag gct ctg att gat ccg atg	355
Cys Ala Val Asp Leu Arg Asp Gly Asn Gln Ala Leu Ile Asp Pro Met	
70 75 80 85	
tct cct gag cgt aag cgc cgc atg ttt gag ctg ctg gtt cag atg ggc	403
Ser Pro Glu Arg Lys Arg Arg Met Phe Glu Leu Leu Val Gln Met Gly	
90 95 100	
ttc aaa gaa atc gag gtc ggt ttc cct tca gct tcc cag act gat ttt	451
Phe Lys Glu Ile Glu Val Gly Phe Pro Ser Ala Ser Gln Thr Asp Phe	
105 110 115	
gat ttc gtt cgt gag atc atc gaa aag ggc atg atc cct gac gat gtc	499
Asp Phe Val Arg Glu Ile Ile Glu Lys Gly Met Ile Pro Asp Asp Val	
120 125 130	
acc att cag gtt ctg gtt cag gct cgt gag cac ctg att cgc cgt act	547
Thr Ile Gln Val Leu Val Gln Ala Arg Glu His Leu Ile Arg Arg Thr	
135 140 145	
ttt gaa gct tgc gaa ggc gca aaa aac gtt atc gtg cac ttc tac aac	595
Phe Glu Ala Cys Glu Gly Ala Lys Asn Val Ile Val His Phe Tyr Asn	
150 155 160 165	
tcc acc tcc atc ctg cag cgc aac gtg gtg ttc cgc atg gac aag gtg	643
Ser Thr Ser Ile Leu Gln Arg Asn Val Val Phe Arg Met Asp Lys Val	
170 175 180	
cag gtg aag aag ctg gct acc gat gcc gct gaa cta atc aag acc atc	691
Gln Val Lys Lys Leu Ala Thr Asp Ala Ala Glu Leu Ile Lys Thr Ile	
185 190 195	
gct cag gat tac cca gac acc aac tgg cgc tgg cag tac tcc cct gag	739
Ala Gln Asp Tyr Pro Asp Thr Asn Trp Arg Trp Gln Tyr Ser Pro Glu	
200 205 210	
tcc ttc acc ggc act gag gtt gag tac gcc aag gaa gtt gtg gac gca	787
Ser Phe Thr Gly Thr Glu Val Glu Tyr Ala Lys Glu Val Val Asp Ala	
215 220 225	
gtt gtt gag gtc atg gat cca act cct gag aac cca atg atc atc aac	835
Val Val Glu Val Met Asp Pro Thr Pro Glu Asn Pro Met Ile Ile Asn	
230 235 240 245	

ggc gca cgc cgt tac ctc aaa aat ggc gag ctg ctc acc gac gag gat 259  
 Gly Ala Arg Arg Tyr Leu Lys Asn Gly Glu Leu Leu Thr Asp Glu Asp  
           40                          45                          50

ctg gca tcc ctg cgc gag cat gac gcg atc ctt ctt ggc gct atc ggt 307  
 Leu Ala Ser Leu Arg Glu His Asp Ala Ile Leu Leu Gly Ala Ile Gly  
           55                          60                          65

gca cca ggt tcc gtc cct cca gga att ctc gag cgt ggt ttg ctg ctg 355  
 Ala Pro Gly Ser Val Pro Pro Gly Ile Leu Glu Arg Gly Leu Leu Leu  
           70                          75                          80                          85

aag atg cga ttc gca ctg gat cac cac gtg aac ctg cgc cca tcc aag 403  
 Lys Met Arg Phe Ala Leu Asp His His Val Asn Leu Arg Pro Ser Lys  
                           90                          95                          100

<210> 272

<211> 101

<212> PRT

<213> Corynebacterium glutamicum

<400> 272

Met Lys Leu Ala Val Ile Gly Gly Asp Gly Ile Gly Pro Glu Val Thr  
           1                          5                          10                          15

Ala Glu Ala Leu Lys Val Leu Asn Ala Val Arg Asp Asp Ile Glu Thr  
                           20                          25                          30

Thr Asp Tyr Asp Leu Gly Ala Arg Arg Tyr Leu Lys Asn Gly Glu Leu  
           35                          40                          45

Leu Thr Asp Glu Asp Leu Ala Ser Leu Arg Glu His Asp Ala Ile Leu  
           50                          55                          60

Leu Gly Ala Ile Gly Ala Pro Gly Ser Val Pro Pro Gly Ile Leu Glu  
           65                          70                          75                          80

Arg Gly Leu Leu Leu Lys Met Arg Phe Ala Leu Asp His His Val Asn  
                           85                          90                          95

Leu Arg Pro Ser Lys  
                           100

<210> 273

<211> 1494

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1471)

<223> RXN00536

<400> 273

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tcgtggaccc acccaaaact ttttaagaag gttgaacaca atg tct cct aac gat 115  
   Met Ser Pro Asn Asp  
   1                          5

<210> 271  
<211> 403  
<212> DNA  
<213> *Corynebacterium glutamicum*

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<400> 271
gccctgcatg atggggtagt gggggttgtt gggcaggta c gagctgtgat caatcagcta 60

cactagtga gtccatatag tgagaaggga atcccacaac atg aaa ctt gct gtt      115
                                         Met Lys Leu Ala Val
                                           1                      5

att ggt gga gat ggt atc ggc cca gag gtt act gca gaa gcc ct c aa g      163
Ile Gly Gly Asp Gly Ile Gly Pro Glu Val Thr Ala Glu Ala Leu Lys
                        10                          15                  20

gtt cta aac gct gtc cgc gac gac atc gag acc acc gat tat gac ctt      211
Val Leu Asn Ala Val Arg Asp Asp Ile Glu Thr Thr Asp Tyr Asp Leu
                    25                30              35
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gca ggc cag gga atc gca gac cca acg gca gca atc cta tcc gct gcg 979  
 Ala Gly Gln Gly Ile Ala Asp Pro Thr Ala Ala Ile Leu Ser Ala Ala  
           280                                  285                                  290

atg ctg ctg cgt cac tta ggt gat gaa gac aac gca gta cgt att gaa  
 1027

Met Leu Leu Arg His Leu Gly Asp Glu Asp Asn Ala Val Arg Ile Glu  
           295                                  300                                  305

aca gcc atc gca gct gat gtg gct ggc cga gat aac tct cag ccg att  
 1075

Thr Ala Ile Ala Ala Asp Val Ala Gly Arg Asp Asn Ser Gln Pro Ile  
           310                                  315                                  320                                  325

tct acc act gag gtg gga gac cgc atc gtc aag gcg ctg caa agc  
 1120

Ser Thr Thr Glu Val Gly Asp Arg Ile Val Lys Ala Leu Gln Ser  
                                   330                                  335                                  340

taaatttcaa cgccgacccc ctt  
 1143

<210> 270

<211> 340

<212> PRT

<213> Corynebacterium glutamicum

<400> 270

Met Lys Leu Ala Val Ile Gly Gly Asp Gly Ile Gly Pro Glu Val Thr  
   1                                  5                                  10                                  15

Ala Glu Ala Leu Lys Val Leu Asn Ala Val Arg Asp Asp Ile Glu Thr  
           20                                  25                                  30

Thr Asp Tyr Asp Leu Gly Ala Arg Arg Tyr Leu Lys Asn Gly Glu Leu  
           35                                  40                                  45

Leu Thr Asp Glu Asp Leu Ala Ser Leu Arg Glu His Asp Ala Ile Leu  
           50                                  55                                  60

Leu Gly Ala Ile Gly Ala Pro Gly Ser Val Pro Pro Gly Ile Leu Glu  
           65                                  70                                  75                                  80

Arg Gly Leu Leu Leu Lys Met Arg Phe Ala Leu Asp His His Val Asn  
                                   85                                  90                                  95

Leu Arg Pro Ser Lys Leu Tyr Asp Gly Val Glu Ser Pro Leu Arg Asn  
           100                                  105                                  110

Pro Gly Lys Ile Asp Phe Val Val Val Arg Glu Gly Thr Glu Gly Ala  
           115                                  120                                  125

Tyr Thr Gly Asn Gly Gly Ala Ile Arg Val Gly Thr Pro His Glu Ile  
           130                                  135                                  140

Ala Asn Glu Thr Ser Val Asn Thr Arg Tyr Gly Ala Glu Arg Val Ile  
           145                                  150                                  155                                  160

Arg Tyr Ala Phe Glu Leu Ala Gln Ser Arg Arg Lys Lys Leu Thr Leu

225		230		235		240
Asp Leu Lys Gly Val Ile Ala Gly Asp Gly Gly Lys Val Gly Thr Gly						
	245		250		255	
Gly Met Ala Ser Lys Val Ser Ala Ala Arg Leu Ala Ser Arg Ser Gly						
	260		265		270	
Val Pro Val Leu Leu Thr Ser Ala Ala Asn Ile Gly Pro Ala Leu Glu						
	275		280		285	
Asp Ala Gln Val Gly Thr Val Phe His Pro Lys Asp Asn Arg Leu Ser						
	290		295		300	
Ala Trp Lys Phe Trp Ala Leu Tyr Ala Ala Asp Thr Ala Gly Lys Ile						
	305		310		315	320
Arg Leu Asp Asp Gly Ala Val Glu Ala Val Thr Ser Gly Gly Lys Ser						
	325		330		335	
Leu Leu Ala Val Gly Ile Thr Glu Ile Ile Gly Asp Phe Gln Gln Gly						
	340		345		350	
Glu Ile Val Glu Ile Leu Gly Pro Ala Gly Gln Ile Ile Gly Arg Gly						
	355		360		365	
Glu Val Ser Tyr Asp Ser Asp Thr Leu Gln Ser Met Val Gly Met Gln						
	370		375		380	
Thr Gln Asp Leu Pro Asp Gly Met Gln Arg Pro Val Val His Ala Asp						
	385		390		395	400
Tyr Leu Ser Asn Tyr Ala Ser Arg Ala						
	405					

&lt;210&gt; 291

&lt;211&gt; 1419

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1396)

&lt;223&gt; RXN02382

&lt;400&gt; 291

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				Met Ser Ser Thr Thr	
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cta act gat gac caa att cgc gac aat gag cgg acc gaa gtt cta gct	163
Leu Thr Asp Asp Gln Ile Arg Asp Asn Glu Arg Thr Glu Val Leu Ala	
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Lys Ala Thr Ala Ala Lys Asn Ile Val Pro Asp Ile Ala Val Leu Gly	
	25 30 35

gat ggc atg cag cgc ccg gta gtg cat gca gat tat ctg tcc aac tac  
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 <213> Corynebacterium glutamicum

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 Lys Arg Val Val Val Lys Ile Gly Ser Ser Ser Leu Thr Asn Asp Glu  
 50 55 60  
 Asp Gly His Thr Val Asp Pro Asn Arg Ile Asn Thr Ile Val Asn Ala  
 65 70 75 80  
 Leu Gln Ala Arg Met Glu Ala Gly Ser Asp Leu Ile Val Val Ser Ser  
 85 90 95  
 Gly Ala Val Ala Ala Gly Met Ala Pro Leu Gly Leu Ser Thr Arg Pro  
 100 105 110  
 Thr Glu Leu Ala Val Lys Gln Ala Ala Ala Val Gly Gln Val His  
 115 120 125  
 Leu Met His Gln Trp Gly Arg Ser Phe Ala Arg Tyr Gly Arg Pro Ile  
 130 135 140  
 Gly Gln Val Leu Leu Thr Ala Ala Asp Ala Gly Lys Arg Asp Arg Ala  
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 Arg Asn Ala Gln Arg Thr Ile Asp Lys Leu Arg Ile Leu Gly Ala Val  
 165 170 175  
 Pro Ile Val Asn Glu Asn Asp Thr Val Ala Thr Thr Gly Val Asn Phe  
 180 185 190  
 Gly Asp Asn Asp Arg Leu Ala Ala Ile Val Ala His Leu Val Ser Ala  
 195 200 205  
 Asp Ala Leu Val Leu Leu Ser Asp Val Asp Gly Leu Phe Asp Lys Asn  
 210 215 220  
 Pro Thr Asp Pro Thr Ala Lys Phe Ile Ser Glu Val Arg Asp Gly Asn

acc atc gac aag ctg cgc att ttg ggc gcg gtt cct atc gtc aat gaa 643  
 Thr Ile Asp Lys Leu Arg Ile Leu Gly Ala Val Pro Ile Val Asn Glu  
 170 175 180

aat gac acc gtg gca acc acc ggt gtg aat ttt ggt gac aac gac cga 691  
 Asn Asp Thr Val Ala Thr Thr Gly Val Asn Phe Gly Asp Asn Asp Arg  
 185 190 195

ctt gct gca att gtg gcg cac ctg gtg tgc gct gat gct ttg gtg ctg 739  
 Leu Ala Ala Ile Val Ala His Leu Val Ser Ala Asp Ala Leu Val Leu  
 200 205 210

ctc agt gac gtg gat gga ctt ttt gat aaa aac cct act gat ccc acc 787  
 Leu Ser Asp Val Asp Gly Leu Phe Asp Lys Asn Pro Thr Asp Pro Thr  
 215 220 225

gcg aag ttt att tcc gag gtt cgt gac ggc aat gat ttg aaa ggt gtc 835  
 Ala Lys Phe Ile Ser Glu Val Arg Asp Gly Asn Asp Leu Lys Gly Val  
 230 235 240 245

att gcc ggc gac ggc gga aaa gtg ggc acc ggt ggc atg gca tca aag 883  
 Ile Ala Gly Asp Gly Gly Lys Val Gly Thr Gly Gly Met Ala Ser Lys  
 250 255 260

gtg tct gct gca cgt ttg gct tcc cga agt ggc gtg cct gtg ctg ttg 931  
 Val Ser Ala Ala Arg Leu Ala Ser Arg Ser Gly Val Pro Val Leu Leu  
 265 270 275

acc tct gcg gca aac att ggc cca gca ctg gaa gac gcc cag gtg ggc 979  
 Thr Ser Ala Ala Asn Ile Gly Pro Ala Leu Glu Asp Ala Gln Val Gly  
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act gta ttc cac ccc aag gac aac cgc ctc tcc gcg tgg aag ttc tgg  
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 Thr Val Phe His Pro Lys Asp Asn Arg Leu Ser Ala Trp Lys Phe Trp  
 295 300 305

gct ttg tat gcc gca gat act gca gga aag atc cga ctc gat gac ggc  
 1075  
 Ala Leu Tyr Ala Ala Asp Thr Ala Gly Lys Ile Arg Leu Asp Asp Gly  
 310 315 320 325

gcg gtg gaa gca gtg acc tcc ggt ggt aaa tct ttg ctg gct gtg ggc  
 1123  
 Ala Val Glu Ala Val Thr Ser Gly Gly Lys Ser Leu Leu Ala Val Gly  
 330 335 340

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 1171  
 Ile Thr Glu Ile Ile Gly Asp Phe Gln Gln Gly Glu Ile Val Glu Ile  
 345 350 355

ttg gga cct gcc ggc caa atc atc ggg cga ggc gag gtg tcc tac gat  
 1219  
 Leu Gly Pro Ala Gly Gln Ile Ile Gly Arg Gly Glu Val Ser Tyr Asp  
 360 365 370

tct gat acc ttg caa tca atg gtt ggt atg caa acg cag gac ctt cca  
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Gly Lys Gly Val Pro Cys Leu Ile  
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Met Ala Pro Val Thr  
1 5  
ggg ctt cct gtc acc ccc tac agc cag gaa gca agc atc ggt gcg agc 163  
Gly Leu Pro Val Thr Pro Tyr Ser Gln Glu Ala Ser Ile Gly Ala Ser  
10 15 20  
ttc ccg gca gtg gat ccg gac acc aaa gac agc gcc gca tac gga cat 211  
Phe Pro Ala Val Asp Pro Asp Thr Lys Asp Ser Ala Ala Tyr Gly His  
25 30 35  
gaa tcc gga atg cgt gag cgc atc tcc aac gct aag cga gtg gtg gtg 259  
Glu Ser Gly Met Arg Glu Arg Ile Ser Asn Ala Lys Arg Val Val Val  
40 45 50  
aaa att ggt tcg tcc tca ttg act aac gat gag gac gga cac acc gtc 307  
Lys Ile Gly Ser Ser Ser Leu Thr Asn Asp Glu Asp Gly His Thr Val  
55 60 65  
gat ccc aac cgc atc aac act att gtc aat gcc ttg caa gca cgc atg 355  
Asp Pro Asn Arg Ile Asn Thr Ile Val Asn Ala Leu Gln Ala Arg Met  
70 75 80 85  
gaa gct ggc tcg gac ctc atc gtt gtg tcc tct ggc gca gtg gcc gcg 403  
Glu Ala Gly Ser Asp Leu Ile Val Val Ser Ser Gly Ala Val Ala Ala  
90 95 100  
gga atg gcc ccg ctt gga ttg agc acc cgg ccc acg gaa ttg gca gtc 451  
Gly Met Ala Pro Leu Gly Leu Ser Thr Arg Pro Thr Glu Leu Ala Val  
105 110 115  
aag cag gct gca gca gca gtg ggg caa gtt cac ctc atg cac cag tgg 499  
Lys Gln Ala Ala Ala Ala Val Gly Gln Val His Leu Met His Gln Trp  
120 125 130  
gga cgt tct ttt gcc cgg tat ggt cgc ccc atc ggc cag gtg ctt ctt 547  
Gly Arg Ser Phe Ala Arg Tyr Gly Arg Pro Ile Gly Gln Val Leu Leu  
135 140 145  
acc gca gct gat gca gga aag cgt gat cgt gcg agg aat gcg cag cgt 595  
Thr Ala Ala Asp Ala Gly Lys Arg Asp Arg Ala Arg Asn Ala Gln Arg  
150 155 160 165



Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu Val Lys Thr Thr Ala  
55 60 65

gag gct gca gct tgg gct gac gtc atc atg ctc ctg gct cca gac acc 355  
Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu Leu Ala Pro Asp Thr  
70 75 80 85

tcc cag gca gaa atc ttc acc aac gac atc gag cca aac ctg aac gca 403  
Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu Pro Asn Leu Asn Ala  
90 95 100

ggc gac gca ctg ctg ttc ggc cac ggc ctg aac att cac ttc gac ctg 451  
Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn Ile His Phe Asp Leu  
105 110 115

atc aag cca gct gac gac atc atc gtt ggc atg gtt gcg cca aag ggc 499  
Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met Val Ala Pro Lys Gly  
120 125 130

cca ggc cac ttg gtt cgc cgt cag ttc gtt gat ggc aag ggt gtt cct 547  
Pro Gly His Leu Val Arg Arg Gln Phe Val Asp Gly Lys Gly Val Pro  
135 140 145

tgc ctc atc 556  
Cys Leu Ile  
150

&lt;210&gt; 288

&lt;211&gt; 152

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 288

Met Ala Ile Glu Leu Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile  
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Gln Gly Arg Lys Val Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala  
20 25 30

His Ser Gln Asn Leu Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu  
35 40 45

Arg Glu Gly Ser Lys Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu  
50 55 60

Val Lys Thr Thr Ala Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu  
65 70 75 80

Leu Ala Pro Asp Thr Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu  
85 90 95

Pro Asn Leu Asn Ala Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn  
100 105 110

Ile His Phe Asp Leu Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met  
115 120 125

Val Ala Pro Lys Gly Pro Gly His Leu Val Arg Arg Gln Phe Val Asp  
130 135 140

Leu Phe Gly Glu Gln Ala Val Leu Cys Gly Gly Thr Glu Glu Leu Val  
 195 200 205  
 Lys Val Gly Phe Glu Val Leu Thr Glu Ala Gly Tyr Glu Pro Glu Met  
 210 215 220  
 Ala Tyr Phe Glu Val Leu His Glu Leu Lys Leu Ile Val Asp Leu Met  
 225 230 235 240  
 Phe Glu Gly Gly Ile Ser Asn Met Asn Tyr Ser Val Ser Asp Thr Ala  
 245 250 255  
 Glu Phe Gly Gly Tyr Leu Ser Gly Pro Arg Val Ile Asp Ala Asp Thr  
 260 265 270  
 Lys Ser Arg Met Lys Asp Ile Leu Thr Asp Ile Gln Asp Gly Thr Phe  
 275 280 285  
 Thr Lys Arg Leu Ile Ala Asn Val Glu Asn Gly Asn Thr Glu Leu Glu  
 290 295 300  
 Gly Leu Arg Ala Ser Tyr Asn Asn His Pro Ile Glu Glu Thr Gly Ala  
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 Lys Leu Arg Asp Leu Met Ser Trp Val Lys Val Asp Ala Arg Ala Glu  
 325 330 335  
 Thr Ala

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 <223> FRXA01145

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 Met Ala Ile Glu Leu  
 1 5  
 ctt tat gat gct gac gct gac ctc tcc ttg atc cag ggc cgt aag gtt 163  
 Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile Gln Gly Arg Lys Val  
 10 15 20  
 gcc atc gtt ggc tac ggc tcc cag ggc cac gca cac tcc cag aac ctc 211  
 Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala His Ser Gln Asn Leu  
 25 30 35  
 cgc gat tct ggc gtt gag gtt gtc att ggt ctg cgc gag ggc tcc aag 259  
 Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu Arg Glu Gly Ser Lys  
 40 45 50  
 tcc gca gag aag gca aag gaa gca ggc ttc gag gtc aag acc acc gct 307

gca aac gtt gag aac ggc aac acc gag ctt gag ggc ctt cgt gct tcc  
1027

Ala Asn Val Glu Asn Gly Asn Thr Glu Leu Glu Gly Leu Arg Ala Ser  
295 300 305

tac aac aac cac cca atc gag gag acc ggc gct aag ctc cgc gac ctc  
1075

Tyr Asn Asn His Pro Ile Glu Glu Thr Gly Ala Lys Leu Arg Asp Leu  
310 315 320 325

atg agc tgg gtc aag gtt gac gct cgc gca gaa acc gct taagtctcac  
1124

Met Ser Trp Val Lys Val Asp Ala Arg Ala Glu Thr Ala  
330 335

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1137

<210> 286

<211> 338

<212> PRT

<213> Corynebacterium glutamicum

<400> 286

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Gln Gly Arg Lys Val Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala  
20 25 30

His Ser Gln Asn Leu Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu  
35 40 45

Arg Glu Gly Ser Lys Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu  
50 55 60

Val Lys Thr Thr Ala Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu  
65 70 75 80

Leu Ala Pro Asp Thr Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu  
85 90 95

Pro Asn Leu Asn Ala Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn  
100 105 110

Ile His Phe Asp Leu Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met  
115 120 125

Val Ala Pro Lys Gly Pro Gly His Leu Val Arg Arg Gln Phe Val Asp  
130 135 140

Gly Lys Gly Val Pro Cys Leu Ile Ala Val Asp Gln Asp Pro Thr Gly  
145 150 155 160

Thr Ala Gln Ala Leu Thr Leu Ser Tyr Ala Ala Ala Ile Gly Gly Ala  
165 170 175

Arg Ala Gly Val Ile Pro Thr Thr Phe Glu Ala Glu Thr Val Thr Asp  
180 185 190

tcc gca gag aag gca aag gaa gca ggc ttc gag gtc aag acc acc gct Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu Val Lys Thr Thr Ala 55 60 65	307
gag gct gca gct tgg gct gac gtc atc atg ctc ctg gct cca gac acc Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu Leu Ala Pro Asp Thr 70 75 80 85	355
tcc cag gca gaa atc ttc acc aac gac atc gag cca aac ctg aac gca Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu Pro Asn Leu Asn Ala 90 95 100	403
ggc gac gca ctg ctg ttc ggc cac ggc ctg aac att cac ttc gac ctg Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn Ile His Phe Asp Leu 105 110 115	451
atc aag cca gct gac gac atc atc gtt ggc atg gtt gcg cca aag ggc Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met Val Ala Pro Lys Gly 120 125 130	499
cca ggc cac ttg gtt cgc cgt cag ttc gtt gat ggc aag ggt gtt cct Pro Gly His Leu Val Arg Arg Gln Phe Val Asp Gly Lys Gly Val Pro 135 140 145	547
tgc ctc atc gca gtc gac cag gac cca acc gga acc gca cag gct ctg Cys Leu Ile Ala Val Asp Gln Asp Pro Thr Gly Thr Ala Gln Ala Leu 150 155 160 165	595
acc ctg tcc tac gca gca gca atc ggt ggc gca cgc gca ggc gtt atc Thr Leu Ser Tyr Ala Ala Ala Ile Gly Gly Ala Arg Ala Gly Val Ile 170 175 180	643
cca acc acc ttc gaa gct gag acc gtc acc gac ctc ttc ggc gag cag Pro Thr Thr Phe Glu Ala Glu Thr Val Thr Asp Leu Phe Gly Glu Gln 185 190 195	691
gct gtt ctc tgc ggt ggc acc gag gaa ctg gtc aag gtt ggc ttc gag Ala Val Leu Cys Gly Gly Thr Glu Glu Leu Val Lys Val Gly Phe Glu 200 205 210	739
gtt ctc acc gaa gct ggc tac gag cca gag atg gca tac ttc gag gtt Val Leu Thr Glu Ala Gly Tyr Glu Pro Glu Met Ala Tyr Phe Glu Val 215 220 225	787
ctt cac gag ctc aag ctc atc gtt gac ctc atg ttc gaa ggt ggc atc Leu His Glu Leu Lys Leu Ile Val Asp Leu Met Phe Glu Gly Gly Ile 230 235 240 245	835
agc aac atg aac tac tct gtt tct gac acc gct gag ttc ggt ggc tac Ser Asn Met Asn Tyr Ser Val Ser Asp Thr Ala Glu Phe Gly Gly Tyr 250 255 260	883
ctc tcc ggc cca cgc gtc atc gat gca gac acc aag tcc cgc atg aag Leu Ser Gly Pro Arg Val Ile Asp Ala Asp Thr Lys Ser Arg Met Lys 265 270 275	931
gac atc ctg acc gat atc cag gac ggc acc ttc acc aag cgc ctc atc Asp Ile Leu Thr Asp Ile Gln Asp Gly Thr Phe Thr Lys Arg Leu Ile 280 285 290	979

145	150	155	160
Ser Val Ile Met Ser Leu Pro Met Ala Phe Val Val Ala Thr Leu Ala	165	170	175
Val Arg Asp Ile Glu Gly Lys Ser Gly Glu Ile Ala Ser Pro Arg Ala	180	185	190
Val Leu Leu Gly Asn Ile Ser Phe Ala Phe Tyr Met Val Gln Phe Pro	195	200	205
Val Met Val Phe Val Gln Arg Tyr Phe Ile Ala Gly Lys Glu Tyr Gly	210	215	220
Phe Leu Gly Trp Ala Phe Tyr Ala Val Val Cys Phe Ile Val Ser Val	225	230	235
Ile Leu Ala Trp Val Leu Phe Thr Phe Val Asp Asp Pro Leu Met Lys	245	250	255
Ala Thr Ala Arg Lys Lys Gly Ser Arg Arg Leu Lys Gln Ser Asn Ile	260	265	270
Leu Val Arg Asp Leu Lys Val Leu Phe Gly Lys Ser Pro Glu Lys Pro	275	280	285
Leu Lys Val Glu Thr Arg Ala Glu Asn Leu Thr Glu Asn Ser Glu Ala	290	295	300
Pro Ala Lys Val Ala Thr Gly Ile Lys Ser	305	310	

&lt;210&gt; 285

&lt;211&gt; 1137

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1114)

&lt;223&gt; RXS01145

&lt;400&gt; 285

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taatgtagtt gtctgccc aa gcgagttaaa ctcccacgat ttacagtggg gggcagacat 60

cttttcacca aaatttttac gaaagggcgag attttctccc atg gct att gaa ctg 115
                               Met Ala Ile Glu Leu
                               1             5

ctt tat gat gct gac gct gac ctc tcc ttg atc cag ggc cgt aag gtt 163
Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile Gln Gly Arg Lys Val
                10             15             20

gcc atc gtt ggc tac ggc tcc cag ggc cac gca cac tcc cag aac ctc 211
Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala His Ser Gln Asn Leu
                25             30             35

cgc gat tct ggc gtt gag gtt gtc att ggt ctg cgc gag ggc tcc aag 259
Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu Arg Glu Gly Ser Lys
                40             45             50

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ttc tat gca gtg gtg tgt ttc atc gtg tcg gtc att ctc gcg tgg gtg 835  
 Phe Tyr Ala Val Val Cys Phe Ile Val Ser Val Ile Leu Ala Trp Val  
 230 235 240 245

ctg ttt acc ttc gtt gat gat cct ttg atg aag gcc acg gcg cgc aag 883  
 Leu Phe Thr Phe Val Asp Asp Pro Leu Met Lys Ala Thr Ala Arg Lys  
 250 255 260

aag ggg agt agg cgc ttg aag cag tcc aat att ttg gtc cgt gac ctg 931  
 Lys Gly Ser Arg Arg Leu Lys Gln Ser Asn Ile Leu Val Arg Asp Leu  
 265 270 275

aaa gtt ctc ttc ggc aaa agc ccc gaa aag ccg tta aaa gtt gag act 979  
 Lys Val Leu Phe Gly Lys Ser Pro Glu Lys Pro Leu Lys Val Glu Thr  
 280 285 290

cgc gct gag aat ctc aca gaa aac tcc gaa gct ccc gct aag gta gct  
 1027  
 Arg Ala Glu Asn Leu Thr Glu Asn Ser Glu Ala Pro Ala Lys Val Ala  
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 Thr Gly Ile Lys Ser  
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<211> 314

<212> PRT

<213> Corynebacterium glutamicum

<400> 284

Val Thr Leu Gly Gly Leu Asn Val Pro Ser Trp Ser Leu Gly Ala Glu  
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Val Lys Gly Val Gly Asn Trp Trp Ala Phe Gly Ile Thr Phe Ala Val  
 35 40 45

Ser Leu Ala Leu Ile Thr Val Ile His Phe Tyr Ala Asp Gly Pro Lys  
 50 55 60

Gly Ile Glu Asn Phe Phe Val Pro Arg Leu Trp Asp Thr Asn Val Ser  
 65 70 75 80

Pro Val Ala Glu Val His Ala Asp Pro Val Trp Phe Met Gln Glu Glu  
 85 90 95

Ile Pro Val Leu Glu Ser Tyr Trp Leu Ser Tyr Tyr Phe Pro Leu Thr  
 100 105 110

Arg Leu Ile Glu Phe Tyr Leu Gly Val Phe Gly Ala Lys Leu Val Ala  
 115 120 125

Glu Gly Met Phe Lys Asn Thr Asn Ile Thr Ile Pro Leu Ile Ala Leu  
 130 135 140

Ala Val Ser Phe Val Ala Thr Trp Phe Val Pro Leu Ala Phe Lys Met

gcggaatgcg	ctgctcatcc	acacgtggaa	tcctgattgg	gtg	acg	ctg	ggt	gga	115							
				Val	Thr	Leu	Gly	Gly								
				1				5								
ttg	aat	gta	cca	tcg	tgg	tcg	ctg	ggc	gcg	gaa	atg	ctg	ttc	tac	ctg	163
Leu	Asn	Val	Pro	Ser	Trp	Ser	Leu	Gly	Ala	Glu	Met	Leu	Phe	Tyr	Leu	
				10				15					20			
acg	ttc	ccg	ctg	ttt	att	ccg	tta	gtg	cgc	aaa	gtg	aag	ggc	gtg	ggc	211
Thr	Phe	Pro	Leu	Phe	Ile	Pro	Leu	Val	Arg	Lys	Val	Lys	Gly	Val	Gly	
			25					30					35			
aac	tgg	tgg	gca	ttt	ggc	atc	acc	ttt	gcc	gtg	agc	ctg	gcg	ctg	att	259
Asn	Trp	Trp	Ala	Phe	Gly	Ile	Thr	Phe	Ala	Val	Ser	Leu	Ala	Leu	Ile	
			40				45					50				
aca	gtg	att	cac	ttt	tat	gcg	gac	gga	cca	aag	ggg	att	gag	aac	ttc	307
Thr	Val	Ile	His	Phe	Tyr	Ala	Asp	Gly	Pro	Lys	Gly	Ile	Glu	Asn	Phe	
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ttt	gtt	cct	cgc	ctg	tgg	gac	acc	aat	gtg	tca	ccg	gtc	gcg	gaa	gtt	355
Phe	Val	Pro	Arg	Leu	Trp	Asp	Thr	Asn	Val	Ser	Pro	Val	Ala	Glu	Val	
	70				75				80					85		
cac	gcc	gat	cca	gtg	tgg	ttt	atg	cag	gaa	gaa	att	ccc	gtg	ctg	gaa	403
His	Ala	Asp	Pro	Val	Trp	Phe	Met	Gln	Glu	Glu	Ile	Pro	Val	Leu	Glu	
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tct	tac	tgg	ctg	tct	tac	tac	ttc	ccg	ctg	acc	aga	ctc	atc	gag	ttc	451
Ser	Tyr	Trp	Leu	Ser	Tyr	Tyr	Phe	Pro	Leu	Thr	Arg	Leu	Ile	Glu	Phe	
			105					110					115			
tac	ctc	ggt	gtg	ttt	ggc	gcg	aag	ctg	gtt	gct	gaa	ggc	atg	ttt	aaa	499
Tyr	Leu	Gly	Val	Phe	Gly	Ala	Lys	Leu	Val	Ala	Glu	Gly	Met	Phe	Lys	
	120					125					130					
aac	acc	aac	atc	acc	atc	ccg	ctg	atc	gca	ctg	gct	gtt	tct	ttt	gtt	547
Asn	Thr	Asn	Ile	Thr	Ile	Pro	Leu	Ile	Ala	Leu	Ala	Val	Ser	Phe	Val	
	135					140					145					
gct	act	tgg	ttt	gtg	cca	ctg	gca	ttc	aag	atg	tct	gtc	atc	atg	tcc	595
Ala	Thr	Trp	Phe	Val	Pro	Leu	Ala	Phe	Lys	Met	Ser	Val	Ile	Met	Ser	
	150				155				160					165		
ctg	cca	atg	gct	ttt	gtt	gtg	gca	acg	ctt	gcg	gtg	aga	gac	att	gaa	643
Leu	Pro	Met	Ala	Phe	Val	Val	Ala	Thr	Leu	Ala	Val	Arg	Asp	Ile	Glu	
			170					175					180			
ggc	aag	agt	ggg	gaa	atc	gcc	tcg	cct	cgc	gca	gtt	ttg	ttg	ggt	aat	691
Gly	Lys	Ser	Gly	Glu	Ile	Ala	Ser	Pro	Arg	Ala	Val	Leu	Leu	Gly	Asn	
			185				190					195				
att	tcc	ttt	gcc	ttc	tac	atg	gtg	caa	ttc	ccc	gtc	atg	gtg	ttt	gtg	739
Ile	Ser	Phe	Ala	Phe	Tyr	Met	Val	Gln	Phe	Pro	Val	Met	Val	Phe	Val	
	200					205					210					
cag	cgc	tat	ttc	att	gct	ggc	aaa	gaa	tac	ggc	ttc	ctt	ggc	tgg	gca	787
Gln	Arg	Tyr	Phe	Ile	Ala	Gly	Lys	Glu	Tyr	Gly	Phe	Leu	Gly	Trp	Ala	
	215				220				225							

Ala Lys Val Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala  
                   20                                  25                                  30  
 Leu Ser Ala Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val  
                   35                                  40                                  45  
 Gly Asp Ser Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser  
                   50                                  55                                  60  
 Ile Thr Leu Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala  
                   65                                  70                                  75                                  80  
 Thr Lys Arg Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr Tyr Glu  
                   85                                  90                                  95  
 Val Ser Pro Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met Arg Glu  
                   100                                  105                                  110  
 Thr Gly Ala Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile Ala Gln  
                   115                                  120                                  125  
 Thr Ile Arg Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly His Ile  
                   130                                  135                                  140  
 Gly Tyr Thr Pro Gln Ser Glu His Ser Leu Gly Gly His Val Val Gln  
                   145                                  150                                  155                                  160  
 Gly Arg Gly Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu  
                   165                                  170                                  175  
 Glu Gln Ala Gly Ala Phe Ala Val Val Leu Glu Met Val Pro Ala Glu  
                   180                                  185                                  190  
 Ala Ala Arg Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile  
                   195                                  200                                  205  
 Gly Ala Gly Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala  
                   210                                  215                                  220  
 Phe Gly Leu Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala  
                   225                                  230                                  235                                  240  
 Thr Leu Gly Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp  
                   245                                  250                                  255  
 Ile His Ala Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe  
                   260                                  265

&lt;210&gt; 283

&lt;211&gt; 1065

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1042)

&lt;223&gt; RXN01420

&lt;400&gt; 283

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Met	Ile	Val	Leu	Ala	Lys	Ala	Val	Thr	Ile	Ala	Thr	Lys	Arg	Ala	Leu	
70					75					80					85	
gtg	gtg	gtt	gat	ctg	ccg	ttt	ggt	acc	tat	gag	gtg	agc	cca	aat	cag	403
Val	Val	Val	Asp	Leu	Pro	Phe	Gly	Thr	Tyr	Glu	Val	Ser	Pro	Asn	Gln	
				90					95					100		
gcg	gtg	gag	tcc	gcg	atc	cgg	gtc	atg	cgt	gaa	acg	ggt	gcg	gct	gcg	451
Ala	Val	Glu	Ser	Ala	Ile	Arg	Val	Met	Arg	Glu	Thr	Gly	Ala	Ala	Ala	
			105					110						115		
gtg	aag	atc	gag	ggt	ggc	gtg	gag	atc	gcg	cag	acg	att	cga	cgc	att	499
Val	Lys	Ile	Glu	Gly	Gly	Val	Glu	Ile	Ala	Gln	Thr	Ile	Arg	Arg	Ile	
		120					125					130				
gtt	gat	gct	gga	att	ccg	gtt	gtc	ggc	cac	atc	ggg	tac	acc	ccg	cag	547
Val	Asp	Ala	Gly	Ile	Pro	Val	Val	Gly	His	Ile	Gly	Tyr	Thr	Pro	Gln	
	135					140					145					
tcc	gag	cat	tcc	ttg	ggc	ggc	cac	gtg	gtt	cag	ggt	cgt	ggc	gcg	agt	595
Ser	Glu	His	Ser	Leu	Gly	Gly	His	Val	Val	Gln	Gly	Arg	Gly	Ala	Ser	
150					155					160					165	
tct	gga	aag	ctc	atc	gcc	gat	gcc	cgc	gcg	ttg	gag	cag	gcg	ggt	gcg	643
Ser	Gly	Lys	Leu	Ile	Ala	Asp	Ala	Arg	Ala	Leu	Glu	Gln	Ala	Gly	Ala	
			170					175						180		
ttt	gcg	gtt	gtg	ttg	gag	atg	gtt	cca	gca	gag	gca	gcg	cgc	gag	gtt	691
Phe	Ala	Val	Val	Leu	Glu	Met	Val	Pro	Ala	Glu	Ala	Ala	Arg	Glu	Val	
			185					190					195			
acc	gag	gat	ctt	tcc	atc	acc	act	atc	gga	atc	ggt	gcc	ggc	aat	ggc	739
Thr	Glu	Asp	Leu	Ser	Ile	Thr	Thr	Ile	Gly	Ile	Gly	Ala	Gly	Asn	Gly	
		200					205					210				
aca	gat	ggg	cag	gtt	ttg	gtg	tgg	cag	gat	gcc	ttc	ggc	ctc	aac	cgc	787
Thr	Asp	Gly	Gln	Val	Leu	Val	Trp	Gln	Asp	Ala	Phe	Gly	Leu	Asn	Arg	
	215					220					225					
ggc	aag	aag	cca	cgc	ttc	gtc	cgc	gag	tac	gcc	acc	ttg	ggc	gat	tcc	835
Gly	Lys	Lys	Pro	Arg	Phe	Val	Arg	Glu	Tyr	Ala	Thr	Leu	Gly	Asp	Ser	
230					235					240					245	
ttg	cac	gac	gcc	gcg	cag	gcc	tac	atc	gcc	gat	atc	cac	gcg	ggt	acc	883
Leu	His	Asp	Ala	Ala	Gln	Ala	Tyr	Ile	Ala	Asp	Ile	His	Ala	Gly	Thr	
			250					255						260		
ttc	cca	ggc	gaa	gcg	gag	tcc	ttt	taatgcaggt	agcaaccaca	aag						930
Phe	Pro	Gly	Glu	Ala	Glu	Ser	Phe									
			265													

&lt;210&gt; 282

&lt;211&gt; 269

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 282

Met	Ser	Gly	Ile	Asp	Ala	Lys	Lys	Ile	Arg	Thr	Arg	His	Phe	Arg	Glu
1					5				10					15	

130	135	140	
His Ile Gly Tyr Thr Pro Gln Ser Glu His Ser Leu Gly Gly His Val 145 150 155 160			
Val Gln Gly Arg Gly Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg 165 170 175			
Ala Leu Glu Gln Ala Gly Ala Phe Ala Val Val Leu Glu Met Val Pro 180 185 190			
Ala Glu Ala Ala Arg Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile 195 200 205			
Gly Ile Gly Ala Gly Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln 210 215 220			
Asp Ala Phe Gly Leu Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu 225 230 235 240			
Tyr Ala Thr Leu Gly Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile 245 250 255			
Ala Asp Ile His Ala Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe 260 265 270			
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<211> 930			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (101)..(907)			
<223> FRXA01929			
<400> 281			
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tattttattct gagctgggtca tcacatctat actcatgccc atg tca ggc att gat			115
		Met Ser Gly Ile Asp	
		1 5	
gca aag aaa atc cgc acc cgt cat ttc cgc gaa gct aaa gta aac ggc			163
Ala Lys Lys Ile Arg Thr Arg His Phe Arg Glu Ala Lys Val Asn Gly			
	10	15 20	
cag aaa gtt tcg gtt ctc acc agc tat gat gcg ctt tcg gcg cgc att			211
Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala Leu Ser Ala Arg Ile			
	25 30	35	
ttt gat gag gct ggc gtc gat atg ctc ctt gtt ggt gat tcc gct gcc			259
Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val Gly Asp Ser Ala Ala			
	40 45	50	
aac gtt gtg ctg ggt cgc gat acc acc ttg tcg atc acc ttg gat gag			307
Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser Ile Thr Leu Asp Glu			
	55 60	65	
atg att gtg ctg gcc aag gcg gtg acg atc gct acg aag cgt gcg ctt			355

tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc 643  
 Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr  
 170 175 180

acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc 691  
 Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser  
 185 190 195

tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag 739  
 Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys  
 200 205 210

cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg 787  
 His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala  
 215 220 225

atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca 835  
 Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro  
 230 235 240 245

gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc 883  
 Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile  
 250 255 260

ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa 931  
 Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys  
 265 270 275

ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc 979  
 Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile  
 280 285 290

acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc  
 1027  
 Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile  
 295 300 305

gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc  
 1075  
 Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser  
 310 315 320 325

ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag  
 1123  
 Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys  
 330 335 340

gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct  
 1171  
 Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala  
 345 350 355

cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa  
 1219  
 Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu  
 360 365 370

gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca  
 1267  
 Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala

Leu Thr Phe Ala Gly Ala Leu Phe  
450 455

<210> 305

<211> 1330

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1330)

<223> FRXA01009

<400> 305

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ttatttaaag acttcataat attttgggga gtgaactggt ttg gca ttg aag ggt 115  
Leu Ala Leu Lys Gly  
1 5  
tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163  
Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala  
10 15 20  
aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211  
Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe  
25 30 35  
cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259  
His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala  
40 45 50  
gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307  
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp  
55 60 65  
atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga 355  
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg  
70 75 80 85  
tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac 403  
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn  
90 95 100  
ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg 451  
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val  
105 110 115  
tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc 499  
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly  
120 125 130  
gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga 547  
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly  
135 140 145  
cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga 595  
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly  
150 155 160 165

115					120					125					
Phe	Thr	Asn	Gly	Gly	Ala	Asp	Ala	Ile	Glu	His	Ser	Ile	Arg	Met	Ala
130						135					140				
Arg	Leu	His	Thr	Gly	Arg	Asn	Lys	Ile	Leu	Ser	Ala	Tyr	Arg	Ser	Tyr
145					150					155					160
His	Gly	Ala	Thr	Gly	Ser	Ala	Met	Met	Leu	Thr	Gly	Glu	His	Arg	Arg
				165					170					175	
Leu	Gly	Asn	Pro	Thr	Thr	Asp	Pro	Asp	Ile	Tyr	His	Phe	Trp	Ala	Pro
			180					185					190		
Phe	Leu	His	His	Ser	Ser	Phe	Phe	Ala	Thr	Thr	Gln	Glu	Glu	Glu	Cys
		195					200					205			
Glu	Arg	Ala	Leu	Lys	His	Leu	Glu	Asp	Val	Ile	Ala	Phe	Glu	Gly	Ala
	210					215					220				
Gly	Met	Ile	Ala	Ala	Ile	Val	Leu	Glu	Pro	Val	Val	Gly	Ser	Ser	Gly
225					230					235					240
Ile	Ile	Leu	Pro	Pro	Ala	Gly	Tyr	Leu	Asn	Gly	Val	Arg	Glu	Leu	Cys
				245					250					255	
Asn	Lys	His	Gly	Ile	Leu	Phe	Ile	Ala	Asp	Glu	Val	Met	Val	Gly	Phe
			260					265					270		
Gly	Arg	Thr	Gly	Lys	Leu	Phe	Ala	Tyr	Glu	His	Ala	Gly	Asp	Asp	Phe
		275					280					285			
Gln	Pro	Asp	Met	Ile	Thr	Phe	Ala	Lys	Gly	Val	Asn	Ala	Gly	Tyr	Ala
	290						295				300				
Pro	Leu	Gly	Gly	Ile	Val	Met	Thr	Gln	Ser	Ile	Arg	Asp	Thr	Phe	Gly
305					310					315					320
Ser	Glu	Ala	Tyr	Ser	Gly	Gly	Leu	Thr	Tyr	Ser	Gly	His	Pro	Leu	Ala
				325					330					335	
Val	Ala	Pro	Ala	Lys	Ala	Ala	Leu	Glu	Ile	Tyr	Ala	Glu	Gly	Glu	Ile
			340					345					350		
Ile	Pro	Arg	Val	Ala	Arg	Leu	Gly	Ala	Glu	Leu	Ile	Glu	Pro	Arg	Leu
		355					360					365			
Arg	Glu	Leu	Ala	Glu	Glu	Asn	Val	Ala	Ile	Ala	Asp	Val	Arg	Gly	Ile
	370					375					380				
Gly	Phe	Phe	Trp	Ala	Val	Glu	Phe	Asn	Ala	Asp	Ala	Thr	Ala	Met	Ala
385					390					395					400
Ala	Gly	Ala	Ala	Glu	Phe	Lys	Glu	Arg	Gly	Val	Trp	Pro	Met	Ile	Ser
				405					410					415	
Gly	Asn	Arg	Phe	His	Ile	Ala	Pro	Pro	Leu	Thr	Thr	Thr	Asp	Asp	Glu
			420					425					430		
Leu	Val	Ala	Leu	Leu	Asp	Ala	Val	Glu	Ala	Ala	Ala	Gln	Ala	Val	Glu
		435					440					445			

360

365

370

gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca  
1267

Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala  
375 380 385

gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa  
1315

Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu  
390 395 400 405

ttc aag gaa cgc ggc gtg tgg ccg atg atc tcc ggc aac cga ttc cac  
1363

Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser Gly Asn Arg Phe His  
410 415 420

atc gcg ccg ccg ctg acc acc act gat gac gaa ttg gta gca ctg ctg  
1411

Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu Leu Val Ala Leu Leu  
425 430 435

gac gcg gtg gaa gct gca gcc caa gct gtc gag ctg acc ttc gct ggg  
1459

Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu Leu Thr Phe Ala Gly  
440 445 450

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1491

Ala Leu Phe  
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<212> PRT

<213> Corynebacterium glutamicum

<400> 304

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20 25 30

Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro  
35 40 45

Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly  
50 55 60

Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly  
65 70 75 80

His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg  
85 90 95

Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val  
100 105 110

Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe

135	140	145	
cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga			595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly			
150	155	160	165
tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc			643
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr			
	170	175	180
acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc			691
Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser			
	185	190	195
tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag			739
Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys			
	200	205	210
cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg			787
His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala			
	215	220	225
atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca			835
Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro			
	230	235	240
gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc			883
Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile			
	250	255	260
ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa			931
Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys			
	265	270	275
ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc			979
Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile			
	280	285	290
acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc			1027
Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile			
	295	300	305
gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc			1075
Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser			
	310	315	320
ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag			1123
Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys			
	330	335	340
gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct			1171
Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala			
	345	350	355
cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa			1219
Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu			

Asn Asp Glu Glu Ile Ile Leu Tyr Ser Val Gly Gly Met Pro Val Glu  
 340 345 350  
 Asp Val Ala Trp Ala Thr Gln Val Tyr Glu Asn Ala Leu Glu Lys Gly  
 355 360 365  
 Val Gly Thr Thr Leu Asn Leu Trp Glu Ser Pro Ala Leu Ala  
 370 375 380  
  
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 <223> RXS02970  
  
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 Leu Ala Leu Lys Gly  
 1 5  
 tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163  
 Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala  
 10 15 20  
 aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211  
 Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe  
 25 30 35  
 cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259  
 His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala  
 40 45 50  
 gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307  
 Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp  
 55 60 65  
 atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga 355  
 Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg  
 70 75 80 85  
 tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac 403  
 Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn  
 90 95 100  
 ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg 451  
 Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val  
 105 110 115  
 tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc 499  
 Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly  
 120 125 130  
 gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga 547  
 Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly



Ser Glu Pro Asp Met Ile Ala Ala Gly Val Lys Asp Val Ala Gln Cys  
 20 25 30  
 Val Asp Val Met Glu Glu Thr Leu Val Leu Leu Ala Gln Gly Asp Tyr  
 35 40 45  
 Lys Met Ala Gly Leu Asn Ser Asn Ser His Gly Ala Met Ile Thr Phe  
 50 55 60  
 Pro Glu Asn Pro Glu Phe Glu Gly Met Pro Lys Asp Gly Pro Asp Arg  
 65 70 75 80  
 Arg Phe Met Ala Met Pro Ala Tyr Leu Gly Gly Arg Phe Lys Asn Thr  
 85 90 95  
 Gly Val Lys Trp Tyr Gly Ser Asn Ala Glu Asn Lys Ala Ser Gly Leu  
 100 105 110  
 Pro Arg Ser Ile His Thr Phe Val Leu Asn Asp Thr Val Thr Gly Ala  
 115 120 125  
 Pro Lys Ala Ile Met Ser Ala Asn Leu Leu Ser Ala Tyr Arg Thr Gly  
 130 135 140  
 Ala Val Pro Gly Val Gly Val Lys His Leu Ala Val Ala Asp Ala Thr  
 145 150 155 160  
 Thr Leu Ala Val Val Gly Pro Gly Val Met Ala Lys Thr Ile Thr Glu  
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 Ala Cys Ile Ala Glu Arg Pro Gly Ile Thr Thr Ile Lys Ile Lys Gly  
 180 185 190  
 Arg Ser Glu Arg Gly Ile Asn Ala Phe Ala Thr Trp Ala Leu Glu Lys  
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 Phe Pro Glu Ile Glu Val Val Ala Val Gly Ser Glu Glu Asp Val Val  
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 Lys Asp Ala Asp Ile Val Ile Ala Ala Thr Thr Thr Asp Ala Ala Gly  
 225 230 235 240  
 Ser Ser Ala Phe Pro Tyr Phe Lys Lys Glu Trp Leu Lys Pro Gly Ala  
 245 250 255  
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 Asp Asp Ala Arg Leu Val Val Asp Tyr Met Gly Leu Tyr Glu Ala Trp  
 275 280 285  
 Ala Glu Glu Tyr Gly Pro Gln Ala Tyr Gln Leu Leu Gly Ile Pro Gly  
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 Thr His Trp Tyr Asp Leu Ala Leu Gln Gly Lys Leu Asp Leu Ala Lys  
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 Ile Ser Gln Ile Gly Asp Ile Cys Ser Gly Lys Leu Pro Gly Arg Thr  
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Val Val Ala Val Gly Ser Glu Glu Asp Val Val Lys Asp Ala Asp Ile  
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 Val Ile Ala Ala Thr Thr Asp Ala Ala Gly Ser Ser Ala Phe Pro  
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 Tyr Phe Lys Lys Glu Trp Leu Lys Pro Gly Ala Leu Leu Leu Leu Pro  
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 265 270 275  
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 Val Val Asp Tyr Met Gly Leu Tyr Glu Ala Trp Ala Glu Tyr Gly  
 280 285 290  
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 1027  
 Pro Gln Ala Tyr Gln Leu Leu Gly Ile Pro Gly Thr His Trp Tyr Asp  
 295 300 305  
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 1075  
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 1123  
 Asp Ile Cys Ser Gly Lys Leu Pro Gly Arg Thr Asn Asp Glu Glu Ile  
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 1171  
 Ile Leu Tyr Ser Val Gly Gly Met Pro Val Glu Asp Val Ala Trp Ala  
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 1219  
 Thr Gln Val Tyr Glu Asn Ala Leu Glu Lys Gly Val Gly Thr Thr Leu  
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 Asn Leu Trp Glu Ser Pro Ala Leu Ala  
 375 380  
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tcgataagca aaaaatcgct gatactcgaa aggcctcaaa atg acc gca acc tac 115  
 Met Thr Ala Thr Tyr  
 1 5

acc act gaa acc gcc atc aat ttc ttg ttc ttg agc gaa ccg gac atg 163  
 Thr Thr Glu Thr Ala Ile Asn Phe Leu Phe Leu Ser Glu Pro Asp Met  
 10 15 20

atc gcg gcc gga gtc aaa gac gtc gcg caa tgc gtc gat gtc atg gag 211  
 Ile Ala Ala Gly Val Lys Asp Val Ala Gln Cys Val Asp Val Met Glu  
 25 30 35

gaa acg ctg gtg ctc ttg gcg cag ggc gac tac aaa atg gcc ggt ttg 259  
 Glu Thr Leu Val Leu Leu Ala Gln Gly Asp Tyr Lys Met Ala Gly Leu  
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aac tcc aac tcg cat ggc gcg atg atc acc ttc ccg gaa aac cca gaa 307  
 Asn Ser Asn Ser His Gly Ala Met Ile Thr Phe Pro Glu Asn Pro Glu  
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ttt gaa ggc atg ccc aag gac ggc ccc gac cgc cga ttc atg gcg atg 355  
 Phe Glu Gly Met Pro Lys Asp Gly Pro Asp Arg Arg Phe Met Ala Met  
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ccc gca tac ctc ggc ggg cga ttc aaa aac acc ggc gtg aag tgg tac 403  
 Pro Ala Tyr Leu Gly Gly Arg Phe Lys Asn Thr Gly Val Lys Trp Tyr  
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gga tcc aac gcg gaa aac aag gcc tca ggc ttg cct cgc tcg atc cac 451  
 Gly Ser Asn Ala Glu Asn Lys Ala Ser Gly Leu Pro Arg Ser Ile His  
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acc ttc gtc ctc aac gac acg gtc acc ggt gca ccg aag gcc atc atg 499  
 Thr Phe Val Leu Asn Asp Thr Val Thr Gly Ala Pro Lys Ala Ile Met  
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tcc gcg aac ctg ctg tcc gcc tac cgc acc ggc gcg gtt ccc ggc gtg 547  
 Ser Ala Asn Leu Leu Ser Ala Tyr Arg Thr Gly Ala Val Pro Gly Val  
 135 140 145

ggc gtg aag cac tta gcg gtc gcc gac gcg aca acc ttg gct gtc gtc 595  
 Gly Val Lys His Leu Ala Val Ala Asp Ala Thr Thr Leu Ala Val Val  
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gga cct ggt gtc atg gcg aaa acc atc acc gaa gcg tgc atc gca gag 643  
 Gly Pro Gly Val Met Ala Lys Thr Ile Thr Glu Ala Cys Ile Ala Glu  
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cgc cca gga atc acc acc atc aag atc aag gga cgc agc gaa cgc ggc 691  
 Arg Pro Gly Ile Thr Thr Ile Lys Ile Lys Gly Arg Ser Glu Arg Gly  
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 145 150 155 160  
 Ser Gly Val Glu Phe Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys  
 165 170 175  
 Met Val Glu Thr Asn Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro  
 180 185 190  
 Ile Gln Gly Glu Thr Gly Val Val Pro Ala Pro Glu Gly Phe Leu Lys  
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 Ala Val Arg Glu Leu Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp  
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 Glu Val Gln Thr Gly Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln  
 225 230 235 240  
 His Asp Gly Val Val Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly  
 245 250 255  
 Gly Gly Leu Pro Ile Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu  
 260 265 270  
 Leu Met Thr Pro Gly Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val  
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 Lys Val Asp Gly Val Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly  
 325 330 335  
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 Lys His Gly Val Ile Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu  
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 Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly Val Val Leu Glu Arg  
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 1171  
 Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe Lys His Gly Val Ile  
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atc acc gac gaa gaa atc gca gac gca gtc aag gct att gcc gag aca  
 1267  
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 Ala Leu Gly His Ala His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln  
 50 55 60  
 Ile Gly Gln Leu Gly His Val Ser Asn Leu Phe Ala Ser Arg Pro Val  
 65 70 75 80  
 Val Glu Val Ala Glu Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala  
 85 90 95  
 Thr Leu Ala Ala Gln Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu  
 100 105 110  
 Ala Asn Glu Ala Ala Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg  
 115 120 125

His Val Ser Asn Leu Phe Ala Ser Arg Pro Val Val Glu Val Ala Glu  
 70 75 80 85  
 gag ctc atc aag cgt ttt tcg ctt gac gac gcc acc ctc gcc gcg caa 403  
 Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala Thr Leu Ala Ala Gln  
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 acc cgg gtt ttc ttc tgc aac tcg ggc gcc gaa gca aac gag gct gct 451  
 Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu Ala Asn Glu Ala Ala  
 105 110 115  
 ttc aag att gca cgc ttg act ggt cgt tcc cgg att ctg gct gca gtt 499  
 Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg Ile Leu Ala Ala Val  
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 cat ggt ttc cac ggc cgc acc atg ggt tcc ctc gcg ctg act ggc cag 547  
 His Gly Phe His Gly Arg Thr Met Gly Ser Leu Ala Leu Thr Gly Gln  
 135 140 145  
 cca gac aag cgt gaa gcg ttc ctg cca atg cca agc ggt gtg gag ttc 595  
 Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro Ser Gly Val Glu Phe  
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 Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys Met Val Glu Thr Asn  
 170 175 180  
 cca acg gat gtg gct gct atc ttc ctc gag cca atc cag ggt gaa acg 691  
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 Gly Val Val Pro Ala Pro Glu Gly Phe Leu Lys Ala Val Arg Glu Leu  
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 Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp Glu Val Gln Thr Gly  
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 Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln His Asp Gly Val Val  
 230 235 240 245  
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 Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly Gly Gly Leu Pro Ile  
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 Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu Leu Met Thr Pro Gly  
 265 270 275  
 aag cac ggc acc act ttc ggt ggc aac cca gtt gct tgt gca gct gcc 979  
 Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val Ala Cys Ala Ala Ala  
 280 285 290  
 aag gca gtg ctg tct gtt gtc gat gac gct ttc tgc gca gaa gtt gcc  
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 Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe Cys Ala Glu Val Ala  
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Val Ala Glu Ser Asp Ile Asp Ala Val Thr Ala Met Ser Gly Ser Ser			
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Pro Ala Tyr Leu Phe Leu Val Thr Glu Ala Leu Ile Glu Ala Gly Val			
	180	185	190
Asn Leu Gly Leu Pro Arg Ala Thr Ala Lys Lys Leu Ala Val Ala Ser			
	195	200	205
Phe Glu Gly Ala Ala Thr Met Met Lys Glu Thr Gly Lys Glu Pro Ser			
210	215	220	
Glu Leu Arg Ala Gly Val Ser Ser Pro Ala Gly Thr Thr Val Ala Ala			
225	230	235	240
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		Met Ser Thr Leu Glu	
		1 5	
act tgg cca cag gtc att att aat acg tac ggc acc cca cca gtt gag			163
Thr Trp Pro Gln Val Ile Ile Asn Thr Tyr Gly Thr Pro Pro Val Glu			
	10	15	20
ctg gtg tcc ggc aag ggc gca acc gtc act gat gac cag ggc aat gtc			211
Leu Val Ser Gly Lys Gly Ala Thr Val Thr Asp Asp Gln Gly Asn Val			
	25	30	35
tac atc gac ttg ctc gcg ggc atc gca gtc aac gcg ttg ggc cac gcc			259
Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn Ala Leu Gly His Ala			
	40	45	50
cac ccg gcg atc atc gag gcg gtc acc aac cag atc ggc caa ctt ggt			307
His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln Ile Gly Gln Leu Gly			
	55	60	65
cac gtc tca aac ttg ttc gca tcc agg ccc gtc gtc gag gtc gcc gag			355

Ile Asp Ala Val Thr Ala Met Ser Gly Ser Ser Pro Ala Tyr Leu Phe  
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 Leu Val Thr Glu Ala Leu Ile Glu Ala Gly Val Asn Leu Gly Leu Pro  
 185 190 195  
 cgc gcg acc gct aaa aag ctc gct gtg gcc tca ttc gaa ggt gct gca 739  
 Arg Ala Thr Ala Lys Lys Leu Ala Val Ala Ser Phe Glu Gly Ala Ala  
 200 205 210  
 acc atg atg aag gaa acc ggc aaa gaa ccc tca gaa ttg cgc gca ggc 787  
 Thr Met Met Lys Glu Thr Gly Lys Glu Pro Ser Glu Leu Arg Ala Gly  
 215 220 225  
 gtt tcc tca ccc gca ggc acc acc gtc gca gcc atc cga gaa ctc gaa 835  
 Val Ser Ser Pro Ala Gly Thr Thr Val Ala Ala Ile Arg Glu Leu Glu  
 230 235 240 245  
 gaa agc gga atc cga ggc gct ttc tac cgc gca gcc caa gct tgc gcc 883  
 Glu Ser Gly Ile Arg Gly Ala Phe Tyr Arg Ala Ala Gln Ala Cys Ala  
 250 255 260  
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 Thr Asn Arg Ser Glu Glu Arg Gly Gln Glu Leu Arg Asp Arg Tyr Gly  
 35 40 45  
 Ile Leu Asn Met Thr Asp Asn Ser Gln Ala Ala Asp Glu Ala Asp Val  
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 Val Phe Leu Cys Val Lys Pro Lys Phe Ile Val Glu Val Leu Ser Glu  
 65 70 75 80  
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 85 90 95  
 Met Ala Ala Gly Ile Ser Ile Ala Ala Met Glu Glu Ser Ala Ser Ala  
 100 105 110  
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195

200

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<213> *Corynebacterium glutamicum*

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<223> RXA02499
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Met Thr Thr Ile Ala  
1 5

gta atc ggc ggc gga caa atc ggc gag gct tta gtc tca ggt ttg atc 163  
Val Ile Gly Gly Gly Gln Ile Gly Glu Ala Leu Val Ser Gly Leu Ile  
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gcg gcc aac atg aat cca caa aat att cgc gtc acc aac cgt tcg gaa 211  
Ala Ala Asn Met Asn Pro Gln Asn Ile Arg Val Thr Asn Arg Ser Glu  
25 30 35

gag cgc ggc caa gag ctg cgt gac cgc tac ggc atc ctc aac atg acg 259  
Glu Arg Gly Gln Glu Leu Arg Asp Arg Tyr Gly Ile Leu Asn Met Thr  
40 45 50

gat aat tcc caa gcc gca gac gaa gcc gac gtg gtg ttc ctg tgc gtg 307  
Asp Asn Ser Gln Ala Ala Asp Glu Ala Asp Val Val Phe Leu Cys Val  
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aag ccg aaa ttt atc gtc gaa gtg ctc tcc gaa atc acc ggc act ttg 355  
Lys Pro Lys Phe Ile Val Glu Val Leu Ser Glu Ile Thr Gly Thr Leu  
70 75 80 85

gat aac aac tcc gca caa agt gtt gtg gtc agc atg gcc gca ggc atc 403  
Asp Asn Asn Ser Ala Gln Ser Val Val Val Ser Met Ala Ala Gly Ile  
90 95 100

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agc atc gct gcc atg gaa gaa agc gcc tct gcg ggg ctc ccc gtc gtg    451
Ser Ile Ala Ala Met Glu Glu Ser Ala Ser Ala Gly Leu Pro Val Val
          105                      110                      115

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cgc gtc atg ccg aac act cca atg ctc gtg ggc aag ggc atg tcg act 499  
 Arg Val Met Pro Asn Thr Pro Met Leu Val Gly Lys Gly Met Ser Thr  
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gtc acc aaa ggc cgc tac gtt gac gcg gaa cag ttg gaa caa gtc aag 547  
Val Thr Lys Gly Arg Tyr Val Asp Ala Glu Gln Leu Glu Gln Val Lys  
135 140 145

gac ttg ttg agc acc gtt gga gac gtc ctc gaa gtc gcg gaa tca gac 595  
Asp Leu Leu Ser Thr Val Gly Asp Val Leu Glu Val Ala Glu Ser Asp  
150 155 160 165

atc gac gca gtc acc gcg atg tcc gga tcc tcc cct gca tac ctg ttc 643

gca gcg gtg atg ata aac gca tcc acc gcc tac acc gat ggg gag cag 480  
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 145 150 155 160

tac ggc atg ggc gcg gag atc ggc att tcc acc cag aaa ctg cat gca 528  
 Tyr Gly Met Gly Ala Glu Ile Gly Ile Ser Thr Gln Lys Leu His Ala  
 165 170 175

cgt gga cca atg gcc ctg cca gag ctg acc tcc acc aag tgg att ctg 576  
 Arg Gly Pro Met Ala Leu Pro Glu Leu Thr Ser Thr Lys Trp Ile Leu  
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cag ggc aca gga caa att agg cct taagtgttgaa gaagtaatca agc 623  
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<211> 200

<212> PRT

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Ala Leu Ser Asp Ser Asp Lys Leu Ala Val Val Gln Ala Leu Gln Glu  
 50 55 60

Ala Gly Val Thr Ile His Gly Arg Val Ala Glu Leu Glu Ala Phe Gly  
 65 70 75 80

Ala Thr Asp Val Val Glu Ala Thr Glu Thr Asp Trp Asp Ser Glu Tyr  
 85 90 95

Leu Ser Phe Asp Ile Ala Val Ala Val Val Asp Gly Val Asp Gly Ala  
 100 105 110

Leu Ala His Ile Ala Lys Tyr Ser Thr Lys His Thr Glu Ala Ile Ala  
 115 120 125

Thr Gln Asn Ile Glu Thr Ala Gln Arg Phe Ala Asp Arg Val Asp Ala  
 130 135 140

Ala Ala Val Met Ile Asn Ala Ser Thr Ala Tyr Thr Asp Gly Glu Gln  
 145 150 155 160

Tyr Gly Met Gly Ala Glu Ile Gly Ile Ser Thr Gln Lys Leu His Ala  
 165 170 175

Arg Gly Pro Met Ala Leu Pro Glu Leu Thr Ser Thr Lys Trp Ile Leu  
 180 185 190

Gln Gly Thr Gly Gln Ile Arg Pro

130	135	140
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Gln Asp Val Leu Glu Arg Phe Glu Leu Pro Arg Glu Thr Val Gln Leu		
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Leu Leu Ala Lys Pro Ala Asp Pro Ser Lys Ile		
195	200	

&lt;210&gt; 295

&lt;211&gt; 623

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

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&lt;223&gt; FRXA02382

&lt;400&gt; 295

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gaa gcc aag ctt gat cag gca atc gcc atg gtc atc aac ggc aag acc	96
Glu Ala Lys Leu Asp Gln Ala Ile Ala Met Val Ile Asn Gly Lys Thr	
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cgc cgc tgc agc gtg tgc aac gct act gaa acc gcg ctt ctc gac gcc	144
Arg Arg Cys Ser Val Cys Asn Ala Thr Glu Thr Ala Leu Leu Asp Ala	
35 40 45	
gcc ctc agc gac tca gac aag ctt gca gtc gtc cag gcg ctc cag gaa	192
Ala Leu Ser Asp Ser Asp Lys Leu Ala Val Val Gln Ala Leu Gln Glu	
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Ala Gly Val Thr Ile His Gly Arg Val Ala Glu Leu Glu Ala Phe Gly	
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Ala Thr Asp Val Val Glu Ala Thr Glu Thr Asp Trp Asp Ser Glu Tyr	
85 90 95	
ctg tcc ttc gat atc gct gtc gct gtg gtt gac ggt gtg gat gga gct	336
Leu Ser Phe Asp Ile Ala Val Ala Val Val Asp Gly Val Asp Gly Ala	
100 105 110	
ctg gca cac atc gct aag tac agc acc aag cac acc gaa gcg atc gcc	384
Leu Ala His Ile Ala Lys Tyr Ser Thr Lys His Thr Glu Ala Ile Ala	
115 120 125	
acc caa aac att gaa acc gct cag cgc ttt gca gat cgc gtc gat gca	432
Thr Gln Asn Ile Glu Thr Ala Gln Arg Phe Ala Asp Arg Val Asp Ala	
130 135 140	

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 Asn Gly Ile Gln Met Lys Gln Val Arg Val Pro Leu Gly Val Met Gly  
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 Met Val Tyr Glu Ala Arg Pro Asn Val Thr Val Asp Ala Phe Gly Leu  
 135 140 145  
 gca ctc aag tcc gga aac gta gct ttg ctg cgc ggt tcc tcc aca gct 595  
 Ala Leu Lys Ser Gly Asn Val Ala Leu Leu Arg Gly Ser Ser Thr Ala  
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 Val His Ser Asn Thr Lys Leu Val Glu Ile Leu Gln Asp Val Leu Glu  
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 cgt ttc gag ctg cca cgc gaa acc gtg cag ttg ctg ctt gcc aaa ccc 691  
 Arg Phe Glu Leu Pro Arg Glu Thr Val Gln Leu Leu Leu Ala Lys Pro  
 185 190 195  
 gcg gat ccg tcc aag att tgatcaccgg acgcg 724  
 Ala Asp Pro Ser Lys Ile  
 200

&lt;210&gt; 294

&lt;211&gt; 203

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 294

Met Ser Ser Thr Thr Leu Thr Asp Asp Gln Ile Arg Asp Asn Glu Arg  
 1 5 10 15  
 Thr Glu Val Leu Ala Lys Ala Thr Ala Ala Lys Asn Ile Val Pro Asp  
 20 25 30  
 Ile Ala Val Leu Gly Thr Gly Pro Lys Asn Ala Ile Leu Arg Ala Ala  
 35 40 45  
 Ala Asp Glu Leu Val Ala Arg Ser Ala Glu Ile Ile Glu Ala Asn Ala  
 50 55 60  
 Ser Asp Ile Glu Ala Gly Arg Ala Asn Gly Met Glu Glu Ser Met Ile  
 65 70 75 80  
 Asp Arg Leu Ala Leu Asp Glu Ser Arg Ile Glu Gly Ile Ala Gly Gly  
 85 90 95  
 Leu Arg Gln Val Ala Gly Leu Thr Asp Pro Val Gly Glu Val Leu Arg  
 100 105 110  
 Gly His Val Met Glu Asn Gly Ile Gln Met Lys Gln Val Arg Val Pro  
 115 120 125  
 Leu Gly Val Met Gly Met Val Tyr Glu Ala Arg Pro Asn Val Thr Val

340	345	350
Thr Lys His Thr Glu Ala Ile Ala Thr Gln Asn Ile Glu Thr Ala Gln		
355	360	365
Arg Phe Ala Asp Arg Val Asp Ala Ala Ala Val Met Ile Asn Ala Ser		
370	375	380
Thr Ala Tyr Thr Asp Gly Glu Gln Tyr Gly Met Gly Ala Glu Ile Gly		
385	390	395
Ile Ser Thr Gln Lys Leu His Ala Arg Gly Pro Met Ala Leu Pro Glu		
405	410	415
Leu Thr Ser Thr Lys Trp Ile Leu Gln Gly Thr Gly Gln Ile Arg Pro		
420	425	430

<210> 293  
 <211> 724  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(709)  
 <223> FRXA02378

<400> 293  
 gagcagatgg ccaccgaggt cgatgtggtg gctggctact aggcctttta tgggtgtgac 60  
 cgacactggt gcttcttaag ggtctgtata gtgggcaacc atg agt tca acg acc 115  
 Met Ser Ser Thr Thr  
 1 5  
 cta act gat gac caa att cgc gac aat gag cgg acc gaa gtt cta gct 163  
 Leu Thr Asp Asp Gln Ile Arg Asp Asn Glu Arg Thr Glu Val Leu Ala  
 10 15 20  
 aaa gca act gca gct aag aac atc gtc ccg gat att gca gtg ttg ggc 211  
 Lys Ala Thr Ala Ala Lys Asn Ile Val Pro Asp Ile Ala Val Leu Gly  
 25 30 35  
 acc gga ccg aag aac gca atc ctg cgt gcg gcg gca gat gaa ctc gtt 259  
 Thr Gly Pro Lys Asn Ala Ile Leu Arg Ala Ala Ala Asp Glu Leu Val  
 40 45 50  
 gca cgc agc gca gaa atc atc gaa gcc aac gct tcc gat atc gaa gcg 307  
 Ala Arg Ser Ala Glu Ile Ile Glu Ala Asn Ala Ser Asp Ile Glu Ala  
 55 60 65  
 ggt cgc gca aac ggc atg gaa gaa tcc atg att gat cgc ctt gcc ctt 355  
 Gly Arg Ala Asn Gly Met Glu Glu Ser Met Ile Asp Arg Leu Ala Leu  
 70 75 80 85  
 gat gaa tct cgc att gag ggc atc gct ggc ggt ttg cgc cag gtt gct 403  
 Asp Glu Ser Arg Ile Glu Gly Ile Ala Gly Gly Leu Arg Gln Val Ala  
 90 95 100

Thr Glu Val Leu Ala Lys Ala Thr Ala Ala Lys Asn Ile Val Pro Asp  
 20 25 30  
 Ile Ala Val Leu Gly Thr Gly Pro Lys Asn Ala Ile Leu Arg Ala Ala  
 35 40 45  
 Ala Asp Glu Leu Val Ala Arg Ser Ala Glu Ile Ile Glu Ala Asn Ala  
 50 55 60  
 Ser Asp Ile Glu Ala Gly Arg Ala Asn Gly Met Glu Glu Ser Met Ile  
 65 70 75 80  
 Asp Arg Leu Ala Leu Asp Glu Ser Arg Ile Glu Gly Ile Ala Gly Gly  
 85 90 95  
 Leu Arg Gln Val Ala Gly Leu Thr Asp Pro Val Gly Glu Val Leu Arg  
 100 105 110  
 Gly His Val Met Glu Asn Gly Ile Gln Met Lys Gln Val Arg Val Pro  
 115 120 125  
 Leu Gly Val Met Gly Met Val Tyr Glu Ala Arg Pro Asn Val Thr Val  
 130 135 140  
 Asp Ala Phe Gly Leu Ala Leu Lys Ser Gly Asn Val Ala Leu Leu Arg  
 145 150 155 160  
 Gly Ser Ser Thr Ala Val His Ser Asn Thr Lys Leu Val Glu Ile Leu  
 165 170 175  
 Gln Asp Val Leu Glu Arg Phe Glu Leu Pro Arg Glu Thr Val Gln Leu  
 180 185 190  
 Leu Pro Cys Gln Thr Arg Gly Ser Val Gln Asp Leu Ile Thr Ala Arg  
 195 200 205  
 Gly Leu Val Asp Val Val Ile Pro Arg Gly Gly Ala Gly Leu Ile Asn  
 210 215 220  
 Ala Val Val Thr Gly Ala Thr Val Pro Thr Ile Glu Thr Gly Thr Gly  
 225 230 235 240  
 Asn Cys His Phe Tyr Ile Asp Ala Glu Ala Lys Leu Asp Gln Ala Ile  
 245 250 255  
 Ala Met Val Ile Asn Gly Lys Thr Arg Arg Cys Ser Val Cys Asn Ala  
 260 265 270  
 Thr Glu Thr Ala Leu Leu Asp Ala Ala Leu Ser Asp Ser Asp Lys Leu  
 275 280 285  
 Ala Val Val Gln Ala Leu Gln Glu Ala Gly Val Thr Ile His Gly Arg  
 290 295 300  
 Val Ala Glu Leu Glu Ala Phe Gly Ala Thr Asp Val Val Glu Ala Thr  
 305 310 315 320  
 Glu Thr Asp Trp Asp Ser Glu Tyr Leu Ser Phe Asp Ile Ala Val Ala  
 325 330 335  
 Val Val Asp Gly Val Asp Gly Ala Leu Ala His Ile Ala Lys Tyr Ser

Leu Asp Ala Ala Leu Ser Asp Ser Asp Lys Leu Ala Val Val Gln Ala  
 280 285 290  
 ctc cag gaa gca gga gtc aca att cat gga cgg gtg gcc gaa ttg gaa  
 1027  
 Leu Gln Glu Ala Gly Val Thr Ile His Gly Arg Val Ala Glu Leu Glu  
 295 300 305  
 gca ttc ggt gca acc gac gtg gtg gaa gca act gaa act gac tgg gat  
 1075  
 Ala Phe Gly Ala Thr Asp Val Val Glu Ala Thr Glu Thr Asp Trp Asp  
 310 315 320 325  
 tct gag tac ctg tcc ttc gat atc gct gtc gct gtg gtt gac ggt gtg  
 1123  
 Ser Glu Tyr Leu Ser Phe Asp Ile Ala Val Ala Val Val Asp Gly Val  
 330 335 340  
 gat gga gct ctg gca cac atc gct aag tac agc acc aag cac acc gaa  
 1171  
 Asp Gly Ala Leu Ala His Ile Ala Lys Tyr Ser Thr Lys His Thr Glu  
 345 350 355  
 gcg atc gcc acc caa aac att gaa acc gct cag cgc ttt gca gat cgc  
 1219  
 Ala Ile Ala Thr Gln Asn Ile Glu Thr Ala Gln Arg Phe Ala Asp Arg  
 360 365 370  
 gtc gat gca gca gcg gtg atg ata aac gca tcc acc gcc tac acc gat  
 1267  
 Val Asp Ala Ala Ala Val Met Ile Asn Ala Ser Thr Ala Tyr Thr Asp  
 375 380 385  
 ggg gag cag tac ggc atg ggc gcg gag atc ggc att tcc acc cag aaa  
 1315  
 Gly Glu Gln Tyr Gly Met Gly Ala Glu Ile Gly Ile Ser Thr Gln Lys  
 390 395 400 405  
 ctg cat gca cgt gga cca atg gcc ctg cca gag ctg acc tcc acc aag  
 1363  
 Leu His Ala Arg Gly Pro Met Ala Leu Pro Glu Leu Thr Ser Thr Lys  
 410 415 420  
 tgg att ctg cag ggc aca gga caa att agg cct taagtttgaa gaagtaatca  
 1416  
 Trp Ile Leu Gln Gly Thr Gly Gln Ile Arg Pro  
 425 430  
 agc  
 1419

&lt;210&gt; 292

&lt;211&gt; 432

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 292

Met Ser Ser Thr Thr Leu Thr Asp Asp Gln Ile Arg Asp Asn Glu Arg  
 1 5 10 15

acc gga ccg aag aac gca atc ctg cgt gcg gcg gca gat gaa ctc gtt	259
Thr Gly Pro Lys Asn Ala Ile Leu Arg Ala Ala Ala Asp Glu Leu Val	
40 45 50	
gca cgc agc gca gaa atc atc gaa gcc aac gct tcc gat atc gaa gcg	307
Ala Arg Ser Ala Glu Ile Ile Glu Ala Asn Ala Ser Asp Ile Glu Ala	
55 60 65	
ggt cgc gca aac ggc atg gaa gaa tcc atg att gat cgc ctt gcc ctt	355
Gly Arg Ala Asn Gly Met Glu Glu Ser Met Ile Asp Arg Leu Ala Leu	
70 75 80 85	
gat gaa tct cgc att gag ggc atc gct ggc ggt ttg cgc cag gtt gct	403
Asp Glu Ser Arg Ile Glu Gly Ile Ala Gly Gly Leu Arg Gln Val Ala	
90 95 100	
ggc ctg acc gac cca gtg ggt gaa gta ctg cgc gga cat gtc atg gaa	451
Gly Leu Thr Asp Pro Val Gly Glu Val Leu Arg Gly His Val Met Glu	
105 110 115	
aac ggc att cag atg aag cag gtc cgt gtg cct ttg ggc gtg atg ggc	499
Asn Gly Ile Gln Met Lys Gln Val Arg Val Pro Leu Gly Val Met Gly	
120 125 130	
atg gtc tat gaa gcc cgc cct aac gtc acc gtc gac gcc ttc ggc ctg	547
Met Val Tyr Glu Ala Arg Pro Asn Val Thr Val Asp Ala Phe Gly Leu	
135 140 145	
gca ctc aag tcc gga aac gta gct ttg ctg cgc ggt tcc tcc aca gct	595
Ala Leu Lys Ser Gly Asn Val Ala Leu Leu Arg Gly Ser Ser Thr Ala	
150 155 160 165	
gtg cat tcc aac acc aag ctc gtg gaa atc ctg cag gac gtc ctc gag	643
Val His Ser Asn Thr Lys Leu Val Glu Ile Leu Gln Asp Val Leu Glu	
170 175 180	
cgt ttc gag ctg cca cgc gaa acc gtg cag ttg ctg cct tgc caa acc	691
Arg Phe Glu Leu Pro Arg Glu Thr Val Gln Leu Leu Pro Cys Gln Thr	
185 190 195	
cgc gga tcc gtc caa gat ttg atc acc gca cgc ggc ctc gtt gac gtg	739
Arg Gly Ser Val Gln Asp Leu Ile Thr Ala Arg Gly Leu Val Asp Val	
200 205 210	
gtc atc cca cgc ggc ggc gca gga cta atc aac gca gtg gtc acc ggt	787
Val Ile Pro Arg Gly Gly Ala Gly Leu Ile Asn Ala Val Val Thr Gly	
215 220 225	
gcg acc gtg ccc acc att gaa acc ggc acc ggc aac tgc cac ttc tac	835
Ala Thr Val Pro Thr Ile Glu Thr Gly Thr Gly Asn Cys His Phe Tyr	
230 235 240 245	
atc gat gcc gaa gcc aag ctt gat cag gca atc gcc atg gtc atc aac	883
Ile Asp Ala Glu Ala Lys Leu Asp Gln Ala Ile Ala Met Val Ile Asn	
250 255 260	
ggc aag acc cgc cgc tgc agc gtg tgc aac gct act gaa acc gcg ctt	931
Gly Lys Thr Arg Arg Cys Ser Val Cys Asn Ala Thr Glu Thr Ala Leu	
265 270 275	
ctc gac gcc gcc ctc agc gac tca gac aag ctt gca gtc gtc cag gcg	979



ggc gtc aaa cca gga acc ttc ttc cac ctc aca gaa gta ttc gga cca  
 2659  
 Gly Val Lys Pro Gly Thr Phe Phe His Leu Thr Glu Val Phe Gly Pro  
           840                                  845                                  850

gtc ctc ggc ctg atg aaa gcc acc gac ctc aat gaa gcc atc gaa ttc  
 2707  
 Val Leu Gly Leu Met Lys Ala Thr Asp Leu Asn Glu Ala Ile Glu Phe  
           855                                  860                                  865

caa aac ggc aac gac ttc gga ctc acc ggc gga ctc caa tcc ctc gac  
 2755  
 Gln Asn Gly Asn Asp Phe Gly Leu Thr Gly Gly Leu Gln Ser Leu Asp  
           870                                  875                                  880                                  885

gcc gac gaa gtc cgc acc tgg ctt gac cac gtc gat gtc gga aac gcc  
 2803  
 Ala Asp Glu Val Arg Thr Trp Leu Asp His Val Asp Val Gly Asn Ala  
                                   890                                  895                                  900

tac gtc aac cgc ggc atc acc ggc gcc att gtc caa cgc caa tcc ttc  
 2851  
 Tyr Val Asn Arg Gly Ile Thr Gly Ala Ile Val Gln Arg Gln Ser Phe  
                                   905                                  910                                  915

gga ggc tgg aaa aaa tcc tcc gtc ggc ctc gga tcc aaa gcc gga gga  
 2899  
 Gly Gly Trp Lys Lys Ser Ser Val Gly Leu Gly Ser Lys Ala Gly Gly  
                                   920                                  925                                  930

ccc aac tat gtc atg ctc atg gga acc tgg gcc gac gcg cca agc cac  
 2947  
 Pro Asn Tyr Val Met Leu Met Gly Thr Trp Ala Asp Ala Pro Ser His  
           935                                  940                                  945

cac gcc cca cgc gaa aca aac ccg ctg atc agc aaa ctg gat ctc ccc  
 2995  
 His Ala Pro Arg Glu Thr Asn Pro Leu Ile Ser Lys Leu Asp Leu Pro  
           950                                  955                                  960                                  965

gga gaa gag ctc gaa tgg ctc gaa aaa gcc aac gcc agc gat gaa aca  
 3043  
 Gly Glu Glu Leu Glu Trp Leu Glu Lys Ala Asn Ala Ser Asp Glu Thr  
                                   970                                  975                                  980

gca tgg aac acg gaa ttc ggc agc cca cgc gac ccc tcc ggc ctc gat  
 3091  
 Ala Trp Asn Thr Glu Phe Gly Ser Pro Arg Asp Pro Ser Gly Leu Asp  
                                   985                                  990                                  995

gta gaa gcc aac att ttc cgc tac cga cca gca  
 3124  
 Val Glu Ala Asn Ile Phe Arg Tyr Arg Pro Ala  
           1000                                  1005

<210> 312

<211> 1008

<212> PRT

<213> Corynebacterium glutamicum

ccc tca aag cct agc caa cat tgc tcc gct gca gtg gtc gaa gcc ctc  
 2083  
 Pro Ser Lys Pro Ser Gln His Cys Ser Ala Ala Val Val Glu Ala Leu  
 650 655 660

tgg gaa gcc ggc gtt ccc cgc gag gtt ctg cat tgc att tac cca gct  
 2131  
 Trp Glu Ala Gly Val Pro Arg Glu Val Leu His Cys Ile Tyr Pro Ala  
 665 670 675

aat cgc gat gtt gga tgt gcg ttg atc agc cat gaa cac gtc gac cgc  
 2179  
 Asn Arg Asp Val Gly Cys Ala Leu Ile Ser His Glu His Val Asp Arg  
 680 685 690

gtc att ttg acc ggc tcc tcc gag acc gcc gcg atg ttc tcc tcc tgg  
 2227  
 Val Ile Leu Thr Gly Ser Ser Glu Thr Ala Ala Met Phe Ser Ser Trp  
 695 700 705

cga cca gaa ctc acc atc aac ggc gaa acc tcc ggc aaa aac gcc atc  
 2275  
 Arg Pro Glu Leu Thr Ile Asn Gly Glu Thr Ser Gly Lys Asn Ala Ile  
 710 715 720 725

gtg gtc acc cca tct gcc gac cgc gac ctc gcc gtc gcc gac ctg gtg  
 2323  
 Val Val Thr Pro Ser Ala Asp Arg Asp Leu Ala Val Ala Asp Leu Val  
 730 735 740

aaa tcc gcc ttc ggc cat gca gga caa aaa tgt tcc gca gcc tcc ctc  
 2371  
 Lys Ser Ala Phe Gly His Ala Gly Gln Lys Cys Ser Ala Ala Ser Leu  
 745 750 755

ggc atc ttg gta ggc agc gtc tac gaa tca gaa cgc ttc cgg aaa cag  
 2419  
 Gly Ile Leu Val Gly Ser Val Tyr Glu Ser Glu Arg Phe Arg Lys Gln  
 760 765 770

ctg gta gac gcc gca tcc tca ctc atc gtc gac tgg cct acc aac ccc  
 2467  
 Leu Val Asp Ala Ala Ser Ser Leu Ile Val Asp Trp Pro Thr Asn Pro  
 775 780 785

tcc gca acc gtc gga cca ctc acc gaa ctc ccc agc gat aaa ctc cac  
 2515  
 Ser Ala Thr Val Gly Pro Leu Thr Glu Leu Pro Ser Asp Lys Leu His  
 790 795 800 805

cac gcc cta acc acc ctc gaa gaa gga gaa agc tgg ctg ctg aaa ccc  
 2563  
 His Ala Leu Thr Thr Leu Glu Glu Gly Glu Ser Trp Leu Leu Lys Pro  
 810 815 820

cga caa ctc gac gac acc ggc cga ctc tgg tca ccc ggc atc aaa gaa  
 2611  
 Arg Gln Leu Asp Asp Thr Gly Arg Leu Trp Ser Pro Gly Ile Lys Glu  
 825 830 835

ctc atc gac gtg ccc gcg ccc ggc ccc aac cac aca caa gac cgc agc  
1507

Leu Ile Asp Val Pro Ala Pro Gly Pro Asn His Thr Gln Asp Arg Ser  
455 460 465

aaa gag acg ctt ctc gac gcc ccc ctc gtc cca ttt atc aac gag ccc  
1555

Lys Glu Thr Leu Leu Asp Ala Pro Leu Val Pro Phe Ile Asn Glu Pro  
470 475 480 485

gac acc aac cca gcg ctc atc caa aac caa cag tgg gcc aca aaa gcc  
1603

Asp Thr Asn Pro Ala Leu Ile Gln Asn Gln Gln Trp Ala Thr Lys Ala  
490 495 500

gtc gcc acc gca gca gag ccc ggt tgg ttg gaa aaa caa aca aag ccg  
1651

Val Ala Thr Ala Ala Glu Pro Gly Trp Leu Glu Lys Gln Thr Lys Pro  
505 510 515

gag gtg ttg gaa gag ggg gac gtc gac aag cta att aac gat gtg cgc  
1699

Glu Val Leu Glu Glu Gly Asp Val Asp Lys Leu Ile Asn Asp Val Arg  
520 525 530

gac gct gct gaa gcg tgg gca gcg cgc cca gcc cgt gaa cgc gct gag  
1747

Asp Ala Ala Glu Ala Trp Ala Ala Arg Pro Ala Arg Glu Arg Ala Glu  
535 540 545

att ttg tac aag acc gcc gag att ttg cgc gtg cga cgc gga cac ctg  
1795

Ile Leu Tyr Lys Thr Ala Glu Ile Leu Arg Val Arg Arg Gly His Leu  
550 555 560 565

atc tca gtg acg gcc gcg gag gtg ggc aaa gct gtg gaa caa acc gac  
1843

Ile Ser Val Thr Ala Ala Glu Val Gly Lys Ala Val Glu Gln Thr Asp  
570 575 580

ccg gaa atc tct gaa gcc att gat ttc gcc cgc tac tac gcg cat ttg  
1891

Pro Glu Ile Ser Glu Ala Ile Asp Phe Ala Arg Tyr Tyr Ala His Leu  
585 590 595

gcc ctg gaa ttg gac gac gta gac aat gcg gaa ttc acc cca gat cgc  
1939

Ala Leu Glu Leu Asp Asp Val Asp Asn Ala Glu Phe Thr Pro Asp Arg  
600 605 610

gtc gtt gtg gtg acc ccg ccc tgg aat ttc ccc atc gcg atc ccc gct  
1987

Val Val Val Val Thr Pro Pro Trp Asn Phe Pro Ile Ala Ile Pro Ala  
615 620 625

gga tcg act ttc gca gca ctc gcg gcg ggc gct ggc gtg atc cac aaa  
2035

Gly Ser Thr Phe Ala Ala Leu Ala Ala Gly Ala Gly Val Ile His Lys  
630 635 640 645

Asn Pro Glu Leu His Glu Leu Glu Ala Gly Ile Val Leu Gln Ala Tyr  
 250 255 260  
 ctt ccc gat gcc ctc ggt gca atc cag gac ttg gcg cag ttc ggc cgc 931  
 Leu Pro Asp Ala Leu Gly Ala Ile Gln Asp Leu Ala Gln Phe Gly Arg  
 265 270 275  
 gag cgc gtc aac aca ggc ggg gcg ggc gtt aag gtt cgc ctg gtc aag 979  
 Glu Arg Val Asn Thr Gly Gly Ala Gly Val Lys Val Arg Leu Val Lys  
 280 285 290  
 ggt gct aat ttg cct atg gag cac gtc cac gcg cag atc acc ggc tgg  
 1027  
 Gly Ala Asn Leu Pro Met Glu His Val His Ala Gln Ile Thr Gly Trp  
 295 300 305  
 cca gtt gcc aca gaa cct tcc aaa caa gcc acc gat gcc aat tac aag  
 1075  
 Pro Val Ala Thr Glu Pro Ser Lys Gln Ala Thr Asp Ala Asn Tyr Lys  
 310 315 320 325  
 cgc gtc ctc tat tgg acg atg cgc aaa gaa aac atg gag ggc ctg cgc  
 1123  
 Arg Val Leu Tyr Trp Thr Met Arg Lys Glu Asn Met Glu Gly Leu Arg  
 330 335 340  
 ctg ggc gtt gcc ggc cac aac ctt ttc gac ata gca ttc gca cat ttg  
 1171  
 Leu Gly Val Ala Gly His Asn Leu Phe Asp Ile Ala Phe Ala His Leu  
 345 350 355  
 ctc tct gtg gag cgt ggg gta gcg gac cgt gtg gag ttc gaa atg ctg  
 1219  
 Leu Ser Val Glu Arg Gly Val Ala Asp Arg Val Glu Phe Glu Met Leu  
 360 365 370  
 cag ggc atg gcg tcc gat cag gcg cgc gcc gtc agc gtt gac gtc ggt  
 1267  
 Gln Gly Met Ala Ser Asp Gln Ala Arg Ala Val Ser Val Asp Val Gly  
 375 380 385  
 gag ctg ctg ctt tac gta cca gcc gtg gcg cca caa gaa ttc gac gtg  
 1315  
 Glu Leu Leu Leu Tyr Val Pro Ala Val Arg Pro Gln Glu Phe Asp Val  
 390 395 400 405  
 gcc att tct tac ctc gtg cgc cgc ctc gag gaa aac gcc gcg agc gaa  
 1363  
 Ala Ile Ser Tyr Leu Val Arg Arg Leu Glu Glu Asn Ala Ala Ser Glu  
 410 415 420  
 aac ttc atg tcc gcc atc ttc gac ctc gac gcc gac aac ccg tcc ttc  
 1411  
 Asn Phe Met Ser Ala Ile Phe Asp Leu Asp Ala Asp Asn Pro Ser Phe  
 425 430 435  
 aag cga gag gag agc cgc ttc cgc gcc tcc ata tct gac ctc gcc acg  
 1459  
 Lys Arg Glu Glu Ser Arg Phe Arg Ala Ser Ile Ser Asp Leu Ala Thr  
 440 445 450

ctg cct att gag ttg gct acg ctg tct gac cag gct gtg gac aag gtg	163
Leu Pro Ile Glu Leu Ala Thr Leu Ser Asp Gln Ala Val Asp Lys Val	
10 15 20	
cgc tcc tgg ctg gag tac agc aaa aag gaa agc gtg ccc aat gcc gat	211
Arg Ser Trp Leu Glu Tyr Ser Lys Lys Glu Ser Val Pro Asn Ala Asp	
25 30 35	
gcg aag cgt cta gct gca gtg ttg cag gat cct aat ggt ttg gaa ttc	259
Ala Lys Arg Leu Ala Ala Val Leu Gln Asp Pro Asn Gly Leu Glu Phe	
40 45 50	
acg gtt ggt ttc gtg gat cga gtg gtt cga act gag gat cgt gaa gcg	307
Thr Val Gly Phe Val Asp Arg Val Val Arg Thr Glu Asp Arg Glu Ala	
55 60 65	
gca gcg cat gcg ttg tat gag ttg ggc aag att gct ccg tcg acg atg	355
Ala Ala His Ala Leu Tyr Glu Leu Gly Lys Ile Ala Pro Ser Thr Met	
70 75 80 85	
tcc ttt ttg gat cgg gcg cag att cag gcc ggt tct ttg gtg ggg cgg	403
Ser Phe Leu Asp Arg Ala Gln Ile Gln Ala Gly Ser Leu Val Gly Arg	
90 95 100	
gcg ttg ccg cag gtt gtg gtt cct gcg gcg cgg gct cga atc cgg cag	451
Ala Leu Pro Gln Val Val Val Pro Ala Ala Arg Ala Arg Ile Arg Gln	
105 110 115	
atg gtt ggg cac atg att gtg gat gcc cgc gac aag cag ttc gcc aag	499
Met Val Gly His Met Ile Val Asp Ala Arg Asp Lys Gln Phe Ala Lys	
120 125 130	
gct gtc gct gag att cag tcg gat ggg cac cgc ctg aac atc aat ttg	547
Ala Val Ala Glu Ile Gln Ser Asp Gly His Arg Leu Asn Ile Asn Leu	
135 140 145	
cta ggt gaa gcg gtg ttg ggc cga aag gaa gca gcg aag cat ttg gat	595
Leu Gly Glu Ala Val Leu Gly Arg Lys Glu Ala Ala Lys His Leu Asp	
150 155 160 165	
gac acg gtg cgg ttg ttg cgc cgt ccg gat gtg gaa tat gtg tcn nnn	643
Asp Thr Val Arg Leu Leu Arg Arg Pro Asp Val Glu Tyr Val Ser Xaa	
170 175 180	
nnn ntc tct tcg gtg gca tcg cag att tcg atg tgg ggt ttc gaa gac	691
Xaa Xaa Ser Ser Val Ala Ser Gln Ile Ser Met Trp Gly Phe Glu Asp	
185 190 195	
acc gtt aat tat gtt gtg gaa cag ctg aca cct tta tat ata gag ccc	739
Thr Val Asn Tyr Val Val Glu Gln Leu Thr Pro Leu Tyr Ile Glu Pro	
200 205 210	
gcg cgg gcg ccg aaa ggc acg aag ttc atc aac ctg gac atg gag gaa	787
Ala Arg Ala Pro Lys Gly Thr Lys Phe Ile Asn Leu Asp Met Glu Glu	
215 220 225	
tac cgc gat ctg cgc ctg act atg gag gtg ttc aag cgg ctg ctc tcc	835
Tyr Arg Asp Leu Arg Leu Thr Met Glu Val Phe Lys Arg Leu Leu Ser	
230 235 240 245	
aat cca gag ctg cat gaa cta gaa gcc gga att gtg ttg cag gcg tac	883

130                                      135                                      140  
 ttg gcg gag gaa ctt aaa cgt tgatcggtttt gcgcatgggt cgc 476  
 Leu Ala Glu Glu Leu Lys Arg  
 145                                      150  
  
 <210> 310  
 <211> 151  
 <212> PRT  
 <213> Corynebacterium glutamicum  
  
 <400> 310  
 His Phe Pro Leu Arg Pro Ala Glu Val Val Leu Arg Leu Asp Asp Ser  
   1                                      5                                      10                                      15  
 Ala Thr Pro Arg Glu Thr Ala Arg Ala Leu Leu Ala Ala Arg Arg Ala  
                                     20                                      25                                      30  
 Gly Val Thr Pro Arg Val Leu Gln Thr Pro Gly Val Ser Glu Gln Val  
                                     35                                      40                                      45  
 Arg Glu Val Leu Ser Ala Ala Gly Val Ser Ala Glu Thr Val Asp Asp  
   50                                      55                                      60  
 Ser Val Phe Ile Ser Asn Val Leu Arg Gly Glu Tyr Asp Glu Asn Ser  
   65                                      70                                      75                                      80  
 Ser Val Arg Val Arg Tyr Leu Gly Lys Val Ser Asp Thr Val Arg Glu  
                                     85                                      90                                      95  
 Arg Leu Ser Val Arg Pro Glu Val Val Leu Leu Asp Asp Ala Val Thr  
                                     100                                      105                                      110  
 Ala Ser Gly Arg Val Glu Leu Arg Tyr Trp Leu Lys Glu Gln Ala Ile  
                                     115                                      120                                      125  
 Ser Met Thr Leu His Arg Phe Gly Asn Pro Val Ala Ala Phe His Glu  
   130                                      135                                      140  
 Leu Ala Glu Glu Leu Lys Arg  
 145                                      150  
  
 <210> 311  
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 <213> Corynebacterium glutamicum  
  
 <220>  
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 <222> (101)..(3124)  
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                                     1                                      5

Gly Lys Val Ser Asp Thr Val Arg Glu Arg Leu Ser Val Arg Pro Glu  
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Arg Tyr Trp Leu Lys Glu Gln Ala Ile Ser Met Thr Leu His Arg Phe  
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Ala Thr Pro Arg Glu Thr Ala Arg Ala Leu Leu Ala Ala Arg Arg Ala	
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Gly Val Thr Pro Arg Val Leu Gln Thr Pro Gly Val Ser Glu Gln Val	
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cgc gaa gta ttg tcc gct gct gga gtg agt gca gaa aca gtc gat gat	192
Arg Glu Val Leu Ser Ala Ala Gly Val Ser Ala Glu Thr Val Asp Asp	
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tcg gta ttt att tcc aac gtg ttg cgc ggc gaa tac gac gag aac tcc	240
Ser Val Phe Ile Ser Asn Val Leu Arg Gly Glu Tyr Asp Glu Asn Ser	
65 70 75 80	
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Ser Val Arg Val Arg Tyr Leu Gly Lys Val Ser Asp Thr Val Arg Glu	
85 90 95	
cgc cta tct gta cgg ccc gaa gtt gtt ctg ctt gac gat gca gta act	336
Arg Leu Ser Val Arg Pro Glu Val Val Leu Leu Asp Asp Ala Val Thr	
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gcc tcc ggt cga gtt gaa tta cgt tac tgg ctc aaa gaa caa gca att	384
Ala Ser Gly Arg Val Glu Leu Arg Tyr Trp Leu Lys Glu Gln Ala Ile	
115 120 125	
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Ser Met Thr Leu His Arg Phe Gly Asn Pro Val Ala Ala Phe His Glu	

Arg Phe Arg Lys Gln Leu Val Asp Ala Ala Ser Ser Leu Ile Val Asp  
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 Trp Pro Thr Asn Pro Ser Ala Thr Val Gly Pro Leu Thr Glu Leu Pro  
 785 790 795 800  
 Ser Asp Lys Leu His His Ala Leu Thr Thr Leu Glu Glu Gly Glu Ser  
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 Trp Leu Leu Lys Pro Arg Gln Leu Asp Asp Thr Gly Arg Leu Trp Ser  
 820 825 830  
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 Glu Val Phe Gly Pro Val Leu Gly Leu Met Lys Ala Thr Asp Leu Asn  
 850 855 860  
 Glu Ala Ile Glu Phe Gln Asn Gly Asn Asp Phe Gly Leu Thr Gly Gly  
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 Leu Gln Ser Leu Asp Ala Asp Glu Val Arg Thr Trp Leu Asp His Val  
 885 890 895  
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 Gln Arg Gln Ser Phe Gly Gly Trp Lys Lys Ser Ser Val Gly Leu Gly  
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 Ser Lys Ala Gly Gly Pro Asn Tyr Val Met Leu Met Gly Thr Trp Ala  
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 980 985 990  
 Pro Ser Gly Leu Asp Val Glu Ala Asn Ile Phe Arg Tyr Arg Pro Ala  
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 Gly Val Ser Ala Glu Thr Val Asp Asp Ser Val Phe Ile Ser Asn Val  
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 Leu Arg Gly Glu Tyr Asp Glu Asn Ser Ser Val Arg Val Arg Tyr Leu  
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Thr	Gln	Asp	Arg	Ser	Lys	Glu	Thr	Leu	Leu	Asp	Ala	Pro	Leu	Val	Pro
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Phe	Ile	Asn	Glu	Pro	Asp	Thr	Asn	Pro	Ala	Leu	Ile	Gln	Asn	Gln	Gln
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Trp	Ala	Thr	Lys	Ala	Val	Ala	Thr	Ala	Ala	Glu	Pro	Gly	Trp	Leu	Glu
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Lys	Gln	Thr	Lys	Pro	Glu	Val	Leu	Glu	Glu	Gly	Asp	Val	Asp	Lys	Leu
		515					520					525			
Ile	Asn	Asp	Val	Arg	Asp	Ala	Ala	Glu	Ala	Trp	Ala	Ala	Arg	Pro	Ala
	530					535					540				
Arg	Glu	Arg	Ala	Glu	Ile	Leu	Tyr	Lys	Thr	Ala	Glu	Ile	Leu	Arg	Val
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Arg	Arg	Gly	His	Leu	Ile	Ser	Val	Thr	Ala	Ala	Glu	Val	Gly	Lys	Ala
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Val	Glu	Gln	Thr	Asp	Pro	Glu	Ile	Ser	Glu	Ala	Ile	Asp	Phe	Ala	Arg
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Tyr	Tyr	Ala	His	Leu	Ala	Leu	Glu	Leu	Asp	Asp	Val	Asp	Asn	Ala	Glu
		595					600					605			
Phe	Thr	Pro	Asp	Arg	Val	Val	Val	Val	Thr	Pro	Pro	Trp	Asn	Phe	Pro
	610					615						620			
Ile	Ala	Ile	Pro	Ala	Gly	Ser	Thr	Phe	Ala	Ala	Leu	Ala	Ala	Gly	Ala
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Gly	Val	Ile	His	Lys	Pro	Ser	Lys	Pro	Ser	Gln	His	Cys	Ser	Ala	Ala
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Val	Val	Glu	Ala	Leu	Trp	Glu	Ala	Gly	Val	Pro	Arg	Glu	Val	Leu	His
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Cys	Ile	Tyr	Pro	Ala	Asn	Arg	Asp	Val	Gly	Cys	Ala	Leu	Ile	Ser	His
		675					680					685			
Glu	His	Val	Asp	Arg	Val	Ile	Leu	Thr	Gly	Ser	Ser	Glu	Thr	Ala	Ala
		690				695					700				
Met	Phe	Ser	Ser	Trp	Arg	Pro	Glu	Leu	Thr	Ile	Asn	Gly	Glu	Thr	Ser
705					710					715					720
Gly	Lys	Asn	Ala	Ile	Val	Val	Thr	Pro	Ser	Ala	Asp	Arg	Asp	Leu	Ala
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Val	Ala	Asp	Leu	Val	Lys	Ser	Ala	Phe	Gly	His	Ala	Gly	Gln	Lys	Cys
			740					745					750		
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Ala Arg Ile Arg Gln Met Val Gly His Met Ile Val Asp Ala Arg Asp  
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 Lys Gln Phe Ala Lys Ala Val Ala Glu Ile Gln Ser Asp Gly His Arg  
 130 135 140  
 Leu Asn Ile Asn Leu Leu Gly Glu Ala Val Leu Gly Arg Lys Glu Ala  
 145 150 155 160  
 Ala Lys His Leu Asp Asp Thr Val Arg Leu Leu Arg Arg Pro Asp Val  
 165 170 175  
 Glu Tyr Val Ser Ile Lys Val Ser Ser Val Ala Ser Gln Ile Ser Met  
 180 185 190  
 Trp Gly Phe Glu Asp Thr Val Asn Tyr Val Val Glu Gln Leu Thr Pro  
 195 200 205  
 Leu Tyr Ile Glu Ala Ala Arg Ala Pro Lys Gly Thr Lys Phe Ile Asn  
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 Leu Asp Met Glu Glu Tyr Arg Asp Leu Arg Leu Thr Met Glu Val Phe  
 225 230 235 240  
 Lys Arg Leu Leu Ser Asn Pro Glu Leu His Glu Leu Glu Ala Gly Ile  
 245 250 255  
 Val Leu Gln Ala Tyr Leu Pro Asp Ala Leu Gly Ala Ile Gln Asp Leu  
 260 265 270  
 Ala Gln Phe Gly Arg Glu Arg Val Asn Thr Gly Gly Ala Gly Val Lys  
 275 280 285  
 Val Arg Leu Val Lys Gly Ala Asn Leu Pro Met Glu His Val His Ala  
 290 295 300  
 Gln Ile Thr Gly Trp Pro Val Ala Thr Glu Pro Ser Lys Gln Ala Thr  
 305 310 315 320  
 Asp Ala Asn Tyr Lys Arg Val Leu Tyr Trp Thr Met Arg Lys Glu Asn  
 325 330 335  
 Met Glu Gly Leu Arg Leu Gly Val Ala Gly His Asn Leu Phe Asp Ile  
 340 345 350  
 Ala Phe Ala His Leu Leu Ser Val Glu Arg Gly Val Ala Asp Arg Val  
 355 360 365  
 Glu Phe Glu Met Leu Gln Gly Met Ala Ser Asp Gln Ala Arg Ala Val  
 370 375 380  
 Ser Val Asp Val Gly Glu Leu Leu Leu Tyr Val Pro Ala Val Arg Pro  
 385 390 395 400  
 Gln Glu Phe Asp Val Ala Ile Ser Tyr Leu Val Arg Arg Leu Glu Glu  
 405 410 415  
 Asn Ala Ala Ser Glu Asn Phe Met Ser Ala Ile Phe Asp Leu Asp Ala  
 420 425 430  
 Asp Asn Pro Ser Phe Lys Arg Glu Glu Ser Arg Phe Arg Ala Ser Ile

aca gtc gat gat tcg gta ttt att tcc aac gtg ttg cgc ggc gaa tac  
3331

Thr Val Asp Asp Ser Val Phe Ile Ser Asn Val Leu Arg Gly Glu Tyr  
1065 1070 1075

gac gag aac tcc agc gtc cga gtc cgc tac ctg ggc aaa gtt agc gac  
3379

Asp Glu Asn Ser Ser Val Arg Val Arg Tyr Leu Gly Lys Val Ser Asp  
1080 1085 1090

act gtc cgt gaa cgc cta tct gta cgg ccc gaa gtt gtt ctg ctt gac  
3427

Thr Val Arg Glu Arg Leu Ser Val Arg Pro Glu Val Val Leu Leu Asp  
1095 1100 1105

gat gca gta act gcc tcc ggt cga gtt gaa tta cgt tac tgg ctc aaa  
3475

Asp Ala Val Thr Ala Ser Gly Arg Val Glu Leu Arg Tyr Trp Leu Lys  
1110 1115 1120 1125

gaa caa gca att tcc atg acg ttg cac cgt ttt gga aac cca gtt gcg  
3523

Glu Gln Ala Ile Ser Met Thr Leu His Arg Phe Gly Asn Pro Val Ala  
1130 1135 1140

gcc ttc cac gag ttg gcg gag gaa ctt aaa cgt tgatcgtttt gcgcatgggt  
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1145 1150

cgc  
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35 40 45

Asn Gly Leu Glu Phe Thr Val Gly Phe Val Asp Arg Val Val Arg Thr  
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Glu Asp Arg Glu Ala Ala Ala His Ala Leu Tyr Glu Leu Gly Lys Ile  
65 70 75 80

Ala Pro Ser Thr Met Ser Phe Leu Asp Arg Ala Gln Ile Gln Ala Gly  
85 90 95

Ser Leu Val Gly Arg Ala Leu Pro Gln Val Val Val Pro Ala Ala Arg  
100 105 110

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 Gln Asn Gly Asn Asp Phe Gly Leu Thr Gly Gly Leu Gln Ser Leu Asp  
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 Ala Asp Glu Val Arg Thr Trp Leu Asp His Val Asp Val Gly Asn Ala  
 890 895 900  
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 gga ggc tgg aaa aaa tcc tcc gtc ggc ctc gga tcc aaa gcc gga gga  
 2899  
 Gly Gly Trp Lys Lys Ser Ser Val Gly Leu Gly Ser Lys Ala Gly Gly  
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 2947  
 Pro Asn Tyr Val Met Leu Met Gly Thr Trp Ala Asp Ala Pro Ser His  
 935 940 945  
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 2995  
 His Ala Pro Arg Glu Thr Asn Pro Leu Ile Ser Lys Leu Asp Leu Pro  
 950 955 960 965  
 gga gaa gag ctc gaa tgg ctc gaa aaa gcc aac gcc agc gat gaa aca  
 3043  
 Gly Glu Glu Leu Glu Trp Leu Glu Lys Ala Asn Ala Ser Asp Glu Thr  
 970 975 980  
 gca tgg aac acg gaa ttc ggc agc cca cgc gac ccc tcc ggc ctc gat  
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 Ala Trp Asn Thr Glu Phe Gly Ser Pro Arg Asp Pro Ser Gly Leu Asp  
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 gta gaa gcc aac att ttc cgc tac cga cca gca gag gta gta ctc cga  
 3139  
 Val Glu Ala Asn Ile Phe Arg Tyr Arg Pro Ala Glu Val Val Leu Arg  
 1000 1005 1010  
 ctc gac gat tcc gcc aca ccc cga gaa act gcc cgc gca ttg ttg gca  
 3187  
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 1015 1020 1025  
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 3235  
 Ala Arg Arg Ala Gly Val Thr Pro Arg Val Leu Gln Thr Pro Gly Val  
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 tca gag caa gtc cgc gaa gta ttg tcc gct gct gga gtg agt gca gaa  
 3283  
 Ser Glu Gln Val Arg Glu Val Leu Ser Ala Ala Gly Val Ser Ala Glu  
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665					670					675				
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2179														
Asn	Arg	Asp	Val	Gly	Cys	Ala	Leu	Ile	Ser	His	Glu	His	Val	Asp
		680					685					690		Arg
gtc att ttg acc ggc tcc tcc gag acc gcc gcg atg ttc tcc tcc tgg														
2227														
Val	Ile	Leu	Thr	Gly	Ser	Ser	Glu	Thr	Ala	Ala	Met	Phe	Ser	Ser
	695					700					705			Trp
cga cca gaa ctc acc atc aac ggc gaa acc tcc ggc aaa aac gcc atc														
2275														
Arg	Pro	Glu	Leu	Thr	Ile	Asn	Gly	Glu	Thr	Ser	Gly	Lys	Asn	Ala
	710					715					720			725
gtg gtc acc cca tct gcc gac cgc gac ctc gcc gtc gcc gac ctg gtg														
2323														
Val	Val	Thr	Pro	Ser	Ala	Asp	Arg	Asp	Leu	Ala	Val	Ala	Asp	Leu
				730					735					740
aaa tcc gcc ttc ggc cat gca gga caa aaa tgt tcc gca gcc tcc ctc														
2371														
Lys	Ser	Ala	Phe	Gly	His	Ala	Gly	Gln	Lys	Cys	Ser	Ala	Ala	Ser
			745					750					755	Leu
ggc atc ttg gta ggc agc gtc tac gaa tca gaa cgc ttc cgg aaa cag														
2419														
Gly	Ile	Leu	Val	Gly	Ser	Val	Tyr	Glu	Ser	Glu	Arg	Phe	Arg	Lys
		760					765					770		Gln
ctg gta gac gcc gca tcc tca ctc atc gtc gac tgg cct acc aac ccc														
2467														
Leu	Val	Asp	Ala	Ala	Ser	Ser	Leu	Ile	Val	Asp	Trp	Pro	Thr	Asn
		775					780				785			Pro
tcc gca acc gtc gga cca ctc acc gaa ctc ccc agc gat aaa ctc cac														
2515														
Ser	Ala	Thr	Val	Gly	Pro	Leu	Thr	Glu	Leu	Pro	Ser	Asp	Lys	Leu
						795					800			805
cac gcc cta acc acc ctc gaa gaa gga gaa agc tgg ctg ctg aaa ccc														
2563														
His	Ala	Leu	Thr	Thr	Leu	Glu	Glu	Gly	Glu	Ser	Trp	Leu	Leu	Lys
				810					815					820
cga caa ctc gac gac acc ggc cga ctc tgg tca ccc ggc atc aaa gaa														
2611														
Arg	Gln	Leu	Asp	Asp	Thr	Gly	Arg	Leu	Trp	Ser	Pro	Gly	Ile	Lys
			825					830					835	Glu
ggc gtc aaa cca gga acc ttc ttc cac ctc aca gaa gta ttc gga cca														
2659														
Gly	Val	Lys	Pro	Gly	Thr	Phe	Phe	His	Leu	Thr	Glu	Val	Phe	Gly
		840					845					850		Pro
gtc ctc ggc ctg atg aaa gcc acc gac ctc aat gaa gcc atc gaa ttc														
2707														
Val	Leu	Gly	Leu	Met	Lys	Ala	Thr	Asp	Leu	Asn	Glu	Ala	Ile	Glu
		855					860					865		Phe

Lys Glu Thr Leu Leu Asp Ala Pro Leu Val Pro Phe Ile Asn Glu Pro  
 470 475 480 485  
 gac acc aac cca gcg ctc atc caa aac caa cag tgg gcc aca aaa gcc  
 1603  
 Asp Thr Asn Pro Ala Leu Ile Gln Asn Gln Gln Trp Ala Thr Lys Ala  
 490 495 500  
 gtc gcc acc gca gca gag ccc ggt tgg ttg gaa aaa caa aca aag ccg  
 1651  
 Val Ala Thr Ala Ala Glu Pro Gly Trp Leu Glu Lys Gln Thr Lys Pro  
 505 510 515  
 gag gtg ttg gaa gag ggg gac gtc gac aag cta att aac gat gtg cgc  
 1699  
 Glu Val Leu Glu Glu Gly Asp Val Asp Lys Leu Ile Asn Asp Val Arg  
 520 525 530  
 gac gct gct gaa gcg tgg gca gcg cgc cca gcc cgt gaa cgc gct gag  
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 535 540 545  
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 1795  
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 550 555 560 565  
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 1843  
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 1891  
 Pro Glu Ile Ser Glu Ala Ile Asp Phe Ala Arg Tyr Tyr Ala His Leu  
 585 590 595  
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 1939  
 Ala Leu Glu Leu Asp Asp Val Asp Asn Ala Glu Phe Thr Pro Asp Arg  
 600 605 610  
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 1987  
 Val Val Val Val Thr Pro Pro Trp Asn Phe Pro Ile Ala Ile Pro Ala  
 615 620 625  
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 2035  
 Gly Ser Thr Phe Ala Ala Leu Ala Ala Gly Ala Gly Val Ile His Lys  
 630 635 640 645  
 ccc tca aag cct agc caa cat tgc tcc gct gca gtg gtc gaa gcc ctc  
 2083  
 Pro Ser Lys Pro Ser Gln His Cys Ser Ala Ala Val Val Glu Ala Leu  
 650 655 660  
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 2131  
 Trp Glu Ala Gly Val Pro Arg Glu Val Leu His Cys Ile Tyr Pro Ala

gag cgc gtc aac aca ggc ggg gcg ggc gtt aag gtt cgc ctg gtc aag 979  
 Glu Arg Val Asn Thr Gly Gly Ala Gly Val Lys Val Arg Leu Val Lys  
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 1027  
 Gly Ala Asn Leu Pro Met Glu His Val His Ala Gln Ile Thr Gly Trp  
 295 300 305

cca gtt gcc aca gaa cct tcc aaa caa gcc acc gat gcc aat tac aag  
 1075  
 Pro Val Ala Thr Glu Pro Ser Lys Gln Ala Thr Asp Ala Asn Tyr Lys  
 310 315 320 325

cgc gtc ctc tat tgg acg atg cgc aaa gaa aac atg gag ggc ctg cgc  
 1123  
 Arg Val Leu Tyr Trp Thr Met Arg Lys Glu Asn Met Glu Gly Leu Arg  
 330 335 340

ctg ggc gtt gcc ggc cac aac ctt ttc gac ata gca ttc gca cat ttg  
 1171  
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 345 350 355

ctc tct gtg gag cgt ggg gta gcg gac cgt gtg gag ttc gaa atg ctg  
 1219  
 Leu Ser Val Glu Arg Gly Val Ala Asp Arg Val Glu Phe Glu Met Leu  
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cag ggc atg gcg tcc gat cag gcg cgc gcc gtc agc gtt gac gtc ggt  
 1267  
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 375 380 385

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 1411  
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 1507  
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 455 460 465

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 55 60 65

gca gcg cat gcg ttg tat gag ttg ggc aag att gct ccg tcg acg atg 355  
 Ala Ala His Ala Leu Tyr Glu Leu Gly Lys Ile Ala Pro Ser Thr Met  
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 Ser Phe Leu Asp Arg Ala Gln Ile Gln Ala Gly Ser Leu Val Gly Arg  
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gcg ttg ccg cag gtt gtg gtt cct gcg gcg cgg gct cga atc cgg cag 451  
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 Met Val Gly His Met Ile Val Asp Ala Arg Asp Lys Gln Phe Ala Lys  
 120 125 130

gct gtc gct gag att cag tcg gat ggg cac cgc ctg aac atc aat ttg 547  
 Ala Val Ala Glu Ile Gln Ser Asp Gly His Arg Leu Asn Ile Asn Leu  
 135 140 145

cta ggt gaa gcg gtg ttg ggc cga aag gag gca gcg aag cat ttg gat 595  
 Leu Gly Glu Ala Val Leu Gly Arg Lys Glu Ala Ala Lys His Leu Asp  
 150 155 160 165

gac acg gtg cgg ttg ttg cgc cgt ccg gat gtg gaa tat gtg tcc atc 643  
 Asp Thr Val Arg Leu Leu Arg Arg Pro Asp Val Glu Tyr Val Ser Ile  
 170 175 180

aag gtc tct tcg gtg gca tcg cag att tcg atg tgg ggt ttc gaa gac 691  
 Lys Val Ser Ser Val Ala Ser Gln Ile Ser Met Trp Gly Phe Glu Asp  
 185 190 195

acc gtt aat tat gtt gtg gaa cag ctg aca cct tta tat ata gag gcc 739  
 Thr Val Asn Tyr Val Val Glu Gln Leu Thr Pro Leu Tyr Ile Glu Ala  
 200 205 210

gcg cgg gcg ccg aaa ggc acg aag ttc atc aac ctg gac atg gag gaa 787  
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 215 220 225

tac cgc gat ctg cgc ctg act atg gag gtg ttc aag cgg ctg ctc tcc 835  
 Tyr Arg Asp Leu Arg Leu Thr Met Glu Val Phe Lys Arg Leu Leu Ser  
 230 235 240 245

aat cca gag ctg cat gaa cta gaa gcc gga att gtg ttg cag gcg tac 883  
 Asn Pro Glu Leu His Glu Leu Glu Ala Gly Ile Val Leu Gln Ala Tyr  
 250 255 260

ctt ccc gat gcc ctc ggt gca atc cag gac ttg gcg cag ttc ggc cgc 931  
 Leu Pro Asp Ala Leu Gly Ala Ile Gln Asp Leu Ala Gln Phe Gly Arg  
 265 270 275



Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly  
 225 230 235 240  
 Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys  
 245 250 255  
 Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe  
 260 265 270  
 Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe  
 275 280 285  
 Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala  
 290 295 300  
 Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly  
 305 310 315 320  
 Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala  
 325 330 335  
 Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile  
 340 345 350  
 Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu  
 355 360 365  
 Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile  
 370 375 380  
 Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala  
 385 390 395 400  
 Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly  
 405 410

<210> 307  
 <211> 3579  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(3556)  
 <223> RXN00023

<400> 307  
 gggattatgt tggggggccac atctgaaaat agttgctggg atccatcaca cctacgatgc 60  
 gaaacggcac ccacaccgct gatcttgaag gagaaccacc atg acg tcg atg aat 115  
 Met Thr Ser Met Asn  
 1 5  
 ctg cct att gag ttg gct acg ctg tct gac cag gct gtg gac aag gtg 163  
 Leu Pro Ile Glu Leu Ala Thr Leu Ser Asp Gln Ala Val Asp Lys Val  
 10 15 20  
 cgc tcc tgg ctg gag tac agc aaa aag gaa agc gtg ccc aat gcc gat 211  
 Arg Ser Trp Leu Glu Tyr Ser Lys Lys Glu Ser Val Pro Asn Ala Asp  
 25 30 35

375

380

385

gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa  
1315

Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu  
390 395 400 405

ttc aag gaa cgc ggc  
1330

Phe Lys Glu Arg Gly  
410

&lt;210&gt; 306

&lt;211&gt; 410

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 306

Leu Ala Leu Lys Gly Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe  
1 5 10 15

Gly Ser Val Gln Ala Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp  
20 25 30

Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro  
35 40 45

Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly  
50 55 60

Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly  
65 70 75 80

His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg  
85 90 95

Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val  
100 105 110

Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe  
115 120 125

Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala  
130 135 140

Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr  
145 150 155 160

His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg  
165 170 175

Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro  
180 185 190

Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Cys  
195 200 205

Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala  
210 215 220

Asp Val Ser Val Val Ser Ile Thr Gly Val Ser Gly Ala Gly Lys Lys  
 185 190 195  
 gca tct gtt gca cta ctt ggc tcg gaa acc atg ggt tca ctc aag gcg 739  
 Ala Ser Val Ala Leu Leu Gly Ser Glu Thr Met Gly Ser Leu Lys Ala  
 200 205 210  
 tac aac acc tcc gga aag cac cgc cac acc ccg gaa att gcc cag aac 787  
 Tyr Asn Thr Ser Gly Lys His Arg His Thr Pro Glu Ile Ala Gln Asn  
 215 220 225  
 ctc ggc gaa gtc agc gac aag cca gtc aag gtg agc ttc acc cca gtg 835  
 Leu Gly Glu Val Ser Asp Lys Pro Val Lys Val Ser Phe Thr Pro Val  
 230 235 240 245  
 ctt gca ccg tta cct cgc gaa ttc tca cca ctg caa ccg cac ctt 880  
 Leu Ala Pro Leu Pro Arg Glu Phe Ser Pro Leu Gln Pro His Leu  
 250 255 260  
 tgaaagaagg cgttaccgca gaa 903

<210> 324  
 <211> 260  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 324  
 Met Ile Met His Asn Val Tyr Gly Val Thr Met Thr Ile Lys Val Ala  
 1 5 10 15  
 Ile Ala Gly Ala Ser Gly Tyr Ala Gly Gly Glu Ile Leu Arg Leu Leu  
 20 25 30  
 Leu Gly His Pro Ala Tyr Ala Ser Gly Glu Leu Glu Ile Gly Ala Leu  
 35 40 45  
 Thr Ala Ala Ser Thr Ala Gly Ser Thr Leu Gly Glu Leu Met Pro His  
 50 55 60  
 Ile Pro Gln Leu Ala Asp Arg Val Ile Gln Asp Thr Thr Ala Glu Thr  
 65 70 75 80  
 Leu Ala Gly His Asp Val Val Phe Leu Gly Leu Pro His Gly Phe Ser  
 85 90 95  
 Ala Glu Ile Ala Leu Gln Leu Gly Pro Asp Val Thr Val Ile Asp Cys  
 100 105 110  
 Ala Ala Asp Phe Arg Leu Gln Asn Ala Ala Asp Trp Glu Lys Phe Tyr  
 115 120 125  
 Gly Ser Glu His Gln Gly Thr Trp Pro Tyr Gly Ile Pro Glu Met Pro  
 130 135 140  
 Gly His Arg Glu Ala Leu Arg Gly Ala Lys Arg Val Ala Val Pro Gly  
 145 150 155 160  
 Cys Phe Pro Thr Gly Ala Thr Leu Ala Leu Leu Pro Ala Val Gln Ala  
 165 170 175



&lt;210&gt; 322

&lt;211&gt; 260

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 322

Met Ile Met His Asn Val Tyr Gly Val Thr Met Thr Ile Lys Val Ala  
 1 5 10 15

Ile Ala Gly Ala Ser Gly Tyr Ala Gly Gly Glu Ile Leu Arg Leu Leu  
 20 25 30

Leu Gly His Pro Ala Tyr Ala Ser Gly Glu Leu Glu Ile Gly Ala Leu  
 35 40 45

Thr Ala Ala Ser Thr Ala Gly Ser Thr Leu Gly Glu Leu Met Pro His  
 50 55 60

Ile Pro Gln Leu Ala Asp Arg Val Ile Gln Asp Thr Thr Ala Glu Thr  
 65 70 75 80

Leu Ala Gly His Asp Val Val Phe Leu Gly Leu Pro His Gly Phe Ser  
 85 90 95

Ala Glu Ile Ala Leu Gln Leu Gly Pro Asp Val Thr Val Ile Asp Cys  
 100 105 110

Ala Ala Asp Phe Arg Leu Gln Asn Ala Ala Asp Trp Glu Lys Phe Tyr  
 115 120 125

Gly Ser Glu His Gln Gly Thr Trp Pro Tyr Gly Ile Pro Glu Met Pro  
 130 135 140

Gly His Arg Glu Ala Leu Arg Gly Ala Lys Arg Val Ala Val Pro Gly  
 145 150 155 160

Cys Phe Pro Thr Gly Ala Thr Leu Ala Leu Leu Pro Ala Val Gln Ala  
 165 170 175

Gly Leu Ile Glu Pro Asp Val Ser Val Val Ser Ile Thr Gly Val Ser  
 180 185 190

Gly Ala Gly Lys Lys Ala Ser Val Ala Leu Leu Gly Ser Glu Thr Met  
 195 200 205

Gly Ser Leu Lys Ala Tyr Asn Thr Ser Gly Lys His Arg His Thr Pro  
 210 215 220

Glu Ile Ala Gln Asn Leu Gly Glu Val Ser Asp Lys Pro Val Lys Val  
 225 230 235 240

Ser Phe Thr Pro Val Leu Ala Pro Leu Pro Arg Glu Phe Ser Pro Leu  
 245 250 255

Gln Pro His Leu  
 260

&lt;210&gt; 323

gga tat gcc ggc gga gaa atc ctt cgt ctc ctt tta ggc cat cca gct	211
Gly Tyr Ala Gly Gly Glu Ile Leu Arg Leu Leu Leu Gly His Pro Ala	
25 30 35	
tat gca tct ggt gaa cta gaa atc gga gca ctc acc gcg gca tca acc	259
Tyr Ala Ser Gly Glu Leu Glu Ile Gly Ala Leu Thr Ala Ala Ser Thr	
40 45 50	
gca ggc agc acg ctc ggt gaa ttg atg cca cac att ccg cag ttg gcg	307
Ala Gly Ser Thr Leu Gly Glu Leu Met Pro His Ile Pro Gln Leu Ala	
55 60 65	
gat cgt gtt att caa gac acc aca gct gaa act cta gcc ggt cat gat	355
Asp Arg Val Ile Gln Asp Thr Thr Ala Glu Thr Leu Ala Gly His Asp	
70 75 80 85	
gtc gta ttt cta gga ctt cca cac gga ttc tct gca gaa att gca ctt	403
Val Val Phe Leu Gly Leu Pro His Gly Phe Ser Ala Glu Ile Ala Leu	
90 95 100	
cag ctc gga cca gat gtc aca gtg att gac tgt gca gct gac ttt cgt	451
Gln Leu Gly Pro Asp Val Thr Val Ile Asp Cys Ala Ala Asp Phe Arg	
105 110 115	
ctg caa aat gct gca gat tgg gag aag ttc tac ggc tca gag cac cag	499
Leu Gln Asn Ala Ala Asp Trp Glu Lys Phe Tyr Gly Ser Glu His Gln	
120 125 130	
gga aca tgg cct tat ggc att cca gaa atg cca gga cac cgc gag gct	547
Gly Thr Trp Pro Tyr Gly Ile Pro Glu Met Pro Gly His Arg Glu Ala	
135 140 145	
ctt cgt ggt gct aag cgt gta gca gtg cca gga tgt ttc cca acc ggt	595
Leu Arg Gly Ala Lys Arg Val Ala Val Pro Gly Cys Phe Pro Thr Gly	
150 155 160 165	
gca acc ttg gct ctt ctt cct gcg gtt caa gcg gga ctt atc gag cca	643
Ala Thr Leu Ala Leu Leu Pro Ala Val Gln Ala Gly Leu Ile Glu Pro	
170 175 180	
gat gtt tcc gta gtg tcc atc acc ggc gta tca ggt gca ggt aag aaa	691
Asp Val Ser Val Val Ser Ile Thr Gly Val Ser Gly Ala Gly Lys Lys	
185 190 195	
gca tct gtt gca cta ctt ggc tcg gaa acc atg ggt tca ctc aag gcg	739
Ala Ser Val Ala Leu Leu Gly Ser Glu Thr Met Gly Ser Leu Lys Ala	
200 205 210	
tac aac acc tcc gga aag cac cgc cac acc ccg gaa att gcc cag aac	787
Tyr Asn Thr Ser Gly Lys His Arg His Thr Pro Glu Ile Ala Gln Asn	
215 220 225	
ctc ggc gaa gtc agc gac aag cca gtc aag gtg agc ttc acc cca gtg	835
Leu Gly Glu Val Ser Asp Lys Pro Val Lys Val Ser Phe Thr Pro Val	
230 235 240 245	
ctt gca ccg tta cct cgc gaa ttc tca cca ctg caa ccg cac ctt	880
Leu Ala Pro Leu Pro Arg Glu Phe Ser Pro Leu Gln Pro His Leu	
250 255 260	
tgaaagaagg cgttaccgca gaa	903

Asp Leu Val Gly Leu Ile Asn Ser His Gly Pro Tyr Ala Val Gly Thr  
 115 120 125  
 Ser Gly Glu Asp Ala Gly Leu Phe Thr Ala Gln Lys Arg Met Val Asn  
 130 135 140  
 Ile Asp Gly Val Pro Thr Asp Ile Gly Leu Val Gly Asp Ile Ile Asn  
 145 150 155 160  
 Val Asp Ala Ser Ser Leu Met Asp Ile Ile Glu Ala Gly Arg Ile Pro  
 165 170 175  
 Val Val Ser Thr Ile Ala Pro Gly Glu Asp Gly Gln Ile Tyr Asn Ile  
 180 185 190  
 Asn Ala Asp Thr Ala Ala Gly Ala Leu Ala Ala Ala Ile Gly Ala Glu  
 195 200 205  
 Arg Leu Leu Val Leu Thr Asn Val Glu Gly Leu Tyr Thr Asp Trp Pro  
 210 215 220  
 Asp Lys Ser Ser Leu Val Ser Lys Ile Lys Ala Thr Glu Leu Glu Ala  
 225 230 235 240  
 Ile Leu Pro Gly Leu Asp Ser Gly Met Ile Pro Lys Met Glu Ser Cys  
 245 250 255  
 Leu Asn Ala Val Arg Gly Gly Val Ser Ala Ala His Val Ile Asp Gly  
 260 265 270  
 Arg Ile Ala His Ser Val Leu Leu Glu Leu Leu Thr Met Gly Gly Ile  
 275 280 285  
 Gly Thr Met Val Leu Pro Asp Val Phe Asp Arg Glu Asn Tyr Pro Glu  
 290 295 300  
 Gly Thr Val Phe Arg Lys Asp Asp Lys Asp Gly Glu Leu  
 305 310 315

<210> 321  
 <211> 903  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(880)  
 <223> RXN02153

<400> 321  
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 cccccgcaat gaatcaaaaa tttatgcatg aataatttgc atg atc atg cat aac 115  
 Met Ile Met His Asn  
 1 5  
 gtg tat ggt gta act atg aca atc aag gtt gca atc gca gga gcc agt 163  
 Val Tyr Gly Val Thr Met Thr Ile Lys Val Ala Ile Ala Gly Ala Ser  
 10 15 20

Ala Gly Ala Leu Ala Ala Ala Ile Gly Ala Glu Arg Leu Leu Val Leu  
 200 205 210

acc aat gtg gaa ggt ctg tac acc gat tgg cct gat aag agc tca ctg 787  
 Thr Asn Val Glu Gly Leu Tyr Thr Asp Trp Pro Asp Lys Ser Ser Leu  
 215 220 225

gtg tcc aag atc aag gcc acc gag ctg gag gcc att ctt ccg gga ctt 835  
 Val Ser Lys Ile Lys Ala Thr Glu Leu Glu Ala Ile Leu Pro Gly Leu  
 230 235 240 245

gat tcc ggc atg att cca aag atg gag tct tgc ttg aac gcg gtg cgt 883  
 Asp Ser Gly Met Ile Pro Lys Met Glu Ser Cys Leu Asn Ala Val Arg  
 250 255 260

ggg gga gta agc gct gct cat gtc att gac ggc cgc atc gcg cac tcg 931  
 Gly Gly Val Ser Ala Ala His Val Ile Asp Gly Arg Ile Ala His Ser  
 265 270 275

gtg ttg ctg gag ctt ttg acc atg ggt gga att ggc acg atg gtg ctg 979  
 Val Leu Leu Glu Leu Leu Thr Met Gly Gly Ile Gly Thr Met Val Leu  
 280 285 290

ccg gat gtt ttt gat cgg gag aat tat cct gaa ggc acc gtt ttt aga  
 1027  
 Pro Asp Val Phe Asp Arg Glu Asn Tyr Pro Glu Gly Thr Val Phe Arg  
 295 300 305

aaa gac gac aag gat ggg gaa ctg taaatgagca cgctggaaac ttg  
 1074  
 Lys Asp Asp Lys Asp Gly Glu Leu  
 310 315

<210> 320  
 <211> 317  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 320  
 Met Asn Asp Leu Ile Lys Asp Leu Gly Ser Glu Val Arg Ala Asn Val  
 1 5 10 15  
 Leu Ala Glu Ala Leu Pro Trp Leu Gln His Phe Arg Asp Lys Ile Val  
 20 25 30  
 Val Val Lys Tyr Gly Gly Asn Ala Met Val Asp Asp Asp Leu Lys Ala  
 35 40 45  
 Ala Phe Ala Ala Asp Met Val Phe Leu Arg Thr Val Gly Ala Lys Pro  
 50 55 60  
 Val Val Val His Gly Gly Gly Pro Gln Ile Ser Glu Met Leu Asn Arg  
 65 70 75 80  
 Val Gly Leu Gln Gly Glu Phe Lys Gly Gly Phe Arg Val Thr Thr Pro  
 85 90 95  
 Glu Val Met Asp Ile Val Arg Met Val Leu Phe Gly Gln Val Gly Arg  
 100 105 110



&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1051)

&lt;223&gt; RXA02156

&lt;400&gt; 319

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aacagcactc caactaacia gcagggaaaa gggcacaggc atg aat gac ttg atc 115
                                         Met Asn Asp Leu Ile
                                         1 5

aaa gat tta ggc tct gag gtg cgc gca aat gtc ctc gct gag gcg ttg 163
Lys Asp Leu Gly Ser Glu Val Arg Ala Asn Val Leu Ala Glu Ala Leu
                               10 15 20

cca tgg ttg cag cac ttc cgc gac aag att gtt gtc gtg aaa tat ggc 211
Pro Trp Leu Gln His Phe Arg Asp Lys Ile Val Val Val Lys Tyr Gly
                               25 30 35

gga aac gcc atg gtg gat gat gat ctc aag gct gct ttt gct gcc gac 259
Gly Asn Ala Met Val Asp Asp Asp Leu Lys Ala Ala Phe Ala Ala Asp
                               40 45 50

atg gtc ttc ttg cgc acc gtg ggc gca aaa cca gtg gtg gtg cac ggt 307
Met Val Phe Leu Arg Thr Val Gly Ala Lys Pro Val Val Val His Gly
                               55 60 65

ggt gga cct cag att tct gag atg cta aac cgt gtg ggt ctc cag ggc 355
Gly Gly Pro Gln Ile Ser Glu Met Leu Asn Arg Val Gly Leu Gln Gly
                               70 75 80 85

gag ttc aag ggt ggt ttc cgt gtg acc act cct gag gtc atg gac att 403
Glu Phe Lys Gly Gly Phe Arg Val Thr Thr Pro Glu Val Met Asp Ile
                               90 95 100

gtg cgc atg gtg ctc ttt ggt cag gtc ggt cgc gat tta gtt ggt ttg 451
Val Arg Met Val Leu Phe Gly Gln Val Gly Arg Asp Leu Val Gly Leu
                               105 110 115

atc aac tct cat ggc cct tac gct gtg gga acc tcc ggt gag gat gcc 499
Ile Asn Ser His Gly Pro Tyr Ala Val Gly Thr Ser Gly Glu Asp Ala
                               120 125 130

ggc ctg ttt acc gcg cag aag cgc atg gtc aac atc gat ggc gta ccc 547
Gly Leu Phe Thr Ala Gln Lys Arg Met Val Asn Ile Asp Gly Val Pro
                               135 140 145

act gat att ggt ttg gtc gga gac atc att aat gtc gat gcc tct tcc 595
Thr Asp Ile Gly Leu Val Gly Asp Ile Ile Asn Val Asp Ala Ser Ser
                               150 155 160 165

ttg atg gat atc atc gag gcc ggt cgc att cct gtg gtc tct acg att 643
Leu Met Asp Ile Ile Glu Ala Gly Arg Ile Pro Val Val Ser Thr Ile
                               170 175 180

gct cca ggc gaa gac ggc cag att tac aac att aac gcc gat acc gca 691
Ala Pro Gly Glu Asp Gly Gln Ile Tyr Asn Ile Asn Ala Asp Thr Ala
                               185 190 195

gca ggt gct ttg gct gca gcg att ggt gca gaa cgc ctg ctg gtt ctc 739

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Gly Leu Ile Gly Glu Leu Leu Pro Met Asp Lys Leu Asn Ala Gly Ile  
 115 120 125  
 Asp Gln Leu Thr Ala Glu Gly Ala Leu Gly Asp Asn Gly Ala Ala Ala  
 130 135 140  
 Ala Lys Ala Ile Met Thr Thr Asp Thr Val Asp Lys Glu Thr Val Val  
 145 150 155 160  
 Phe Ala Asp Gly Trp Thr Val Gly Gly Met Gly Lys Gly Val Gly Met  
 165 170 175  
 Met Ala Pro Ser Leu Ala Thr Met Leu Val Cys Leu Thr Thr Asp Ala  
 180 185 190  
 Ser Val Thr Gln Glu Met Ala Gln Ile Ala Leu Ala Asn Ala Thr Ala  
 195 200 205  
 Val Thr Phe Asp Thr Leu Asp Ile Asp Gly Ser Thr Ser Thr Asn Asp  
 210 215 220  
 Thr Val Phe Leu Leu Ala Ser Gly Ala Ser Gly Ile Thr Pro Thr Gln  
 225 230 235 240  
 Asp Glu Leu Asn Asp Ala Val Tyr Ala Ala Cys Ser Asp Ile Ala Ala  
 245 250 255  
 Lys Leu Gln Ala Asp Ala Glu Gly Val Thr Lys Arg Val Ala Val Thr  
 260 265 270  
 Val Val Gly Thr Thr Asn Asn Glu Gln Ala Ile Asn Ala Ala Arg Thr  
 275 280 285  
 Val Ala Arg Asp Asn Leu Phe Lys Cys Ala Met Phe Gly Ser Asp Pro  
 290 295 300  
 Asn Trp Gly Arg Val Leu Ala Ala Val Gly Met Ala Asp Ala Asp Met  
 305 310 315 320  
 Glu Pro Glu Lys Ile Ser Val Phe Phe Asn Gly Gln Ala Val Cys Leu  
 325 330 335  
 Asp Ser Thr Gly Ala Pro Gly Ala Arg Glu Val Asp Leu Ser Gly Ala  
 340 345 350  
 Asp Ile Asp Val Arg Ile Asp Leu Gly Thr Ser Gly Glu Gly Gln Ala  
 355 360 365  
 Thr Val Arg Thr Thr Asp Leu Ser Phe Ser Tyr Val Glu Ile Asn Ser  
 370 375 380  
 Ala Tyr Ser Ser  
 385

&lt;210&gt; 319

&lt;211&gt; 1074

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

ttg ttc aag tgc gca atg ttt gga tct gat cca aac tgg ggt cgc gtg  
1027

Leu Phe Lys Cys Ala Met Phe Gly Ser Asp Pro Asn Trp Gly Arg Val  
295 300 305

ttg gct gca gtc ggc atg gct gat gct gat atg gaa cca gag aag att  
1075

Leu Ala Ala Val Gly Met Ala Asp Ala Asp Met Glu Pro Glu Lys Ile  
310 315 320 325

tct gtg ttc ttc aat ggt caa gca gta tgc ctt gat tcc act ggc gct  
1123

Ser Val Phe Phe Asn Gly Gln Ala Val Cys Leu Asp Ser Thr Gly Ala  
330 335 340

cct ggt gct cgt gag gtg gat ctt tcc ggc gct gac att gat gtc cga  
1171

Pro Gly Ala Arg Glu Val Asp Leu Ser Gly Ala Asp Ile Asp Val Arg  
345 350 355

att gat ttg ggc acc agt ggg gaa ggc cag gca aca gtt cga acc act  
1219

Ile Asp Leu Gly Thr Ser Gly Glu Gly Gln Ala Thr Val Arg Thr Thr  
360 365 370

gac ctg agc ttc tcc tac gtg gag atc aac tcc gcg tac agc tct  
1264

Asp Leu Ser Phe Ser Tyr Val Glu Ile Asn Ser Ala Tyr Ser Ser  
375 380 385

taaaaagaaa cagcactcca act  
1287

<210> 318

<211> 388

<212> PRT

<213> Corynebacterium glutamicum

<400> 318

Met Ala Glu Lys Gly Ile Thr Ala Pro Lys Gly Phe Val Ala Ser Ala  
1 5 10 15

Thr Thr Ala Gly Ile Lys Ala Ser Gly Asn Pro Asp Met Ala Leu Val  
20 25 30

Val Asn Gln Gly Pro Glu Phe Ser Ala Ala Ala Val Phe Thr Arg Asn  
35 40 45

Arg Val Phe Ala Ala Pro Val Lys Val Ser Arg Glu Asn Val Ala Asp  
50 55 60

Gly Gln Ile Arg Ala Val Leu Tyr Asn Ala Gly Asn Ala Asn Ala Cys  
65 70 75 80

Asn Gly Leu Gln Gly Glu Lys Asp Ala Arg Glu Ser Val Ser His Leu  
85 90 95

Ala Gln Asn Leu Gly Leu Glu Asp Ser Asp Ile Gly Val Cys Ser Thr  
100 105 110

40	45	50	
cct gtg aag gtg agc cga gag aac gtt gct gat ggc cag atc agg gct Pro Val Lys Val Ser Arg Glu Asn Val Ala Asp Gly Gln Ile Arg Ala 55 60 65			307
gtt ttg tac aac gct ggt aat gct aat gcg tgt aat ggt ctg cag ggt Val Leu Tyr Asn Ala Gly Asn Ala Asn Ala Cys Asn Gly Leu Gln Gly 70 75 80 85			355
gag aag gat gct cgt gag tct gtt tct cat cta gct caa aat ttg ggc Glu Lys Asp Ala Arg Glu Ser Val Ser His Leu Ala Gln Asn Leu Gly 90 95 100			403
ttg gag gat tcc gat att ggt gtg tgt tcc act ggt ctt att ggt gag Leu Glu Asp Ser Asp Ile Gly Val Cys Ser Thr Gly Leu Ile Gly Glu 105 110 115			451
ttg ctt ccg atg gat aag ctc aat gca ggt att gat cag ctg acc gct Leu Leu Pro Met Asp Lys Leu Asn Ala Gly Ile Asp Gln Leu Thr Ala 120 125 130			499
gag ggc gct ttg ggt gac aat ggt gca gct gct gcc aag gcg atc atg Glu Gly Ala Leu Gly Asp Asn Gly Ala Ala Ala Ala Lys Ala Ile Met 135 140 145			547
acc act gac acg gtg gat aag gaa acc gtc gtg ttt gct gat ggt tgg Thr Thr Asp Thr Val Asp Lys Glu Thr Val Val Phe Ala Asp Gly Trp 150 155 160 165			595
act gtc ggc gga atg ggc aag ggc gtg ggc atg atg gcg ccg tct ctt Thr Val Gly Gly Met Gly Lys Gly Val Gly Met Met Ala Pro Ser Leu 170 175 180			643
gcc acc atg ctg gtc tgc ttg acc act gat gca tcc gtt act cag gaa Ala Thr Met Leu Val Cys Leu Thr Thr Asp Ala Ser Val Thr Gln Glu 185 190 195			691
atg gct cag atc gcg ctg gct aat gct acg gcc gtt acg ttt gac acc Met Ala Gln Ile Ala Leu Ala Asn Ala Thr Ala Val Thr Phe Asp Thr 200 205 210			739
ctg gat att gat gga tca acc tcc acc aat gac acc gtg ttc ctg ctg Leu Asp Ile Asp Gly Ser Thr Ser Thr Asn Asp Thr Val Phe Leu Leu 215 220 225			787
gca tct ggc gct agc gga atc acc cca act cag gat gaa ctc aac gat Ala Ser Gly Ala Ser Gly Ile Thr Pro Thr Gln Asp Glu Leu Asn Asp 230 235 240 245			835
gcg gtg tac gca gct tgt tct gat atc gca gcg aag ctt cag gct gat Ala Val Tyr Ala Ala Cys Ser Asp Ile Ala Ala Lys Leu Gln Ala Asp 250 255 260			883
gca gag ggt gtg acc aag cgc gtt gct gtg aca gtg gtg gga acc acc Ala Glu Gly Val Thr Lys Arg Val Ala Val Thr Val Val Gly Thr Thr 265 270 275			931
aac aac gag cag gcg att aat gcg gct cgc act gtt gct cgt gac aat Asn Asn Glu Gln Ala Ile Asn Ala Ala Arg Thr Val Ala Arg Asp Asn 280 285 290			979

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<210> 317
<211> 1287
<212> DNA
<213> Corynebacterium glutamicum
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<400> 317
tcggcgctgc accttaaagt agcgccttaa agcggcgctt caaaccaagc gccctaacca 60

gcaaacacaa caaacacatc taattcagta ggagttccac atg gca gaa aaa ggc 115
Met Ala Glu Lys Gly
1 5

att acc gcg ccg aaa ggc ttc gtt gct tct gca acg acc gcg ggt att 163
Ile Thr Ala Pro Lys Gly Phe Val Ala Ser Ala Thr Thr Ala Gly Ile
10 15 20

aaa gct tct ggc aat cct gac atg gcg ttg gtg gtt aac cag ggt cca 211
Lys Ala Ser Gly Asn Pro Asp Met Ala Leu Val Val Asn Gln Gly Pro
25 30 35

gag ttt tcc gca gcg gcc gtg ttt aca cgt aac cga gtt ttc gca gcg 259
Glu Phe Ser Ala Ala Ala Val Phe Thr Arg Asn Arg Val Phe Ala Ala

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tgg tgt gca cat cag gca ctc caa gct ttg gga cga gat agc ggt gat 307  
 Trp Cys Ala His Gln Ala Leu Gln Ala Leu Gly Arg Asp Ser Gly Asp  
 55 60 65

ccc att ttg cgt ggg gaa cga gga atg cca ttg tgg cct tct tcg gtg 355  
 Pro Ile Leu Arg Gly Glu Arg Gly Met Pro Leu Trp Pro Ser Ser Val  
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tct ggt tca ttg acc cac act gac gga ttc cga gct gct gtt gtg gcg 403  
 Ser Gly Ser Leu Thr His Thr Asp Gly Phe Arg Ala Ala Val Val Ala  
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cca cga ttg ttg gtg cgt tct atg gga ttg gat gcc gaa cct gcg gag 451  
 Pro Arg Leu Leu Val Arg Ser Met Gly Leu Asp Ala Glu Pro Ala Glu  
 105 110 115

ccg ttg ccc aag gat gtt ttg ggt tca atc gct cgg gtg ggg gag att 499  
 Pro Leu Pro Lys Asp Val Leu Gly Ser Ile Ala Arg Val Gly Glu Ile  
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cct caa ctt aag cgc ttg gag gaa caa ggt gtg cac tgc gcg gat cgc 547  
 Pro Gln Leu Lys Arg Leu Glu Glu Gln Gly Val His Cys Ala Asp Arg  
 135 140 145

ctg ctg ttt tgt gcc aag gaa gca aca tac aaa gcg tgg ttc ccg ctg 595  
 Leu Leu Phe Cys Ala Lys Glu Ala Thr Tyr Lys Ala Trp Phe Pro Leu  
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acg cat agg tgg ctt ggt ttt gaa caa gct gag atc gac ttg cgt gat 643  
 Thr His Arg Trp Leu Gly Phe Glu Gln Ala Glu Ile Asp Leu Arg Asp  
 170 175 180

gat ggc act ttt gtg tcc tat ttg ctg gtt cga cca act cca gtg ccg 691  
 Asp Gly Thr Phe Val Ser Tyr Leu Leu Val Arg Pro Thr Pro Val Pro  
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ttt att tca ggt aaa tgg gta ctg cgt gat ggt tat gtc ata gct gcg 739  
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 Thr Ala Val Thr  
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 Leu Glu Lys Ala Leu Val Ala His Ser Val Asp Ile Arg Lys Ala Glu  
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Glu	Lys	Asp	Ala	Asp	Val	Glu	Thr	Ala	Val	Lys	Ala	Asp	Phe	Ala	Glu
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Val	Glu	Val	Asp	Asn	Thr	Asp	Thr	Thr	Gln	Met	Ala	Val	Val	Glu	Glu
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Val	Asp	Glu	Glu	Pro	Glu	Gln	Glu	Asn	Lys	Met	Ser	Val	Phe	Ala	Ile
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Arg	Thr	Ser	Arg	Asp	Gly	Phe	Ser	Met	Val	Leu	Ala	Gly	Ile	Val	Gly
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&lt;211&gt; 774

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(751)

&lt;223&gt; RXA01491

&lt;400&gt; 315

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Val	Asn	Leu	Asp	His	Phe	His	Gln	Leu	His	Pro	Leu	Glu	Lys	Ala	Leu	
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Val	Ala	His	Ser	Val	Asp	Ile	Arg	Lys	Ala	Glu	Phe	Gly	Asp	Ala	Arg	
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 gtg gag act gcc gta aag gca gat ttc gca gag gtg gaa gtc gat aac 595  
 Val Glu Thr Ala Val Lys Ala Asp Phe Ala Glu Val Glu Val Asp Asn  
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 act gac acc acg cag atg gct gtg gtg gaa gaa gtt gac gag gag cca 643  
 Thr Asp Thr Thr Gln Met Ala Val Val Glu Glu Val Asp Glu Glu Pro  
 170 175 180  
 gag caa gaa aac aaa atg tcc gta ttc gcg atc atc atg atg gcg atc 691  
 Glu Gln Glu Asn Lys Met Ser Val Phe Ala Ile Ile Met Met Ala Ile  
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 gtc gga gtt gtt ctc ggt gtc gtt gta ttc ctc ggc ttt gaa atg ctg 739  
 Val Gly Val Val Leu Gly Val Val Val Phe Leu Gly Phe Glu Met Leu  
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 Trp Glu Arg Leu Asn Lys Trp Ile Val Ala Val Leu Ala Val Gly Val  
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 Thr Leu Gly Met Val Gly Ile Ile His Ala Leu Arg Thr Ser Arg Asp  
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 ggt ttc agc atg gtt ctc gca gga atc gtg ggc ctg gtc atg acg ttc 883  
 Gly Phe Ser Met Val Leu Ala Gly Ile Val Gly Leu Val Met Thr Phe  
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 Asp Ala Pro Ala Glu Pro Glu Val Val Glu Ala Pro Lys Pro Glu Pro  
 65 70 75 80  
 Ala Glu Glu Val Glu Val Ala Ser Val Glu Gly Asp Val Asp Lys Gln  
 85 90 95  
 Glu Thr Pro Glu Arg Pro Ala Pro Ser Asn Glu Glu Thr Met Val Leu





645	650	655
Val Val Glu Ala Leu Trp Glu Ala Gly Val Pro Arg Glu Val Leu His		
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Cys Ile Tyr Pro Ala Asn Arg Asp Val Gly Cys Ala Leu Ile Ser His		
675	680	685
Glu His Val Asp Arg Val Ile Leu Thr Gly Ser Ser Glu Thr Ala Ala		
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Met Phe Ser Ser Trp Arg Pro Glu Leu Thr Ile Asn Gly Glu Thr Ser		
705	710	715
Gly Lys Asn Ala Ile Val Val Thr Pro Ser Ala Asp Arg Asp Leu Ala		
725	730	735
Val Ala Asp Leu Val Lys Ser Ala Phe Gly His Ala Gly Gln Lys Cys		
740	745	750
Ser Ala Ala Ser Leu Gly Ile Leu Val Gly Ser Val Tyr Glu Ser Glu		
755	760	765
Arg Phe Arg Lys Gln Leu Val Asp Ala Ala Ser Ser Leu Ile Val Asp		
770	775	780
Trp Pro Thr Asn Pro Ser Ala Thr Val Gly Pro Leu Thr Glu Leu Pro		
785	790	795
Ser Asp Lys Leu His His Ala Leu Thr Thr Leu Glu Glu Gly Glu Ser		
805	810	815
Trp Leu Leu Lys Pro Arg Gln Leu Asp Asp Thr Gly Arg Leu Trp Ser		
820	825	830
Pro Gly Ile Lys Glu Gly Val Lys Pro Gly Thr Phe Phe His Leu Thr		
835	840	845
Glu Val Phe Gly Pro Val Leu Gly Leu Met Lys Ala Thr Asp Leu Asn		
850	855	860
Glu Ala Ile Glu Phe Gln Asn Gly Asn Asp Phe Gly Leu Thr Gly Gly		
865	870	875
Leu Gln Ser Leu Asp Ala Asp Glu Val Arg Thr Trp Leu Asp His Val		
885	890	895
Asp Val Gly Asn Ala Tyr Val Asn Arg Gly Ile Thr Gly Ala Ile Val		
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Gln Arg Gln Ser Phe Gly Gly Trp Lys Lys Ser Ser Val Gly Leu Gly		
915	920	925
Ser Lys Ala Gly Gly Pro Asn Tyr Val Met Leu Met Gly Thr Trp Ala		
930	935	940
Asp Ala Pro Ser His His Ala Pro Arg Glu Thr Asn Pro Leu Ile Ser		
945	950	955
Lys Leu Asp Leu Pro Gly Glu Glu Leu Glu Trp Leu Glu Lys Ala Asn		
965	970	975

Asp Ala Asn Tyr Lys Arg Val Leu Tyr Trp Thr Met Arg Lys Glu Asn  
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 Met Glu Gly Leu Arg Leu Gly Val Ala Gly His Asn Leu Phe Asp Ile  
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 Ala Phe Ala His Leu Leu Ser Val Glu Arg Gly Val Ala Asp Arg Val  
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 Glu Phe Glu Met Leu Gln Gly Met Ala Ser Asp Gln Ala Arg Ala Val  
 370 375 380  
 Ser Val Asp Val Gly Glu Leu Leu Leu Tyr Val Pro Ala Val Arg Pro  
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 Gln Glu Phe Asp Val Ala Ile Ser Tyr Leu Val Arg Arg Leu Glu Glu  
 405 410 415  
 Asn Ala Ala Ser Glu Asn Phe Met Ser Ala Ile Phe Asp Leu Asp Ala  
 420 425 430  
 Asp Asn Pro Ser Phe Lys Arg Glu Glu Ser Arg Phe Arg Ala Ser Ile  
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 Ser Asp Leu Ala Thr Leu Ile Asp Val Pro Ala Pro Gly Pro Asn His  
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 Thr Gln Asp Arg Ser Lys Glu Thr Leu Leu Asp Ala Pro Leu Val Pro  
 465 470 475 480  
 Phe Ile Asn Glu Pro Asp Thr Asn Pro Ala Leu Ile Gln Asn Gln Gln  
 485 490 495  
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 500 505 510  
 Lys Gln Thr Lys Pro Glu Val Leu Glu Glu Gly Asp Val Asp Lys Leu  
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 530 535 540  
 Arg Glu Arg Ala Glu Ile Leu Tyr Lys Thr Ala Glu Ile Leu Arg Val  
 545 550 555 560  
 Arg Arg Gly His Leu Ile Ser Val Thr Ala Ala Glu Val Gly Lys Ala  
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 Val Glu Gln Thr Asp Pro Glu Ile Ser Glu Ala Ile Asp Phe Ala Arg  
 580 585 590  
 Tyr Tyr Ala His Leu Ala Leu Glu Leu Asp Asp Val Asp Asn Ala Glu  
 595 600 605  
 Phe Thr Pro Asp Arg Val Val Val Val Thr Pro Pro Trp Asn Phe Pro  
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 35 40 45  
 Asn Gly Leu Glu Phe Thr Val Gly Phe Val Asp Arg Val Val Arg Thr  
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 Glu Asp Arg Glu Ala Ala His Ala Leu Tyr Glu Leu Gly Lys Ile  
 65 70 75 80  
 Ala Pro Ser Thr Met Ser Phe Leu Asp Arg Ala Gln Ile Gln Ala Gly  
 85 90 95  
 Ser Leu Val Gly Arg Ala Leu Pro Gln Val Val Val Pro Ala Ala Arg  
 100 105 110  
 Ala Arg Ile Arg Gln Met Val Gly His Met Ile Val Asp Ala Arg Asp  
 115 120 125  
 Lys Gln Phe Ala Lys Ala Val Ala Glu Ile Gln Ser Asp Gly His Arg  
 130 135 140  
 Leu Asn Ile Asn Leu Leu Gly Glu Ala Val Leu Gly Arg Lys Glu Ala  
 145 150 155 160  
 Ala Lys His Leu Asp Asp Thr Val Arg Leu Leu Arg Arg Pro Asp Val  
 165 170 175  
 Glu Tyr Val Ser Xaa Xaa Xaa Ser Ser Val Ala Ser Gln Ile Ser Met  
 180 185 190  
 Trp Gly Phe Glu Asp Thr Val Asn Tyr Val Val Glu Gln Leu Thr Pro  
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 Leu Asp Met Glu Glu Tyr Arg Asp Leu Arg Leu Thr Met Glu Val Phe  
 225 230 235 240  
 Lys Arg Leu Leu Ser Asn Pro Glu Leu His Glu Leu Glu Ala Gly Ile  
 245 250 255  
 Val Leu Gln Ala Tyr Leu Pro Asp Ala Leu Gly Ala Ile Gln Asp Leu  
 260 265 270  
 Ala Gln Phe Gly Arg Glu Arg Val Asn Thr Gly Gly Ala Gly Val Lys  
 275 280 285  
 Val Arg Leu Val Lys Gly Ala Asn Leu Pro Met Glu His Val His Ala  
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 Gln Ile Thr Gly Trp Pro Val Ala Thr Glu Pro Ser Lys Gln Ala Thr  
 305 310 315 320

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cct gaa gaa ggc cca gca ggc ctt aag ggt aag aag gct gtg tac ctg 595  
 Pro Glu Glu Gly Pro Ala Gly Leu Lys Gly Lys Lys Ala Val Tyr Leu  
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 Gly Asp Gly Asp Asn Asn Met Ala Asn Ser Tyr Met Ile Gly Phe Ala  
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acc gcg ggc atg gat att tcc atc atc gct cct gaa ggg ttc cag cct 691  
 Thr Ala Gly Met Asp Ile Ser Ile Ile Ala Pro Glu Gly Phe Gln Pro  
 185 190 195

cgt gcg gaa ttc gtg gag cgc gcg gaa aag cgt ggc cag gaa acc ggc 739  
 Arg Ala Glu Phe Val Glu Arg Ala Glu Lys Arg Gly Gln Glu Thr Gly  
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gcg aag gtt gtt gtc acc gac agc ctc gac gag gtt gcc ggc gcc gat 787  
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 Val Val Ile Thr Asp Thr Trp Val Ser Met Gly Met Glu Asn Asp Gly  
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 Ile Asp Arg Thr Thr Pro Phe Val Pro Tyr Gln Val Asn Asp Glu Val  
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tac cgt ggc aaa gaa gtg gca gcc tcc gtg att gat gga cca gcg tcc 979  
 Tyr Arg Gly Lys Glu Val Ala Ala Ser Val Ile Asp Gly Pro Ala Ser  
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 1027  
 Lys Val Phe Asp Glu Ala Glu Asn Arg Leu His Ala Gln Lys Ala Leu  
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aac  
 1080

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Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile  
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Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu  
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<223> RXA02158
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					Met	Thr	Ser	Gln	Pro						
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cag gtt cgc	cat ttt	ctg gct	gat gat	gat ctc	acc cct	gca gag	cag								163
Gln Val Arg	His Phe	Leu Ala	Asp Asp	Asp Leu	Thr Pro	Ala Glu	Gln								
	10			15		20									
gca gag gtt	ttg acc	cta gcc	gca aag	ctc aag	gca gcg	ccg ttt	tcg								211
Ala Glu Val	Leu Thr	Leu Ala	Ala Lys	Leu Lys	Ala Ala	Pro Phe	Ser								
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Glu Arg	Pro	Leu Glu	Gly Pro	Lys Ser	Val Ala	Val Leu	Phe Asp	Lys							
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Thr Ser	Thr Arg	Thr Arg	Phe Ser	Phe Asp	Ala Gly	Ile Ala	His Leu								
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Gly Gly His	Ala Ile	Val Val	Asp Ser	Gly Ser	Ser Gln	Met Gly	Lys								
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 Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly  
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 Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly  
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 His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg  
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 Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe  
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 Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr  
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 His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg  
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 Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly  
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 Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly  
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cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa  
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gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca  
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Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala	
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Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe	
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His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala	
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Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp	
55 60 65	
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Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg	
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Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn	
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Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val	
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Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly	
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Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly	
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cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga	595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly	
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tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc	643
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr	
170 175 180	
acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc	691
Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser	
185 190 195	
tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag	739
Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys	
200 205 210	
cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg	787
His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala	
215 220 225	

Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala  
 210 215 220  
 Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly  
 225 230 235 240  
 Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys  
 245 250 255  
 Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe  
 260 265 270  
 Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe  
 275 280 285  
 Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala  
 290 295 300  
 Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly  
 305 310 315 320  
 Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala  
 325 330 335  
 Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile  
 340 345 350  
 Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu  
 355 360 365  
 Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile  
 370 375 380  
 Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala  
 385 390 395 400  
 Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser  
 405 410 415  
 Gly Asn Arg Phe His Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu  
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 Leu Val Ala Leu Leu Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu  
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 Leu Thr Phe Ala Gly Ala Leu Phe  
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 <213> Corynebacterium glutamicum

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 <223> FRXA01009

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 1411  
 Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu Leu Val Ala Leu Leu  
                   425                                  430                                  435

gac gcg gtg gaa gct gca gcc caa gct gtc gag ctg acc ttc gct ggg  
 1459  
 Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu Leu Thr Phe Ala Gly  
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gcg ttg ttc taagttttct agataacaag gcc  
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 Ala Leu Phe  
                   455

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<211> 456

<212> PRT

<213> Corynebacterium glutamicum

<400> 330

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Gly Ser Val Gln Ala Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp  
                   20                                  25                                  30

Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro  
                   35                                  40                                  45

Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly  
   50                                  55                                  60

Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly  
   65                                  70                                  75                                  80

His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg  
                   85                                  90                                  95

Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val  
                   100                                  105                                  110

Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe  
                   115                                  120                                  125

Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala  
   130                                  135                                  140

Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr  
   145                                  150                                  155                                  160

His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg  
                   165                                  170                                  175

Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro  
                   180                                  185                                  190

Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys  
                   195                                  200                                  205

cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg 787  
 His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala  
 215 220 225

atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca 835  
 Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro  
 230 235 240 245

gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc 883  
 Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile  
 250 255 260

ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa 931  
 Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys  
 265 270 275

ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc 979  
 Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile  
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acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc  
 1027  
 Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile  
 295 300 305

gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc  
 1075  
 Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser  
 310 315 320 325

ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag  
 1123  
 Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys  
 330 335 340

gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct  
 1171  
 Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala  
 345 350 355

cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa  
 1219  
 Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu  
 360 365 370

gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca  
 1267  
 Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala  
 375 380 385

gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa  
 1315  
 Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu  
 390 395 400 405

ttc aag gaa cgc ggc gtg tgg ccg atg atc tcc ggc aac cga ttc cac  
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 Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser Gly Asn Arg Phe His  
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&lt;222&gt; (101)..(1468)

&lt;223&gt; RXS02970

&lt;400&gt; 329

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ttatttaaag acttcataat attttgggga gtgaactggt ttg gca ttg aag ggt 115
                                         Leu Ala Leu Lys Gly
                                         1           5

tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163
Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala
                        10                15                20

aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211
Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe
                        25                30                35

cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259
His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala
                        40                45                50

gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp
                        55                60                65

atg ggt tcc caa ctt gtc tgc gca aac tta ggc cac aac aac cct cga 355
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg
                        70                75                80                85

tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac 403
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn
                        90                95                100

ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg 451
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val
                        105                110                115

tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc 499
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly
                        120                125                130

gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga 547
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly
                        135                140                145

cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga 595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly
                        150                155                160                165

tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc 643
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr
                        170                175                180

acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc 691
Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser
                        185                190                195

tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag 739
Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys
                        200                205                210

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115	120	125
Ile Leu Ala Ala Val His Gly Phe His Gly Arg Thr Met Gly Ser Leu 130	135	140
Ala Leu Thr Gly Gln Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro 145	150	155 160
Ser Gly Val Glu Phe Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys 165	170	175
Met Val Glu Thr Asn Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro 180	185	190
Ile Gln Gly Glu Thr Gly Val Val Pro Ala Pro Glu Gly Phe Leu Lys 195	200	205
Ala Val Arg Glu Leu Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp 210	215	220
Glu Val Gln Thr Gly Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln 225	230	235 240
His Asp Gly Val Val Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly 245	250	255
Gly Gly Leu Pro Ile Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu 260	265	270
Leu Met Thr Pro Gly Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val 275	280	285
Ala Cys Ala Ala Ala Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe 290	295	300
Cys Ala Glu Val Ala Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala 305	310	315 320
Lys Val Asp Gly Val Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly 325	330	335
Val Val Leu Glu Arg Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe 340	345	350
Lys His Gly Val Ile Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu 355	360	365
Thr Pro Pro Leu Val Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys 370	375	380
Ala Ile Ala Glu Thr Ile Ala 385	390	

&lt;210&gt; 329

&lt;211&gt; 1491

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

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 Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala Lys Val Asp Gly Val  
 310                      315                      320                      325  
 gta gac gtc cgt ggc agg ggc ttg atg ttg ggc gtg gtg ctg gag cgc  
 1123  
 Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly Val Val Leu Glu Arg  
 330                      335                      340  
 gac gtc gca aag caa gct gtt ctt gat ggt ttt aag cac ggc gtt att  
 1171  
 Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe Lys His Gly Val Ile  
 345                      350                      355  
 ttg aat gca ccg gcg gac aac att atc cgt ttg acc ccg ccg ctg gtg  
 1219  
 Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu Thr Pro Pro Leu Val  
 360                      365                      370  
 atc acc gac gaa gaa atc gca gac gca gtc aag gct att gcc gag aca  
 1267  
 Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys Ala Ile Ala Glu Thr  
 375                      380                      385  
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 1296  
 Ile Ala  
 390

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 20                      25                      30  
 Asp Gln Gly Asn Val Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn  
 35                      40                      45  
 Ala Leu Gly His Ala His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln  
 50                      55                      60  
 Ile Gly Gln Leu Gly His Val Ser Asn Leu Phe Ala Ser Arg Pro Val  
 65                      70                      75                      80  
 Val Glu Val Ala Glu Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala  
 85                      90                      95  
 Thr Leu Ala Ala Gln Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu  
 100                      105                      110  
 Ala Asn Glu Ala Ala Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg

55	60	65	
cac gtc tca aac ttg ttc gca tcc agg ccc gtc gtc gag gtc gcc gag			355
His Val Ser Asn Leu Phe Ala Ser Arg Pro Val Val Glu Val Ala Glu			
70	75	80	85
gag ctc atc aag cgt ttt tcg ctt gac gac gcc acc ctc gcc gcg caa			403
Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala Thr Leu Ala Ala Gln			
	90	95	100
acc cgg gtt ttc ttc tgc aac tcg ggc gcc gaa gca aac gag gct gct			451
Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu Ala Asn Glu Ala Ala			
	105	110	115
ttc aag att gca cgc ttg act ggt cgt tcc cgg att ctg gct gca gtt			499
Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg Ile Leu Ala Ala Val			
	120	125	130
cat ggt ttc cac ggc cgc acc atg ggt tcc ctc gcg ctg act ggc cag			547
His Gly Phe His Gly Arg Thr Met Gly Ser Leu Ala Leu Thr Gly Gln			
	135	140	145
cca gac aag cgt gaa gcg ttc ctg cca atg cca agc ggt gtg gag ttc			595
Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro Ser Gly Val Glu Phe			
	150	155	160
tac cct tac ggc gac acc gat tac ttg cgc aaa atg gta gaa acc aac			643
Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys Met Val Glu Thr Asn			
	170	175	180
cca acg gat gtg gct gct atc ttc ctc gag cca atc cag ggt gaa acg			691
Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro Ile Gln Gly Glu Thr			
	185	190	195
ggc gtt gtt cca gca cct gaa gga ttc ctc aag gca gtg cgc gag ctg			739
Gly Val Val Pro Ala Pro Glu Gly Phe Leu Lys Ala Val Arg Glu Leu			
	200	205	210
tgc gat gag tac ggc atc ttg atg atc acc gat gaa gtc cag act ggc			787
Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp Glu Val Gln Thr Gly			
	215	220	225
gtt ggc cgt acc ggc gat ttc ttt gca cat cag cac gat ggc gtt gtt			835
Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln His Asp Gly Val Val			
	230	235	240
ccc gat gtg gtg acc atg gcc aag gga ctt ggc ggc ggt ctt ccc atc			883
Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly Gly Gly Leu Pro Ile			
	250	255	260
ggt gct tgt ttg gcc act ggc cgt gca gct gaa ttg atg acc cca ggc			931
Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu Leu Met Thr Pro Gly			
	265	270	275
aag cac ggc acc act ttc ggt ggc aac cca gtt gct tgt gca gct gcc			979
Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val Ala Cys Ala Ala Ala			
	280	285	290
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Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe Cys Ala Glu Val Ala			



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caccgttttt agaaaagacg acaaggatgg ggaactgtaa atg agc acg ctg gaa 115
Met Ser Thr Leu Glu
1 5

act tgg cca cag gtc att att aat acg tac ggc acc cca cca gtt gag 163
Thr Trp Pro Gln Val Ile Ile Asn Thr Tyr Gly Thr Pro Pro Val Glu
10 15 20

ctg gtg tcc ggc aag ggc gca acc gtc act gat gac cag ggc aat gtc 211
Leu Val Ser Gly Lys Gly Ala Thr Val Thr Asp Asp Gln Gly Asn Val
25 30 35

tac atc gac ttg ctc gcg ggc atc gca gtc aac gcg ttg ggc cac gcc 259
Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn Ala Leu Gly His Ala
40 45 50

cac ccg gcg atc atc gag gcg gtc acc aac cag atc ggc caa ctt ggt 307
His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln Ile Gly Gln Leu Gly

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Gly Leu Ile Glu Pro Asp Val Ser Val Val Ser Ile Thr Gly Val Ser  
 180 185 190

Gly Ala Gly Lys Lys Ala Ser Val Ala Leu Leu Gly Ser Glu Thr Met  
 195 200 205

Gly Ser Leu Lys Ala Tyr Asn Thr Ser Gly Lys His Arg His Thr Pro  
 210 215 220

Glu Ile Ala Gln Asn Leu Gly Glu Val Ser Asp Lys Pro Val Lys Val  
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Ser Phe Thr Pro Val Leu Ala Pro Leu Pro Arg Glu Phe Ser Pro Leu  
 245 250 255

Gln Pro His Leu  
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 <223> RXA02154

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 Leu Lys Glu Gly Val  
 1 5

acc gca gaa cag gct cgc gca gta tat gaa gag ttc tat gca cag gaa 163  
 Thr Ala Glu Gln Ala Arg Ala Val Tyr Glu Glu Phe Tyr Ala Gln Glu  
 10 15 20

acc ttc gtg cat gtt ctt cca gaa ggt gca cag cca caa acc caa gca 211  
 Thr Phe Val His Val Leu Pro Glu Gly Ala Gln Pro Gln Thr Gln Ala  
 25 30 35

gtt ctt ggc tcc aac atg tgc cac gtg cag gta gaa att gat gag gaa 259  
 Val Leu Gly Ser Asn Met Cys His Val Gln Val Glu Ile Asp Glu Glu  
 40 45 50

gca ggc aaa gtc ctt gtt acc tcc gca atc gat aac ctc acc aag gga 307  
 Ala Gly Lys Val Leu Val Thr Ser Ala Ile Asp Asn Leu Thr Lys Gly  
 55 60 65

act gcc ggc gcc gct gtt cag tgc atg aac tta agc gtt ggt ttt gat 355  
 Thr Ala Gly Ala Ala Val Gln Cys Met Asn Leu Ser Val Gly Phe Asp  
 70 75 80 85

gag gca gca ggc ctg cca cag gtc ggc gtc gca cct taaagtagcg 401  
 Glu Ala Ala Gly Leu Pro Gln Val Gly Val Ala Pro  
 90 95

ccttaaagcg gcg 414

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Glu	Ala	Met	Phe	Ala	Leu	Ser	Val	Ser	Thr	His	Phe	Asp	Trp	Val	Leu														
			25					30					35																
gcc	cct	tat	gat	gtg	ttg	gcc	tcc	aag	gca	cac	gcc	aag	gtt	ttg	cac	259													
Ala	Pro	Tyr	Asp	Val	Leu	Ala	Ser	Lys	Ala	His	Ala	Lys	Val	Leu	His														
		40					45					50																	
caa	gca	gat	cta	ctt	tct	gat	gaa	gat	cta	gcc	acc	atg	ctg	gct	ggg	307													
Gln	Ala	Asp	Leu	Leu	Ser	Asp	Glu	Asp	Leu	Ala	Thr	Met	Leu	Ala	Gly														
	55					60					65																		
ctt	gat	cag	ctg	ggc	aag	gat	gtc	gcc	gac	gga	acc	ttc	ggt	ccg	ctg	355													
Leu	Asp	Gln	Leu	Gly	Lys	Asp	Val	Ala	Asp	Gly	Thr	Phe	Gly	Pro	Leu														
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cct	tct	gat	gag	gat	gtg	cac	ggc	gcg	atg	gaa	cgc	ggt	gtg	att	gac	403													
Pro	Ser	Asp	Glu	Asp	Val	His	Gly	Ala	Met	Glu	Arg	Gly	Val	Ile	Asp														
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cgc	gtt	ggt	cct	gag	gtg	ggc	ggc	cgt	ctg	cgc	gct	ggt	cgt	tcc	cgc	451													
Arg	Val	Gly	Pro	Glu	Val	Gly	Gly	Arg	Leu	Arg	Ala	Gly	Arg	Ser	Arg														
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Asn	Asp	Gln	Val	Ala	Thr	Leu	Phe	Arg	Met	Trp	Val	Arg	Asp	Ala	Val														
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cgc	gac	atc	gcg	ctg	gga	aca	acc	gag	ctt	gtc	gac	gcc	ctc	agc	gcc	547													
Arg	Asp	Ile	Ala	Leu	Gly	Thr	Thr	Glu	Leu	Val	Asp	Ala	Leu	Ser	Ala														
	135					140					145																		
caa	gct	aag	gca	cat	gca	ggc	gcg	atc	atg	cca	ggc	aag	acc	cac	ttc	595													
Gln	Ala	Lys	Ala	His	Ala	Gly	Ala	Ile	Met	Pro	Gly	Lys	Thr	His	Phe														
	150				155					160					165														
cag	gca	gct	cag	ccg	gtc	ctt	ctg	gca	cac	cag	ctg	ctg	gca	cac	gca	643													
Gln	Ala	Ala	Gln	Pro	Val	Leu	Leu	Ala	His	Gln	Leu	Leu	Ala	His	Ala														
				170					175					180															
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Gln	Pro	Leu	Leu	Arg	Asp	Ile	Asp	Arg	Ile	Arg	Asp	Leu	Asp	Lys	Arg														
			185					190					195																
ctt	gcg	gtg	tct	cct	tac	ggt	tcc	ggc	gca	ctt	gct	ggt	tcc	tct	ttg	739													
Leu	Ala	Val	Ser	Pro	Tyr	Gly	Ser	Gly	Ala	Leu	Ala	Gly	Ser	Ser	Leu														
		200					205					210																	
aag	ctc	aac	cct	gaa	gca	atc	gct	gaa	gaa	ctc	ggc	ttt	gat	tcc	gca	787													
Lys	Leu	Asn	Pro	Glu	Ala	Ile	Ala	Glu	Glu	Leu	Gly	Phe	Asp	Ser	Ala														
	215					220					225																		
gca	gat	aac	tcc	att	gat	gcc	acc	agc	tcc	cgc	gat	ttc	gca	tct	gaa	835													
Ala	Asp	Asn	Ser	Ile	Asp	Ala	Thr	Ser	Ser	Arg	Asp	Phe	Ala	Ser	Glu														
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Gln Pro Leu Ala Tyr Asn Arg Asp Leu Gln Glu Asp Lys Glu Pro Ile 325 330 335		
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Ala Lys Val Leu His Gln Ala Asp Leu Leu Ser Asp Glu Asp Leu Ala  
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Thr Met Leu Ala Gly Leu Asp Gln Leu Gly Lys Asp Val Ala Asp Gly  
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Thr Phe Gly Pro Leu Pro Ser Asp Glu Asp Val His Gly Ala Met Glu  
85 90 95

Arg Gly Val Ile Asp Arg Val Gly Pro Glu Val Gly Gly Arg Leu Arg  
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Ala Gly Arg Ser Arg Asn Asp Gln Val Ala Thr Leu Phe Arg Met Trp  
115 120 125

Val Arg Asp Ala Val Arg Asp Ile Ala Leu Gly Thr Thr Glu Leu Val  
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Asp Ala Leu Ser Ala Gln Ala Lys Ala His Ala Gly Ala Ile Met Pro  
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Gly Lys Thr His Phe Gln Ala Ala Gln Pro Val Leu Leu Ala His Gln  
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Leu Leu Ala His Ala Gln Pro Leu Leu Arg Asp Ile Asp Arg Ile Arg  
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Leu Lys Lys Met Ile Asp Gly Glu Val Ile Ala Val Ser Leu Asp Leu
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Gly Gln Gly Gly Glu Asn Met Asp Asn Val Arg Gln Arg Ala Leu Asp
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Cys Thr Gly Lys Gly Asn Asp Gln Val Arg Phe Glu Val Gly Phe Met
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Lys	Ala	Val	Tyr	Leu	Gly	Asp	Gly	Asp	Asn	Asn	Met	Ala	Asn	Ser	Tyr
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Ala Asp Ala Lys Thr Thr Gly Ser Leu Val Ala Thr Leu Asn Ala Ala			
135 140 145			
gat tac ctt ggc gca ctt tta ggt ggc ctg gcc tgg cct ttt gtg ttg	595		
Asp Tyr Leu Gly Ala Leu Leu Gly Gly Leu Ala Trp Pro Phe Val Leu			

<210> 346  
 <211> 314  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 346

Val	Ala	Arg	Lys	Lys	Asn	Thr	Ser	Asp	Gln	Ser	Arg	Ser	Gln	Ala	Ala	1	5	10	15
Asn	Thr	Pro	Ile	Ala	Gly	Thr	Tyr	Glu	Gly	Glu	Tyr	Ser	Val	Ile	Glu	20	25	30	
Leu	Glu	Ala	Asp	Ser	Tyr	Thr	Thr	Asp	Gly	Trp	Leu	Ile	Ser	Ile	Asn	35	40	45	
Gly	Val	Pro	Ser	Ser	His	Ile	Val	Leu	Gly	Gln	Pro	Gln	Ala	Leu	Glu	50	55	60	
Phe	Glu	Tyr	Met	Arg	Trp	Ile	Ala	Thr	Gly	Ala	Arg	Ala	Phe	Ile	Asp	65	70	75	80
Ala	His	Gln	Asp	Ala	Ser	Lys	Leu	Arg	Ile	Thr	His	Leu	Gly	Gly	Gly	85	90	95	
Ala	Cys	Thr	Met	Ala	Arg	Tyr	Phe	Ala	Asp	Val	Tyr	Pro	Gln	Ser	Arg	100	105	110	
Asn	Thr	Val	Val	Glu	Leu	Asp	Ala	Glu	Leu	Ala	Arg	Leu	Ser	Arg	Glu	115	120	125	
Trp	Phe	Asp	Ile	Pro	Arg	Ala	Pro	Arg	Val	Lys	Ile	Arg	Val	Asp	Asp	130	135	140	
Ala	Arg	Met	Val	Ala	Glu	Ser	Phe	Thr	Pro	Ala	Ser	Arg	Asp	Val	Ile	145	150	155	160
Ile	Arg	Asp	Val	Phe	Ala	Gly	Ala	Ile	Thr	Pro	Gln	Asn	Phe	Thr	Thr	165	170	175	
Val	Glu	Phe	Phe	Glu	His	Cys	His	Arg	Gly	Leu	Ala	Pro	Gly	Gly	Leu	180	185	190	
Tyr	Val	Ala	Asn	Cys	Gly	Asp	His	Ser	Asp	Leu	Arg	Gly	Ala	Lys	Ser	195	200	205	
Glu	Leu	Ala	Gly	Met	Met	Glu	Val	Phe	Glu	His	Val	Ala	Val	Ile	Ala	210	215	220	
Asp	Pro	Pro	Met	Leu	Lys	Gly	Arg	Arg	Tyr	Gly	Asn	Ile	Ile	Leu	Met	225	230	235	240
Gly	Ser	Asp	Thr	Glu	Phe	Phe	Ser	Ser	Asn	Ser	Thr	Glu	Ala	Ser	Ala	245	250	255	
Ile	Thr	Arg	Glu	Leu	Leu	Gly	Gly	Gly	Val	Pro	Ala	Gln	Tyr	Lys	Asp	260	265	270	
Glu	Ser	Trp	Val	Arg	Lys	Phe	Ala	Ser	Gly	Ala	Gln	Ala	Arg	His	Asp	275	280	285	
Gly	Val	Ser	Thr	Leu	Gln	Met	Pro	Ser	Asp	Thr	Pro	Gln	His	Pro	Ala				

	90	95	100	
agg tat ttc gcg gat gtt tac ccg cag tca cgc aac act gtc gtg gaa				451
Arg Tyr Phe Ala Asp Val Tyr Pro Gln Ser Arg Asn Thr Val Val Glu				
	105	110	115	
ttg gat gca gag ctt gcc cgc ctg tcg cgt gaa tgg ttc gac att ccg				499
Leu Asp Ala Glu Leu Ala Arg Leu Ser Arg Glu Trp Phe Asp Ile Pro				
	120	125	130	
cgc gcg cca cgg gta aag att cgt gtg gat gat gcc cga atg gtg gca				547
Arg Ala Pro Arg Val Lys Ile Arg Val Asp Asp Ala Arg Met Val Ala				
	135	140	145	
gaa tct ttc act ccc gca agc cgc gat gtg atc atc cgt gac gtt ttt				595
Glu Ser Phe Thr Pro Ala Ser Arg Asp Val Ile Ile Arg Asp Val Phe				
	150	155	160	165
gcc gga gct atc acg ccg cag aac ttc acc acc gtg gag ttc ttt gag				643
Ala Gly Ala Ile Thr Pro Gln Asn Phe Thr Thr Val Glu Phe Phe Glu				
	170	175	180	
cac tgt cac cgt ggc ctt gct ccc ggc gga ttg tac gtt gcc aac tgt				691
His Cys His Arg Gly Leu Ala Pro Gly Gly Leu Tyr Val Ala Asn Cys				
	185	190	195	
ggc gat cat tcg gat ctg cgc gga gct aaa tct gag ctc gcg gga atg				739
Gly Asp His Ser Asp Leu Arg Gly Ala Lys Ser Glu Leu Ala Gly Met				
	200	205	210	
atg gag gtg ttc gag cac gtc gcg gtc atc gcc gat ccc ccg atg ctt				787
Met Glu Val Phe Glu His Val Ala Val Ile Ala Asp Pro Pro Met Leu				
	215	220	225	
aaa ggg cgc cgt tac ggc aac atc att ttg atg ggt tca gac acc gag				835
Lys Gly Arg Arg Tyr Gly Asn Ile Ile Leu Met Gly Ser Asp Thr Glu				
	230	235	240	245
ttc ttt agc tcc aac agc acg gaa gcg tcc gcg att acc cgt gag ctt				883
Phe Phe Ser Ser Asn Ser Thr Glu Ala Ser Ala Ile Thr Arg Glu Leu				
	250	255	260	
ctt ggc ggc ggc gtt cca gcg cag tac aag gat gaa tcc tgg gtg cgg				931
Leu Gly Gly Gly Val Pro Ala Gln Tyr Lys Asp Glu Ser Trp Val Arg				
	265	270	275	
aaa ttc gcc tcg gga gcc cag gcc cgc cac gat ggg gtc tct acc ctc				979
Lys Phe Ala Ser Gly Ala Gln Ala Arg His Asp Gly Val Ser Thr Leu				
	280	285	290	
caa atg ccg agt gat act cca caa cac cct gcg gaa acg ccg gag cat				
1027				
Gln Met Pro Ser Asp Thr Pro Gln His Pro Ala Glu Thr Pro Glu His				
	295	300	305	
tca aac aca cag cca taaaaaatc cgctggcgcg tcc				
1065				
Ser Asn Thr Gln Pro				
310				

Asp Asp Ala Arg Leu Val Val Asp Tyr Met Gly Leu Tyr Glu Ala Trp  
 275 280 285  
 Ala Glu Glu Tyr Gly Pro Gln Ala Tyr Gln Leu Leu Gly Ile Pro Gly  
 290 295 300  
 Thr His Trp Tyr Asp Leu Ala Leu Gln Gly Lys Leu Asp Leu Ala Lys  
 305 310 315 320  
 Ile Ser Gln Ile Gly Asp Ile Cys Ser Gly Lys Leu Pro Gly Arg Thr  
 325 330 335  
 Asn Asp Glu Glu Ile Ile Leu Tyr Ser Val Gly Gly Met Pro Val Glu  
 340 345 350  
 Asp Val Ala Trp Ala Thr Gln Val Tyr Glu Asn Ala Leu Glu Lys Gly  
 355 360 365  
 Val Gly Thr Thr Leu Asn Leu Trp Glu Ser Pro Ala Leu Ala  
 370 375 380

<210> 345  
 <211> 1065  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (101)..(1042)  
 <223> RXA00219

<400> 345  
 ttgcccgtac atgcgcgagc acctcctcaa cagcccgac caccgaccaa tcacataaga 60  
 cacaagcact aaaacagcat taaagaaaga aagctttttc gtg gcc cgt aag aaa 115  
 Val Ala Arg Lys Lys  
 1 5  
 aac acg tcc gat caa tcc cgc tcc caa gct gcc aac acg ccc att gct 163  
 Asn Thr Ser Asp Gln Ser Arg Ser Gln Ala Ala Asn Thr Pro Ile Ala  
 10 15 20  
 ggc acc tat gag ggt gaa tat tcc gtc atc gag ttg gag gcc gat tcc 211  
 Gly Thr Tyr Glu Gly Glu Tyr Ser Val Ile Glu Leu Glu Ala Asp Ser  
 25 30 35  
 tac acc acc gat ggc tgg ttg atc agc att aat ggc gtg ccc agc tct 259  
 Tyr Thr Thr Asp Gly Trp Leu Ile Ser Ile Asn Gly Val Pro Ser Ser  
 40 45 50  
 cat att gtc ctg ggg caa ccg cag gca ctg gaa ttt gag tac atg cgg 307  
 His Ile Val Leu Gly Gln Pro Gln Ala Leu Glu Phe Glu Tyr Met Arg  
 55 60 65  
 tgg atc gct acc ggc gct cgg gcg ttc atc gat gcg cat cag gat gca 355  
 Trp Ile Ala Thr Gly Ala Arg Ala Phe Ile Asp Ala His Gln Asp Ala  
 70 75 80 85  
 tcc aag ctg cgg att act cac ctc ggc ggc ggt gcg tgc acg atg gcc 403  
 Ser Lys Leu Arg Ile Thr His Leu Gly Gly Gly Ala Cys Thr Met Ala



aaa  
1269

<210> 344

<211> 382

<212> PRT

<213> Corynebacterium glutamicum

<400> 344

Met Thr Ala Thr Tyr Thr Thr Glu Thr Ala Ile Asn Phe Leu Phe Leu  
1 5 10 15

Ser Glu Pro Asp Met Ile Ala Ala Gly Val Lys Asp Val Ala Gln Cys  
20 25 30

Val Asp Val Met Glu Glu Thr Leu Val Leu Leu Ala Gln Gly Asp Tyr  
35 40 45

Lys Met Ala Gly Leu Asn Ser Asn Ser His Gly Ala Met Ile Thr Phe  
50 55 60

Pro Glu Asn Pro Glu Phe Glu Gly Met Pro Lys Asp Gly Pro Asp Arg  
65 70 75 80

Arg Phe Met Ala Met Pro Ala Tyr Leu Gly Gly Arg Phe Lys Asn Thr  
85 90 95

Gly Val Lys Trp Tyr Gly Ser Asn Ala Glu Asn Lys Ala Ser Gly Leu  
100 105 110

Pro Arg Ser Ile His Thr Phe Val Leu Asn Asp Thr Val Thr Gly Ala  
115 120 125

Pro Lys Ala Ile Met Ser Ala Asn Leu Leu Ser Ala Tyr Arg Thr Gly  
130 135 140

Ala Val Pro Gly Val Gly Val Lys His Leu Ala Val Ala Asp Ala Thr  
145 150 155 160

Thr Leu Ala Val Val Gly Pro Gly Val Met Ala Lys Thr Ile Thr Glu  
165 170 175

Ala Cys Ile Ala Glu Arg Pro Gly Ile Thr Thr Ile Lys Ile Lys Gly  
180 185 190

Arg Ser Glu Arg Gly Ile Asn Ala Phe Ala Thr Trp Ala Leu Glu Lys  
195 200 205

Phe Pro Glu Ile Glu Val Val Ala Val Gly Ser Glu Glu Asp Val Val  
210 215 220

Lys Asp Ala Asp Ile Val Ile Ala Ala Thr Thr Thr Asp Ala Ala Gly  
225 230 235 240

Ser Ser Ala Phe Pro Tyr Phe Lys Lys Glu Trp Leu Lys Pro Gly Ala  
245 250 255

Leu Leu Leu Leu Pro Ala Ala Gly Arg Phe Asp Asp Ala Tyr Leu Leu  
260 265 270

170	175	180	
cgc cca gga atc acc acc atc aag atc aag gga cgc agc gaa cgc ggc Arg Pro Gly Ile Thr Thr Ile Lys Ile Lys Gly Arg Ser Glu Arg Gly 185 190 195			691
atc aac gcc ttt gca aca tgg gcg ttg gaa aaa ttc ccc gag atc gaa Ile Asn Ala Phe Ala Thr Trp Ala Leu Glu Lys Phe Pro Glu Ile Glu 200 205 210			739
gtg gtc gcc gtc gga tct gaa gaa gac gtg gtc aaa gac gcc gac atc Val Val Ala Val Gly Ser Glu Glu Asp Val Val Lys Asp Ala Asp Ile 215 220 225			787
gtc atc gcc gcc acc acc acg gac gcc gcc ggc tcc tcc gcc ttc cca Val Ile Ala Ala Thr Thr Asp Ala Ala Gly Ser Ser Ala Phe Pro 230 235 240 245			835
tac ttc' aaa aaa gaa tgg ctc aag ccg ggc gca ttg ctg ctg ctt cca Tyr Phe Lys Lys Glu Trp Leu Lys Pro Gly Ala Leu Leu Leu Leu Pro 250 255 260			883
gcc gcc ggt cgc ttc gac gac gct tat ttg ctt gac gac gcc cgc ctc Ala Ala Gly Arg Phe Asp Asp Ala Tyr Leu Leu Asp Asp Ala Arg Leu 265 270 275			931
gtt gtt gac tac atg ggg ctc tac gaa gcc tgg gca gaa gaa tac ggc Val Val Asp Tyr Met Gly Leu Tyr Glu Ala Trp Ala Glu Glu Tyr Gly 280 285 290			979
cca cag gcc tac caa cta ctc ggc att cca gga acc cac tgg tac gac 1027 Pro Gln Ala Tyr Gln Leu Leu Gly Ile Pro Gly Thr His Trp Tyr Asp 295 300 305			
ctg gcg ctg caa gga aaa ctc gac ctt gca aag att tcc cag att ggc 1075 Leu Ala Leu Gln Gly Lys Leu Asp Leu Ala Lys Ile Ser Gln Ile Gly 310 315 320 325			
gat atc tgc tcc ggc aag cta ccc gga cgc acc aac gat gag gaa atc 1123 Asp Ile Cys Ser Gly Lys Leu Pro Gly Arg Thr Asn Asp Glu Glu Ile 330 335 340			
atc ctc tat tcc gtc ggc ggc atg cca gta gaa gac gtc gcc tgg gca 1171 Ile Leu Tyr Ser Val Gly Gly Met Pro Val Glu Asp Val Ala Trp Ala 345 350 355			
acc caa gtg tat gaa aac gcc ctg gaa aaa ggc gtc ggc acc aca ttg 1219 Thr Gln Val Tyr Glu Asn Ala Leu Glu Lys Gly Val Gly Thr Thr Leu 360 365 370			
aac ctg tgg gaa tca ccc gca ctg gct tgagagaaga aacaacaatg 1266 Asn Leu Trp Glu Ser Pro Ala Leu Ala 375 380			

<210> 343  
 <211> 1269  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1246)  
 <223> RXA02262

<400> 343  
 gcaccaatttt cggacctgaa atccccgagg aaaccgtgcc cgacgccgtg caggtgggcg 60

tcgataagca aaaaatcgct gatactcgaa aggcctcaaa atg acc gca acc tac 115  
 Met Thr Ala Thr Tyr  
 1 5

acc act gaa acc gcc atc aat ttc ttg ttc ttg agc gaa ccg gac atg 163  
 Thr Thr Glu Thr Ala Ile Asn Phe Leu Phe Leu Ser Glu Pro Asp Met  
 10 15 20

atc gcg gcc gga gtc aaa gac gtc gcg caa tgc gtc gat gtc atg gag 211  
 Ile Ala Ala Gly Val Lys Asp Val Ala Gln Cys Val Asp Val Met Glu  
 25 30 35

gaa acg ctc gtg ctc ttg gcg cag ggc gac tac aaa atg gcc ggt ttg 259  
 Glu Thr Leu Val Leu Leu Ala Gln Gly Asp Tyr Lys Met Ala Gly Leu  
 40 45 50

aac tcc aac tcg cat ggc gcg atg atc acc ttc ccg gaa aac cca gaa 307  
 Asn Ser Asn Ser His Gly Ala Met Ile Thr Phe Pro Glu Asn Pro Glu  
 55 60 65

ttt gaa ggc atg ccc aag gac ggc ccc gac cgc cga ttc atg gcg atg 355  
 Phe Glu Gly Met Pro Lys Asp Gly Pro Asp Arg Arg Phe Met Ala Met  
 70 75 80 85

ccc gca tac ctc ggc ggg cga ttc aaa aac acc ggc gtg aag tgg tac 403  
 Pro Ala Tyr Leu Gly Gly Arg Phe Lys Asn Thr Gly Val Lys Trp Tyr  
 90 95 100

gga tcc aac gcg gaa aac aag gcc tca ggc ttg cct cgc tcg atc cac 451  
 Gly Ser Asn Ala Glu Asn Lys Ala Ser Gly Leu Pro Arg Ser Ile His  
 105 110 115

acc ttc gtc ctc aac gac acg gtc acc ggt gca ccg aag gcc atc atg 499  
 Thr Phe Val Leu Asn Asp Thr Val Thr Gly Ala Pro Lys Ala Ile Met  
 120 125 130

tcc gcg aac ctg ctg tcc gcc tac cgc acc ggc gcg gtt ccc ggc gtg 547  
 Ser Ala Asn Leu Leu Ser Ala Tyr Arg Thr Gly Ala Val Pro Gly Val  
 135 140 145

ggc gtg aag cac tta gcg gtc gcc gac gcg aca acc ttg gct gtc gtc 595  
 Gly Val Lys His Leu Ala Val Ala Asp Ala Thr Thr Leu Ala Val Val  
 150 155 160 165

gga cct ggt gtc atg gcg aaa acc atc acc gaa gcg tgc atc gca gag 643  
 Gly Pro Gly Val Met Ala Lys Thr Ile Thr Glu Ala Cys Ile Ala Glu

gca gtg gct tcc cgt gca acg cgc ggt gga acc gcg ggc gtg cgg gtt 691  
 Ala Val Ala Ser Arg Ala Thr Arg Gly Gly Thr Ala Gly Val Arg Val  
                   185                                  190                                  195

gcg gag caa cgc gca cgt gtc gat gcc gca agt acc gct cac gcg gag 739  
 Ala Glu Gln Arg Ala Arg Val Asp Ala Ala Ser Thr Ala His Ala Glu  
                   200                                  205                                  210

tgg gca cgt gcg ggg gta cgt cga taagcattag tttatggcct gtg 786  
 Trp Ala Arg Ala Gly Val Arg Arg  
                   215                                  220

<210> 342

<211> 221

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 342

Met Ser Arg Leu Ala Glu Glu Ile Ile Ala Trp Cys Thr Pro Glu Phe  
           1                                  5                                  10                                  15

Gly Tyr Ile Thr Leu Ser Asp Ser Trp Ser Thr Gly Ser Ser Ile Met  
                   20                                  25                                  30

Pro Gln Lys Lys Asn Pro Asp Val Ala Glu Leu Thr Arg Gly Lys Ser  
                   35                                  40                                  45

Gly Arg Leu Ile Gly Asn Leu Thr Gly Leu Leu Ala Thr Leu Lys Ala  
           50                                  55                                  60

Gln Pro Leu Ala Tyr Asn Arg Asp Leu Gln Glu Asp Lys Glu Pro Ile  
           65                                  70                                  75                                  80

Val Asp Ser Val Ala Gln Leu Asn Leu Leu Leu Pro Ala Met Thr Gly  
                   85                                  90                                  95

Leu Val Ser Thr Leu Thr Phe Asn Thr Glu Arg Met Arg Glu Leu Ala  
                   100                                  105                                  110

Pro Ala Gly Phe Thr Leu Ala Thr Asp Leu Ala Glu Trp Met Val Arg  
                   115                                  120                                  125

Gln Gly Val Pro Phe Arg Glu Ala His Glu Ala Ser Gly Ala Cys Val  
           130                                  135                                  140

Arg Ile Ala Glu Ser Arg Gly Val Asp Leu Ile Asp Leu Thr Asp Glu  
           145                                  150                                  155                                  160

Glu Leu Ser Gly Val Asp Ala Arg Leu Thr Pro Glu Val Arg Glu Val  
                   165                                  170                                  175

Leu Thr Ile Asp Gly Ala Val Ala Ser Arg Ala Thr Arg Gly Gly Thr  
                   180                                  185                                  190

Ala Gly Val Arg Val Ala Glu Gln Arg Ala Arg Val Asp Ala Ala Ser  
                   195                                  200                                  205

Thr Ala His Ala Glu Trp Ala Arg Ala Gly Val Arg Arg  
           210                                  215                                  220

<210> 341  
 <211> 786  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(763)  
 <223> FRXA02162

<400> 341  
 ctccggctttg attccgcagc agataactcc attgatgccca ccagctcccg cgatttcgca 60

tctgaaaccg ccttcgtgct ggcgcagctt gcangtggat atg tcc cgc ttg gct 115  
 Met Ser Arg Leu Ala  
 1 5

gaa gaa atc atc gca tgg tgc acc cca gaa ttt ggt tac atc acc ttg 163  
 Glu Glu Ile Ile Ala Trp Cys Thr Pro Glu Phe Gly Tyr Ile Thr Leu  
 10 15 20

tct gat tcc tgg tcc aca ggc agc tca atc atg ccg cag aag aag aac 211  
 Ser Asp Ser Trp Ser Thr Gly Ser Ser Ile Met Pro Gln Lys Lys Asn  
 25 30 35

cct gac gtg gca gag ctg acc cgt ggc aag tct ggt cgc ttg atc ggt 259  
 Pro Asp Val Ala Glu Leu Thr Arg Gly Lys Ser Gly Arg Leu Ile Gly  
 40 45 50

aac ctc acc ggt ctg ctg gct acc ctg aag gca cag cct tta gcg tac 307  
 Asn Leu Thr Gly Leu Leu Ala Thr Leu Lys Ala Gln Pro Leu Ala Tyr  
 55 60 65

aac cgc gac ctg cag gaa gat aag gaa cca atc gta gat tcc gtg gcg 355  
 Asn Arg Asp Leu Gln Glu Asp Lys Glu Pro Ile Val Asp Ser Val Ala  
 70 75 80 85

cag ctc aac ctg ctg ctc cct gca atg act ggt ttg gtt tcc acc ttg 403  
 Gln Leu Asn Leu Leu Leu Pro Ala Met Thr Gly Leu Val Ser Thr Leu  
 90 95 100

acc ttc aac acc gag cgc atg cgt gaa ctt gca cca gca ggt ttc acc 451  
 Thr Phe Asn Thr Glu Arg Met Arg Glu Leu Ala Pro Ala Gly Phe Thr  
 105 110 115

ctt gcc acc gac ttg gct gag tgg atg gtg cgc cag ggc gtt cca ttc 499  
 Leu Ala Thr Asp Leu Ala Glu Trp Met Val Arg Gln Gly Val Pro Phe  
 120 125 130

cgt gag gca cac gaa gca tcc ggc gct tgc gtg cgg atc gcg gag tcc 547  
 Arg Glu Ala His Glu Ala Ser Gly Ala Cys Val Arg Ile Ala Glu Ser  
 135 140 145

agg gga gtg gac ctt atc gat ctc act gat gaa gaa ctc agt ggc gtt 595  
 Arg Gly Val Asp Leu Ile Asp Leu Thr Asp Glu Glu Leu Ser Gly Val  
 150 155 160 165

gat gca cgt ctg acc cca gag gta cgg gaa gtg ctc acc att gat ggt 643  
 Asp Ala Arg Leu Thr Pro Glu Val Arg Glu Val Leu Thr Ile Asp Gly  
 170 175 180

tgaagaaatc atcgcatggt gca

906

&lt;210&gt; 340

&lt;211&gt; 261

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 340

Met Glu Gln His Gly Thr Asn Glu Gly Ala Leu Trp Gly Gly Arg Phe  
 1 5 10 15

Ser Gly Gly Pro Ser Glu Ala Met Phe Ala Leu Ser Val Ser Thr His  
 20 25 30

Phe Asp Trp Val Leu Ala Pro Tyr Asp Val Leu Ala Ser Lys Ala His  
 35 40 45

Ala Lys Val Leu His Gln Ala Asp Leu Leu Ser Asp Glu Asp Leu Ala  
 50 55 60

Thr Met Leu Ala Gly Leu Asp Gln Leu Gly Lys Asp Val Ala Asp Gly  
 65 70 75 80

Thr Phe Gly Pro Leu Pro Ser Asp Glu Asp Val His Gly Ala Met Glu  
 85 90 95

Arg Gly Val Ile Asp Arg Val Gly Pro Glu Val Gly Gly Arg Leu Arg  
 100 105 110

Ala Gly Arg Ser Arg Asn Asp Gln Val Ala Thr Leu Phe Arg Met Trp  
 115 120 125

Val Arg Asp Ala Val Arg Asp Ile Ala Leu Gly Thr Thr Glu Leu Val  
 130 135 140

Asp Ala Leu Ser Ala Gln Ala Lys Ala His Ala Gly Ala Ile Met Pro  
 145 150 155 160

Gly Lys Thr His Phe Gln Ala Ala Gln Pro Val Leu Leu Ala His Gln  
 165 170 175

Leu Leu Ala His Ala Gln Pro Leu Leu Arg Asp Ile Asp Arg Ile Arg  
 180 185 190

Asp Leu Asp Lys Arg Leu Ala Val Ser Pro Tyr Gly Ser Gly Ala Leu  
 195 200 205

Ala Gly Ser Ser Leu Lys Leu Asn Pro Glu Ala Ile Ala Glu Glu Leu  
 210 215 220

Gly Phe Asp Ser Ala Ala Asp Asn Ser Ile Asp Ala Thr Ser Ser Arg  
 225 230 235 240

Asp Phe Ala Ser Glu Thr Ala Phe Val Leu Ala Gln Leu Ala Xaa Gly  
 245 250 255

Tyr Val Pro Leu Gly  
 260

Thr Thr Leu Asn Leu Thr Tyr Val Val Glu Gly Ser Glu Glu Met Gly  
 150 155 160 165  
 ggc gga gcg ctc agc gcg ctc atc aag gac aag cct gag ctt ttc gac 643  
 Gly Gly Ala Leu Ser Ala Leu Ile Lys Asp Lys Pro Glu Leu Phe Asp  
 170 175 180  
 gca gat gtc atc ttg att gca gac agc gga aac gct tcc gtg ggc acc 691  
 Ala Asp Val Ile Leu Ile Ala Asp Ser Gly Asn Ala Ser Val Gly Thr  
 185 190 195  
 cca acc ttg acc act acc ctg cgc ggt ggc gga cag gtc acc gtc acc 739  
 Pro Thr Leu Thr Thr Thr Leu Arg Gly Gly Gly Gln Val Thr Val Thr  
 200 205 210  
 gtg gac acc ctt gaa ggc gct gtt cac tcc ggc cag aac ggt ggc gct 787  
 Val Asp Thr Leu Glu Gly Ala Val His Ser Gly Gln Asn Gly Gly Ala  
 215 220 225  
 gcc cca gat gct gtt gct gct ctc gtg cgc gtt ctg gat act ttg cgc 835  
 Ala Pro Asp Ala Val Ala Ala Leu Val Arg Val Leu Asp Thr Leu Arg  
 230 235 240 245  
 gat gaa cac gga cgc acc gtt atc gac ggc tgt caa cac cac cgc aaa 883  
 Asp Glu His Gly Arg Thr Val Ile Asp Gly Cys Gln His His Arg Lys  
 250 255 260  
 ctg gaa ggg cga gcc tta tgatccagag actttccgca gcg 924  
 Leu Glu Gly Arg Ala Leu  
 265

&lt;210&gt; 358

&lt;211&gt; 267

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 358

Met Thr Gln Phe Glu Asn Ala Gln Val Leu Lys Glu Asn Ile Glu Asn  
 1 5 10 15  
 Gln Arg Glu Gln Ile Phe Thr Gln Leu Lys Glu Ile Val Ser Phe Asn  
 20 25 30  
 Ser Val His Ser Asp Pro Asn Leu Leu Glu Asp Tyr Ala Gly Ala Lys  
 35 40 45  
 Glu Trp Val Lys Glu Thr Leu Thr Asn Ala Gly Leu Thr Val Ser Glu  
 50 55 60  
 Phe Ala Ala Glu Asp Gly Thr Thr Asn Phe Ile Gly Thr Arg Lys Gly  
 65 70 75 80  
 Ser Glu Gly Ala Pro Lys Val Leu Leu Tyr Ser His Phe Asp Val Val  
 85 90 95  
 Pro Ser Gly Pro Leu Asp Leu Trp Asp Thr Asn Pro Phe Glu Leu Thr  
 100 105 110  
 Glu Arg Asp Ala Gly His Gly Thr Arg Trp Tyr Gly Arg Gly Ala Ala  
 115 120 125

Gly Pro Asn Asp Ala Ser Pro Leu Phe Asp Gln Phe Val Glu Leu Met  
 370 375 380

Asp Ala Asp Ala Gln Lys Lys Gly Ala  
 385 390

<210> 357  
 <211> 924  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(901)  
 <223> RXS00905

<400> 357  
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 tctgcatcga gtcgggtcga cgtatataag gtggaaaggc atg acc caa ttc gaa 115  
 Met Thr Gln Phe Glu  
 1 5  
 aac gcg caa gta ctt aaa gag aac atc gaa aac caa cgc gag cag atc 163  
 Asn Ala Gln Val Leu Lys Glu Asn Ile Glu Asn Gln Arg Glu Gln Ile  
 10 15 20  
 ttt acc cag ttg aaa gaa att gtg tct ttc aac tcc gtg cac agc gat 211  
 Phe Thr Gln Leu Lys Glu Ile Val Ser Phe Asn Ser Val His Ser Asp  
 25 30 35  
 cca aac cta ctg gag gac tac gcc gcc gcg aaa gaa tgg gta aaa gaa 259  
 Pro Asn Leu Leu Glu Asp Tyr Ala Gly Ala Lys Glu Trp Val Lys Glu  
 40 45 50  
 aca ctg acc aac gca ggt ctc acc gtc agc gaa ttc gct gcc gaa gat 307  
 Thr Leu Thr Asn Ala Gly Leu Thr Val Ser Glu Phe Ala Ala Glu Asp  
 55 60 65  
 gga acc acc aac ttc atc gcc acc cgc aag gcc tcc gaa ggt gca cca 355  
 Gly Thr Thr Asn Phe Ile Gly Thr Arg Lys Gly Ser Glu Gly Ala Pro  
 70 75 80 85  
 aag gta ctg ctg tac agc cac ttc gac gtt gtc cca tcc gcc cct ttg 403  
 Lys Val Leu Leu Tyr Ser His Phe Asp Val Val Pro Ser Gly Pro Leu  
 90 95 100  
 gat ctc tgg gac acc aat cct ttt gaa ctc acc gag cgc gac gct gcc 451  
 Asp Leu Trp Asp Thr Asn Pro Phe Glu Leu Thr Glu Arg Asp Ala Gly  
 105 110 115  
 cac gcc acc cgc tgg tac gcc cgc gcc gcc gct gac tgc aag gcc aac 499  
 His Gly Thr Arg Trp Tyr Gly Arg Gly Ala Ala Asp Cys Lys Gly Asn  
 120 125 130  
 ctg gtc atg cac ctc gca gca ctg cgc gcc gtc gaa gcc agc gcc gac 547  
 Leu Val Met His Leu Ala Ala Leu Arg Ala Val Glu Ala Ser Gly Asp  
 135 140 145  
 acc aca ctc aac ctc acc tac gtg gtc gag gcc tcc gag gaa atg gga 595



Ala Met Thr Gly Tyr Gln Glu Thr Met Thr Asp Pro Ser Tyr His Arg  
 50 55 60  
 Gln Ile Val Val Ala Thr Ala Pro Gln Ile Gly Asn Thr Gly Trp Asn  
 65 70 75 80  
 Asp Glu Asp Asn Glu Ser Arg Asp Gly Lys Ile Trp Val Ala Gly Leu  
 85 90 95  
 Val Ile Arg Asp Leu Ala Ala Arg Val Ser Asn Trp Arg Ala Thr Thr  
 100 105 110  
 Ser Leu Gln Gln Glu Met Ala Gly Gln Gly Ile Val Gly Ile Gly Gly  
 115 120 125  
 Ile Asp Thr Arg Ala Leu Val Arg His Leu Arg Asn Glu Gly Ser Ile  
 130 135 140  
 Ala Ala Gly Ile Phe Ser Gly Ala Asp Ala Gln Arg Pro Val Glu Glu  
 145 150 155 160  
 Leu Val Glu Ile Val Lys Asn Gln Pro Ala Met Thr Gly Ala Asn Leu  
 165 170 175  
 Ser Val Glu Val Ser Ala Asp Glu Thr Tyr Val Ile Glu Ala Glu Gly  
 180 185 190  
 Glu Glu Arg His Thr Val Val Ala Tyr Asp Leu Gly Ile Lys Gln Asn  
 195 200 205  
 Thr Pro Arg Arg Phe Ser Ala Arg Gly Val Arg Thr Val Ile Val Pro  
 210 215 220  
 Ala Glu Thr Pro Phe Glu Asp Ile Lys Gln Tyr Asn Pro Ser Gly Val  
 225 230 235 240  
 Phe Ile Ser Asn Gly Pro Gly Asp Pro Ala Ala Ala Asp Val Met Val  
 245 250 255  
 Asp Ile Val Arg Glu Val Leu Glu Ala Asp Ile Pro Phe Phe Gly Ile  
 260 265 270  
 Cys Phe Gly Asn Gln Ile Leu Gly Arg Ala Phe Gly Met Glu Thr Tyr  
 275 280 285  
 Lys Leu Lys Phe Gly His Arg Gly Ile Asn Val Pro Val Lys Asn His  
 290 295 300  
 Ile Thr Gly Lys Ile Asp Ile Thr Ala Gln Asn His Gly Phe Ala Leu  
 305 310 315 320  
 Lys Gly Glu Ala Gly Gln Glu Phe Glu Thr Asp Phe Gly Thr Ala Ile  
 325 330 335  
 Val Thr His Thr Cys Leu Asn Asp Gly Val Val Glu Gly Ile Ala Leu  
 340 345 350  
 Lys Ser Gly Arg Ala Tyr Ser Val Gln Tyr His Pro Glu Ala Ala Ala  
 355 360 365

Pro Gly Asp Pro Ala Ala Ala Asp Val Met Val Asp Ile Val Arg Glu  
 250 255 260

gtt ctt gaa gcc gac att cca ttc ttt ggc atc tgc ttc ggc aac cag 931  
 Val Leu Glu Ala Asp Ile Pro Phe Phe Gly Ile Cys Phe Gly Asn Gln  
 265 270 275

att ctt ggc cgc gca ttc ggc atg gag acc tac aag ctg aag ttc ggc 979  
 Ile Leu Gly Arg Ala Phe Gly Met Glu Thr Tyr Lys Leu Lys Phe Gly  
 280 285 290

cac cgc ggc atc aac gtt cca gtg aag aac cac atc acc ggc aag atc  
 1027

His Arg Gly Ile Asn Val Pro Val Lys Asn His Ile Thr Gly Lys Ile  
 295 300 305

gac atc acc gcc cag aac cac ggc ttc gca ctc aag ggt gaa gca ggc  
 1075

Asp Ile Thr Ala Gln Asn His Gly Phe Ala Leu Lys Gly Glu Ala Gly  
 310 315 320 325

cag gaa ttc gag acc gat ttc ggc act gca att gtc acc cac acc tgc  
 1123

Gln Glu Phe Glu Thr Asp Phe Gly Thr Ala Ile Val Thr His Thr Cys  
 330 335 340

ctc aac gac ggc gtc gtt gaa ggt att gcg ctg aag tcc gga cgc gca  
 1171

Leu Asn Asp Gly Val Val Glu Gly Ile Ala Leu Lys Ser Gly Arg Ala  
 345 350 355

tac tcc gtt cag tac cac cca gag gcc gct gcc ggc cca aat gat gca  
 1219

Tyr Ser Val Gln Tyr His Pro Glu Ala Ala Ala Gly Pro Asn Asp Ala  
 360 365 370

agc ccc ctg ttt gac cag ttt gtt gag ctg atg gat gca gac gct cag  
 1267

Ser Pro Leu Phe Asp Gln Phe Val Glu Leu Met Asp Ala Asp Ala Gln  
 375 380 385

aag aaa ggc gca taaataacat gccaaagcgt tca  
 1302

Lys Lys Gly Ala  
 390

&lt;210&gt; 356

&lt;211&gt; 393

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 356

Val Ser Lys Asp Thr Thr Thr Tyr Gln Gly Val Thr Glu Ile Gly Ser  
 1 5 10 15

Val Pro Ala Tyr Leu Val Leu Ala Asp Gly Arg Thr Phe Thr Gly Phe  
 20 25 30

Gly Phe Gly Ala Ile Gly Thr Thr Leu Gly Glu Ala Val Phe Thr Thr  
 35 40 45

acc acc tac cag gga gtc acc gag atc gga tcc gtt ccg gca tac ctg	163
Thr Thr Tyr Gln Gly Val Thr Glu Ile Gly Ser Val Pro Ala Tyr Leu	
10 15 20	
ggt ctt gca gac gga cgt acc ttc acc gga ttt ggc ttt gga gct atc	211
Val Leu Ala Asp Gly Arg Thr Phe Thr Gly Phe Gly Phe Gly Ala Ile	
25 30 35	
ggc acc acc ctt ggt gag gca gtg ttc act acc gcc atg acc ggt tac	259
Gly Thr Thr Leu Gly Glu Ala Val Phe Thr Thr Ala Met Thr Gly Tyr	
40 45 50	
caa gaa acc atg acc gat cct tcc tat cac cgc cag att gtt gtg gct	307
Gln Glu Thr Met Thr Asp Pro Ser Tyr His Arg Gln Ile Val Val Ala	
55 60 65	
acc gca cca cag atc ggc aac acc ggc tgg aac gat gag gac aac gag	355
Thr Ala Pro Gln Ile Gly Asn Thr Gly Trp Asn Asp Glu Asp Asn Glu	
70 75 80 85	
tcc cgc gac ggc aag att tgg gtt gca ggc ctt gtt atc cgc gac ctc	403
Ser Arg Asp Gly Lys Ile Trp Val Ala Gly Leu Val Ile Arg Asp Leu	
90 95 100	
gca gca cgt gtg tcc aac tgg cgc gcc acc acc tcc ttg cag cag gaa	451
Ala Ala Arg Val Ser Asn Trp Arg Ala Thr Thr Ser Leu Gln Gln Glu	
105 110 115	
atg gca ggc cag ggc atc gtc ggc atc ggc gga atc gac acc cgc gca	499
Met Ala Gly Gln Gly Ile Val Gly Ile Gly Gly Ile Asp Thr Arg Ala	
120 125 130	
ctg gtt cgc cac ctg cgc aat gaa ggt tcc att gca gcg ggc atc ttc	547
Leu Val Arg His Leu Arg Asn Glu Gly Ser Ile Ala Ala Gly Ile Phe	
135 140 145	
tcc ggc gct gac gca cag cgc cca gtt gaa gaa ctc gta gag atc gtc	595
Ser Gly Ala Asp Ala Gln Arg Pro Val Glu Glu Leu Val Glu Ile Val	
150 155 160 165	
aag aat cag cca gca atg acc ggc gca aac ctc tcc gtt gag gtc tct	643
Lys Asn Gln Pro Ala Met Thr Gly Ala Asn Leu Ser Val Glu Val Ser	
170 175 180	
gct gat gaa acc tac gtc atc gaa gct gaa ggc gaa gag cgc cac acc	691
Ala Asp Glu Thr Tyr Val Ile Glu Ala Glu Gly Glu Glu Arg His Thr	
185 190 195	
gtc gtg gcc tac gac ctg ggc att aag caa aac acc cca cgt cgt ttc	739
Val Val Ala Tyr Asp Leu Gly Ile Lys Gln Asn Thr Pro Arg Arg Phe	
200 205 210	
tct gca cgc ggt gtt cgc acc gtc atc gtg cct gct gaa acc cca ttc	787
Ser Ala Arg Gly Val Arg Thr Val Ile Val Pro Ala Glu Thr Pro Phe	
215 220 225	
gag gat atc aag cag tac aac cca tca ggc gtg ttc atc tcc aac ggc	835
Glu Asp Ile Lys Gln Tyr Asn Pro Ser Gly Val Phe Ile Ser Asn Gly	
230 235 240 245	
cct ggc gat cct gca gca gca gac gtc atg gtt gat atc gtc cgc gaa	883

526

1	5	10	15
Thr Arg Thr	Ala Arg Gln Ala Leu	Ile Leu Gln Ile Leu	Asp Lys Gln
	20	25	30
Lys Val Thr	Ser Gln Val Gln Leu	Ser Glu Leu Leu Leu	Asp Glu Gly
	35	40	45
Ile Asp Ile	Thr Gln Ala Thr Leu	Ser Arg Asp Leu Asp	Glu Leu Gly
	50	55	60
Ala Arg Lys	Val Arg Pro Asp Gly	Gly Arg Ala Tyr Tyr	Ala Val Gly
	65	70	75
Pro Val Asp	Ser Ile Ala Arg Glu	Asp Leu Arg Gly Pro	Ser Glu Lys
	85	90	95
Leu Arg Arg	Met Leu Asp Glu Leu	Leu Val Ser Thr Asp	His Ser Gly
	100	105	110
Asn Ile Ala	Met Leu Arg Thr Pro	Pro Gly Ala Ala Gln	Tyr Leu Ala
	115	120	125
Ser Phe Ile	Asp Arg Val Gly Leu	Lys Glu Val Val Gly	Thr Ile Ala
	130	135	140
Gly Asp Asp	Thr Val Phe Val Leu	Ala Arg Asp Pro Leu	Thr Gly Lys
	145	150	155
Glu Leu Gly	Glu Leu Leu Ser Gly	Arg Thr Thr	
	165	170	

&lt;210&gt; 353

&lt;211&gt; 414

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(391)

&lt;223&gt; RXN02154

&lt;400&gt; 353

cccagaacct cggcgaagtc agcgacaagc cagtcaaggt gagcttcacc ccagtgcttg 60

caccgttacc	tcgcgaattc	tcaccactgc	aaccgcacct	ttg aaa gaa ggc gtt	115
				Leu Lys Glu Gly Val	
				1 5	

acc gca gaa	cag gct cgc	gca gta tat	gaa gag ttc	tat gca cag gaa	163
Thr Ala Glu	Gln Ala Arg	Ala Val Tyr	Glu Glu Phe	Tyr Ala Gln Glu	
	10		15	20	

acc ttc gtg	cat gtt ctt	cca gaa ggt	gca cag cca	caa acc caa gca	211
Thr Phe Val	His Val Leu	Pro Glu Gly	Ala Gln Pro	Gln Thr Gln Ala	
	25		30	35	

gtt ctt ggc	tcc aac atg	tgc cac gtg	cag gta gaa	att gat gag gaa	259
Val Leu Gly	Ser Asn Met	Cys His Val	Gln Val Glu	Ile Asp Glu Glu	
	40		45	50	



&lt;400&gt; 350

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Met Pro Thr Ala Ser Pro Ile Tyr Asp Val Val Val Val Gly Ala Gly
 1              5              10              15

Ile Ser Gly Leu Ile Ala Thr Gln Leu Leu Asp Arg Ala Gly Leu Asn
      20              25              30

Ile Lys Cys Phe Glu Ala Cys Ser Arg Val Gly Gly Arg Ala Val Ser
      35              40              45

Val Gln Gln Ser Asp Leu Phe Leu Asp Leu Gly Ala Thr Trp Phe Trp
      50              55              60

Leu Asn Glu Pro Leu Val Gln Gln Leu Val Asn Asn Leu Gly Leu Gly
      65              70              75              80

Thr Phe Pro Gln Ala Ile Glu Gly Asp Ala Leu Phe Glu Thr Leu Val
      85              90              95

Asp Ala Pro Ser Arg Leu Arg Gly Asn Pro Ile Asp Ala Ala Ser Gly
      100             105             110

Arg Phe Gln Ala Gly Ala Ser Ser Leu Ala Leu Gly Leu Ala Ala Gln
      115             120             125

Leu Lys Pro Gly Val Leu Glu Leu Gly Asp Pro Val His Ser Leu Ser
      130             135             140

Glu Glu Asp Gly Glu Ile Val Val Lys Ser Ser Lys Gln Ile Val Arg
      145             150             155             160

Ala Lys His Val Ile Ile Ala Val Pro Pro Ala Leu Ala Ala Glu Leu
      165             170             175

Ile Gly Phe Thr Leu Asp Leu Pro Ala Asp Val Arg Lys Ala Ala His
      180             185             190

Pro Gln His Ile Ala Val Met Asn Trp Ala Lys Glu Lys Tyr Thr Leu
      195             200             205

Pro Thr Gln Ala Ala Ser Ala Gly Gly Phe Gly His Glu Leu Phe Gln
      210             215             220

Gln Pro Leu Gly His Gly Arg Ile His Trp Ala Ser Thr Glu Val Ala
      225             230             235             240

Thr Glu Phe Gly Gly His Leu Glu Gly Ala Val Arg Ala Gly Ile Gln
      245             250             255

Ala Ala Leu Gln Thr Gly Phe Asn Leu Lys Ser
      260             265

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&lt;210&gt; 351

&lt;211&gt; 636

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(613)

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Leu Phe Leu Asp Leu Gly Ala Thr Trp Phe Trp Leu Asn Glu Pro Leu
  55                                60                                65

gtg cag caa ctc gtc aat aat ctc ggc ctc ggc aca ttc cct cag gcc 355
Val Gln Gln Leu Val Asn Asn Leu Gly Leu Gly Thr Phe Pro Gln Ala
  70                                75                                80                                85

atc gag ggt gat gcg ctt ttt gag acg ctt gtc gac gcc ccg agc cgc 403
Ile Glu Gly Asp Ala Leu Phe Glu Thr Leu Val Asp Ala Pro Ser Arg
                                90                                95                                100

ctg cgg ggt aac ccc ata gac gct gct tca ggc agg ttc caa gca ggg 451
Leu Arg Gly Asn Pro Ile Asp Ala Ala Ser Gly Arg Phe Gln Ala Gly
                                105                                110                                115

gcc tcc tcg ctt gcg ctc ggg ctt gca gcc cag ctc aag cca gga gtt 499
Ala Ser Ser Leu Ala Leu Gly Leu Ala Ala Gln Leu Lys Pro Gly Val
                                120                                125                                130

tta gaa ctc ggg gac ccc gtc cat tct ctc agt gag gaa gat ggg gaa 547
Leu Glu Leu Gly Asp Pro Val His Ser Leu Ser Glu Glu Asp Gly Glu
                                135                                140                                145

atc gtt gtg aag tct tcc aaa cag att gtg agg gca aag cac gtc atc 595
Ile Val Val Lys Ser Ser Lys Gln Ile Val Arg Ala Lys His Val Ile
                                150                                155                                160                                165

att gcg gtt cca ccg gca ctc gct gcc gag ttg att ggt ttc acc cta 643
Ile Ala Val Pro Pro Ala Leu Ala Ala Glu Leu Ile Gly Phe Thr Leu
                                170                                175                                180

gat tta cca gct gac gtg cga aaa gca gcg cat cca caa cat ata gct 691
Asp Leu Pro Ala Asp Val Arg Lys Ala Ala His Pro Gln His Ile Ala
                                185                                190                                195

gtg atg aat tgg gca aag gag aaa tac acc tta ccc aca caa gcc gca 739
Val Met Asn Trp Ala Lys Glu Lys Tyr Thr Leu Pro Thr Gln Ala Ala
                                200                                205                                210

tcg gct ggg ggt ttt ggg cat gag ctg ttc caa caa cca ctc gga cat 787
Ser Ala Gly Gly Phe Gly His Glu Leu Phe Gln Gln Pro Leu Gly His
                                215                                220                                225

ggg cga att cat tgg gca tca acg gaa gtt gcc act gag ttt ggt gga 835
Gly Arg Ile His Trp Ala Ser Thr Glu Val Ala Thr Glu Phe Gly Gly
                                230                                235                                240                                245

cac ctt gaa ggc gca gtt cgt gca gga att cag gct gcg ctt caa aca 883
His Leu Glu Gly Ala Val Arg Ala Gly Ile Gln Ala Ala Leu Gln Thr
                                250                                255                                260

gga ttt aat cta aaa tct taaacctcgt attttccctg ata 924
Gly Phe Asn Leu Lys Ser
                                265

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&lt;210&gt; 350

&lt;211&gt; 267

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum



Ser Ile Ile Ile Asp Leu Pro Asp Pro Asn Asn Asp Thr Met Ala Arg  
 370 375 380

Leu Tyr Ser Glu Glu Phe Tyr Thr Leu Ala Arg Ala Arg Leu Asn Glu  
 385 390 395 400

Gln Gly Arg Met Val Val Gln Ser Ser Ser Ala Tyr Thr Thr Pro Asp  
 405 410 415

Val Phe Trp Arg Val Gly Ala Thr Leu Lys Ser Ala Gly Cys Glu Gln  
 420 425 430

Val Ile Pro Tyr His Val His Val Pro Thr Phe Gly Asp Trp Gly Phe  
 435 440 445

Gln Leu Cys Gly Pro Ala Asp Met Glu Leu Glu Leu Arg Glu Asp Thr  
 450 455 460

Pro Pro Leu Thr Phe Leu Asn Asp Glu Val Leu Val Ala Ala Gly Val  
 465 470 475 480

Phe Gly Leu Asp Asn Gln Pro Arg Glu Leu Glu Pro Ser Thr Leu Asp  
 485 490 495

His Pro Arg Val Val Glu Asp Leu Arg Lys Gly Tyr Arg Glu Ser Gly  
 500 505 510

Asp

<210> 349  
 <211> 924  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(901)  
 <223> RXA01757

<400> 349  
 cgcttattga acggatgcct ctcgatcaag ccaacgaggc tattgcacgt atttcagctg 60

gtaaaccacg tttccgtatt gtcttggagc cgaattcata atg cca aca gca agc 115  
 Met Pro Thr Ala Ser  
 1 5

cca att tat gat gtc gtt gtc gtc gga gcc ggc att tct ggc ctc atc 163  
 Pro Ile Tyr Asp Val Val Val Val Gly Ala Gly Ile Ser Gly Leu Ile  
 10 15 20

gcc acg caa ctg ttg gac cgc gca ggt cta aac atc aaa tgc ttc gaa 211  
 Ala Thr Gln Leu Leu Asp Arg Ala Gly Leu Asn Ile Lys Cys Phe Glu  
 25 30 35

gcc tgc tca aga gtt ggc ggc cga gca gtg tct gtc caa cag tcc gat 259  
 Ala Cys Ser Arg Val Gly Gly Arg Ala Val Ser Val Gln Gln Ser Asp  
 40 45 50

ttg ttc ctg gac ctc ggc gca aca tgg ttc tgg ctc aac gaa cca ctt 307

Val Ala Gly Tyr Val Ala Ala Leu Gly Leu Gly Ala Leu Leu Val Lys  
 50 55 60  
 Pro Phe Leu Asn Trp Pro Ala Gln Thr Phe Leu Gly Val Glu Thr Leu  
 65 70 75 80  
 Leu Gly Leu Ile Gly Gly Cys Ser Ala Leu Val Leu Tyr Phe Thr Phe  
 85 90 95  
 Ala Thr Ile Gly Gln Ser Leu Trp Ile Leu Val Ile Ala Thr Ala Ala  
 100 105 110  
 Ile Gly Ile Leu Val Gly Ala Glu Leu Pro Leu Leu Met Thr Met Ile  
 115 120 125  
 Gln Gln Gly Arg Leu Ala Asp Ala Lys Thr Thr Gly Ser Leu Val Ala  
 130 135 140  
 Thr Leu Asn Ala Ala Asp Tyr Leu Gly Ala Leu Leu Gly Gly Leu Ala  
 145 150 155 160  
 Trp Pro Phe Val Leu Leu Pro Trp Leu Gly Met Met Arg Gly Ala Ala  
 165 170 175  
 Ala Ala Gly Met Ile Asn Leu Val Ala Ala Leu Phe Val Gly Cys Val  
 180 185 190  
 Leu Leu Arg His Leu Leu Pro Arg Thr His Phe Phe Val Ser Val Val  
 195 200 205  
 Ala Leu Leu Leu Ala Ile Ala Ala Leu Ala Thr Val Leu Val Lys Ser  
 210 215 220  
 Asp Gly Ile Val Ala Thr Ala Arg Ala Gln Leu Tyr Arg Asp Pro Val  
 225 230 235 240  
 Ile Tyr Ser His Gln Ser Asp Tyr Gln Asp Ile Val Val Thr Glu Arg  
 245 250 255  
 Gly Lys Asp Arg Arg Leu Tyr Leu Asn Gly Gly Leu Gln Tyr Ser Thr  
 260 265 270  
 Arg Asp Gln His Arg Tyr Thr Glu Ser Leu Val Tyr Pro Ser Leu Asn  
 275 280 285  
 Pro Glu Ala Glu Ser Val Leu Ile Ile Gly Gly Gly Asp Gly Leu Ala  
 290 295 300  
 Ala Arg Glu Leu Leu Arg Phe Pro Ser Met Gln Ile Thr Gln Val Glu  
 305 310 315 320  
 Leu Asp Pro Glu Val Ile Glu Val Ala Asn Thr Val Leu Arg Ser Asp  
 325 330 335  
 Asn Gly Gly Ala Met Glu Asp Pro Arg Val Ser Ile Ile Val Asp Asp  
 340 345 350  
 Ala Phe Thr Trp Leu Arg Ser Gly Gly Asn Asn Gly Glu Thr Tyr Asp  
 355 360 365

Leu Pro Asp Pro Asn Asn Asp Thr Met Ala Arg Leu Tyr Ser Glu Glu  
375 380 385

ttc tac acc ttg gcc cga gca cga ctg aac gaa caa ggc cgc atg gtg  
1315

Phe Tyr Thr Leu Ala Arg Ala Arg Leu Asn Glu Gln Gly Arg Met Val  
390 395 400 405

gtg caa tcc tcc agc gcc tac acc act cca gat gtg ttc tgg cga gtt  
1363

Val Gln Ser Ser Ser Ala Tyr Thr Thr Pro Asp Val Phe Trp Arg Val  
410 415 420

gga gca acc ttg aaa tcg gcg ggc tgt gaa caa gtc atc cca tat cac  
1411

Gly Ala Thr Leu Lys Ser Ala Gly Cys Glu Gln Val Ile Pro Tyr His  
425 430 435

gtg cat gtt ccc aca ttt ggc gac tgg ggc ttc caa ctg tgt ggc cct  
1459

Val His Val Pro Thr Phe Gly Asp Trp Gly Phe Gln Leu Cys Gly Pro  
440 445 450

gcc gac atg gaa tta gag ctt cgg gaa gac acc ccg cca ctg act ttc  
1507

Ala Asp Met Glu Leu Glu Leu Arg Glu Asp Thr Pro Pro Leu Thr Phe  
455 460 465

ctt aat gat gaa gtt ctg gtg gct gct ggg gtg ttt ggg ttg gat aat  
1555

Leu Asn Asp Glu Val Leu Val Ala Ala Gly Val Phe Gly Leu Asp Asn  
470 475 480 485

cag cct cgt gaa ttg gaa cct tcc acg ctg gat cat ccc cgc gtg gtg  
1603

Gln Pro Arg Glu Leu Glu Pro Ser Thr Leu Asp His Pro Arg Val Val  
490 495 500

gag gat ctg cgc aag gga tac cgc gaa tca ggc gac tagctgcaac  
1649

Glu Asp Leu Arg Lys Gly Tyr Arg Glu Ser Gly Asp  
505 510

gatgcgctgt gtg  
1662

<210> 348

<211> 513

<212> PRT

<213> Corynebacterium glutamicum

<400> 348

Met Ser Asp Leu Gly Pro Ile Trp Arg Trp Leu Leu Leu Val Ser Val  
1 5 10 15

Ser Ile Cys Ala Ala Ser Gly Leu Val Tyr Glu Leu Ala Leu Val Ser  
20 25 30

Leu Ser Thr Ser Leu Asn Gly Gly Gly Ile Val Glu Thr Ser Leu Ile  
35 40 45

150	155	160	165	
ctg ccg tgg ctt ggc atg atg cgc ggt gcc gca gca gcc gga atg atc				643
Leu Pro Trp Leu Gly Met Met Arg Gly Ala Ala Ala Ala Gly Met Ile				
	170	175	180	
aac ctc gtt gca gca cta ttc gtg ggc tgt gtg ctg ctg cga cat ttg				691
Asn Leu Val Ala Ala Leu Phe Val Gly Cys Val Leu Leu Arg His Leu				
	185	190	195	
ctt ccg cgc acc cac ttc ttc gta tcc gtg gtg gcg ctt ctt ctc gcg				739
Leu Pro Arg Thr His Phe Phe Val Ser Val Val Ala Leu Leu Leu Ala				
	200	205	210	
atc gca gcg cta gcc acc gtg ttg gtg aaa tcc gac ggg atc gtt gcc				787
Ile Ala Ala Leu Ala Thr Val Leu Val Lys Ser Asp Gly Ile Val Ala				
	215	220	225	
acc gcc cgc gca cag ctc tac cgc gac ccc gtg atc tat tca cac caa				835
Thr Ala Arg Ala Gln Leu Tyr Arg Asp Pro Val Ile Tyr Ser His Gln				
	230	235	240	245
tct gac tac caa gac atc gta gtg aca gaa cga gcc aaa gac cga cgc				883
Ser Asp Tyr Gln Asp Ile Val Val Thr Glu Arg Gly Lys Asp Arg Arg				
	250	255	260	
ctc tac ctc aat ggc ggt ttg cag tat tcc act cgt gac cag cat aga				931
Leu Tyr Leu Asn Gly Gly Leu Gln Tyr Ser Thr Arg Asp Gln His Arg				
	265	270	275	
tat aca gaa tca ctg gtg tat cca agc ctt aat cca gag gca gaa tcg				979
Tyr Thr Glu Ser Leu Val Tyr Pro Ser Leu Asn Pro Glu Ala Glu Ser				
	280	285	290	
gtg tta atc atc ggc ggt ggc gat ggc ctc gca gca cgg gaa ctc ctc				1027
Val Leu Ile Ile Gly Gly Gly Asp Gly Leu Ala Ala Arg Glu Leu Leu				
	295	300	305	
cga ttc cca tca atg cag atc acc caa gtt gaa tta gac cca gaa gtc				1075
Arg Phe Pro Ser Met Gln Ile Thr Gln Val Glu Leu Asp Pro Glu Val				
	310	315	320	325
atc gaa gta gcc aac aca gtg ctg cgc tct gac aat ggg gga gcg atg				1123
Ile Glu Val Ala Asn Thr Val Leu Arg Ser Asp Asn Gly Gly Ala Met				
	330	335	340	
gaa gat ccc cgc gtc tcc atc atc gtt gac gac gct ttc acc tgg ctg				1171
Glu Asp Pro Arg Val Ser Ile Ile Val Asp Asp Ala Phe Thr Trp Leu				
	345	350	355	
cgc tcc ggc gga aat aat ggc gaa act tac gat tcc atc atc atc gat				1219
Arg Ser Gly Gly Asn Asn Gly Glu Thr Tyr Asp Ser Ile Ile Ile Asp				
	360	365	370	
ctt ccc gac cca aac aac gac acc atg gcc agg ctg tat tca gaa gag				1267

aac cca gag acc gtg tcc acc gac tac gac acc gct gac cgc ctg tac  
 1987  
 Asn Pro Glu Thr Val Ser Thr Asp Tyr Asp Thr Ala Asp Arg Leu Tyr  
 615 620 625

ttc gag cca ctg acc ttc gaa gac gtc atg gag gtc tac cac gct gag  
 2035  
 Phe Glu Pro Leu Thr Phe Glu Asp Val Met Glu Val Tyr His Ala Glu  
 630 635 640 645

gcg cag tcc ggc acc gtc gca ggt gtt atc gtc cag ctt ggt ggc cag  
 2083  
 Ala Gln Ser Gly Thr Val Ala Gly Val Ile Val Gln Leu Gly Gly Gln  
 650 655 660

act cct ctg ggc ttg gca gat cgt ttg aag aag gct ggc gtc cct gtc  
 2131  
 Thr Pro Leu Gly Leu Ala Asp Arg Leu Lys Lys Ala Gly Val Pro Val  
 665 670 675

att ggt acc tcc cca gag gca atc gac atg gct gag gac cgt ggc gag  
 2179  
 Ile Gly Thr Ser Pro Glu Ala Ile Asp Met Ala Glu Asp Arg Gly Glu  
 680 685 690

ttc ggt gca ctg ctg aac cgc gag cag ctt cct gct cca gca ttc ggc  
 2227  
 Phe Gly Ala Leu Leu Asn Arg Glu Gln Leu Pro Ala Pro Ala Phe Gly  
 695 700 705

acc gca acc tct ttc gaa gag gct cgc aca gta gcc gat gag atc agc  
 2275  
 Thr Ala Thr Ser Phe Glu Glu Ala Arg Thr Val Ala Asp Glu Ile Ser  
 710 715 720 725

tac cca gtg ctg gtt cgc cct tcc tac gtc ttg ggt ggc cgt ggc atg  
 2323  
 Tyr Pro Val Leu Val Arg Pro Ser Tyr Val Leu Gly Gly Arg Gly Met  
 730 735 740

gag att gtc tac gat gag gct tcc ctc gag gat tac atc aac cgc gca  
 2371  
 Glu Ile Val Tyr Asp Glu Ala Ser Leu Glu Asp Tyr Ile Asn Arg Ala  
 745 750 755

act gag ttg tct tct gac cac cca gtg ctg gtt gac cgc ttc cta gac  
 2419  
 Thr Glu Leu Ser Ser Asp His Pro Val Leu Val Asp Arg Phe Leu Asp  
 760 765 770

aac gct att gag atc gac gtc gac gca ctg tgc gac ggc gac gag gtc  
 2467  
 Asn Ala Ile Glu Ile Asp Val Asp Ala Leu Cys Asp Gly Asp Glu Val  
 775 780 785

tac ctg gca ggc gtc atg gag cac atc gag gaa gcc ggc att cac tcc  
 2515  
 Tyr Leu Ala Gly Val Met Glu His Ile Glu Glu Ala Gly Ile His Ser  
 790 795 800 805

gca ggg gag cgc gct acc gat aag gca gct gtt ctg gaa gat ctc aag  
 1411  
 Ala Gly Glu Arg Ala Thr Asp Lys Ala Ala Val Leu Glu Asp Leu Lys  
 425 430 435  
 cgc cca acc gaa ggc cgc ctc tac gac gtt gag ctg gca atg cgc ctt  
 1459  
 Arg Pro Thr Glu Gly Arg Leu Tyr Asp Val Glu Leu Ala Met Arg Leu  
 440 445 450  
 ggc gca agc gtg gaa gaa ctc tac gaa gca tct tct att gat cct tgg  
 1507  
 Gly Ala Ser Val Glu Glu Leu Tyr Glu Ala Ser Ser Ile Asp Pro Trp  
 455 460 465  
 ttc ctc gcc gag ctt gaa gct ctc gtg cag ttc cgc cag aag ctc gtt  
 1555  
 Phe Leu Ala Glu Leu Glu Ala Leu Val Gln Phe Arg Gln Lys Leu Val  
 470 475 480 485  
 gac gca cca ttc cta aac gaa gat ctc ctg cgc gaa gca aag ttc atg  
 1603  
 Asp Ala Pro Phe Leu Asn Glu Asp Leu Leu Arg Glu Ala Lys Phe Met  
 490 495 500  
 ggt ctg tcc gac ctg cag atc gca gcc ctt cgc cca gag ttc gct ggc  
 1651  
 Gly Leu Ser Asp Leu Gln Ile Ala Ala Leu Arg Pro Glu Phe Ala Gly  
 505 510 515  
 gaa gac ggc gta cgc acc ttg cgt ctg tcc cta ggc atc cgc cca gta  
 1699  
 Glu Asp Gly Val Arg Thr Leu Arg Leu Ser Leu Gly Ile Arg Pro Val  
 520 525 530  
 ttc aag act gtg gat acc tgt gca gca gag ttt gaa gct aag act ccg  
 1747  
 Phe Lys Thr Val Asp Thr Cys Ala Ala Glu Phe Glu Ala Lys Thr Pro  
 535 540 545  
 tac cac tac tcc gca tac gag ctg gat cca gca gct gag tct gag gtc  
 1795  
 Tyr His Tyr Ser Ala Tyr Glu Leu Asp Pro Ala Ala Glu Ser Glu Val  
 550 555 560 565  
 gca cca cag act gag cgt gaa aag gtc ctg atc ttg ggc tcc ggt cca  
 1843  
 Ala Pro Gln Thr Glu Arg Glu Lys Val Leu Ile Leu Gly Ser Gly Pro  
 570 575 580  
 aac cgc atc ggc cag ggc atc gag ttc gac tac tcc tgt gtt cac gca  
 1891  
 Asn Arg Ile Gly Gln Gly Ile Glu Phe Asp Tyr Ser Cys Val His Ala  
 585 590 595  
 gct ctt gag ctc tcc cgc gtc ggc tac gaa act gtc atg gtc aac tgc  
 1939  
 Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu Thr Val Met Val Asn Cys  
 600 605 610

tcc atc ctt ggt tgg aag gaa ttc gag ctc gag ctc atg cgc gat acc 787  
 Ser Ile Leu Gly Trp Lys Glu Phe Glu Leu Glu Leu Met Arg Asp Thr  
 215 220 225

gca gac aac gtt gtg gtt atc tgc tcc att gaa aac gtc gac gca ctg 835  
 Ala Asp Asn Val Val Ile Cys Ser Ile Glu Asn Val Asp Ala Leu  
 230 235 240 245

ggc gtg cac acc ggc gac tct gtc acc gtg gca cct gcc ctg acc ctg 883  
 Gly Val His Thr Gly Asp Ser Val Thr Val Ala Pro Ala Leu Thr Leu  
 250 255 260

act gac cgt gaa ttc cag aag atg cgc gat cag ggt atc gcc atc atc 931  
 Thr Asp Arg Glu Phe Gln Lys Met Arg Asp Gln Gly Ile Ala Ile Ile  
 265 270 275

cgc gag gtc ggc gtg gac acc ggt gga tgt aac atc cag ttc gcc atc 979  
 Arg Glu Val Gly Val Asp Thr Gly Gly Cys Asn Ile Gln Phe Ala Ile  
 280 285 290

aac cca gtt gat ggc cgc atc atc acc att gag atg aac cca cgt gtg  
 1027  
 Asn Pro Val Asp Gly Arg Ile Ile Thr Ile Glu Met Asn Pro Arg Val  
 295 300 305

tct cgt tcc tcc gct ctg gca tcc aag gca acg ggc ttc cca att gcc  
 1075  
 Ser Arg Ser Ser Ala Leu Ala Ser Lys Ala Thr Gly Phe Pro Ile Ala  
 310 315 320 325

aag atg gct gcc aag ctg gct atc gga tac acc ctg gat gag atc acc  
 1123  
 Lys Met Ala Ala Lys Leu Ala Ile Gly Tyr Thr Leu Asp Glu Ile Thr  
 330 335 340

aac gac atc act ggt gaa acc cca gct gcg ttt gag ccc acc atc gac  
 1171  
 Asn Asp Ile Thr Gly Glu Thr Pro Ala Ala Phe Glu Pro Thr Ile Asp  
 345 350 355

tac gtc gtg gtc aag gcc cca cgc ttt gct ttc gag aag ttt gtc ggc  
 1219  
 Tyr Val Val Val Lys Ala Pro Arg Phe Ala Phe Glu Lys Phe Val Gly  
 360 365 370

gct gat gac act ttg acc acc acc atg aag tcc gtc ggt gag gtc atg  
 1267  
 Ala Asp Asp Thr Leu Thr Thr Thr Met Lys Ser Val Gly Glu Val Met  
 375 380 385

tcc ctg ggc cgc aac tac att gca gca ctg aac aag gca ctg cgt tcc  
 1315  
 Ser Leu Gly Arg Asn Tyr Ile Ala Ala Leu Asn Lys Ala Leu Arg Ser  
 390 395 400 405

ctg gaa acc aag cag cag ggt ttc tgg acc aag cct gat gag ttc ttc  
 1363  
 Leu Glu Thr Lys Gln Gln Gly Phe Trp Thr Lys Pro Asp Glu Phe Phe  
 410 415 420

&lt;222&gt; (101)..(3439)

&lt;223&gt; RXS02234

&lt;400&gt; 367

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accagagggc cgctgccggc ccaaagatg caagccccct gtttgaccag tttgttgagc 60
tgatggatgc agacgctcag aagaaaggcg cataaataac atg cca aag cgt tca 115
                                         Met Pro Lys Arg Ser
                                         1           5

gat att aac cac gtc ctc gtc atc ggt tcc ggc ccc atc gtc att ggc 163
Asp Ile Asn His Val Leu Val Ile Gly Ser Gly Pro Ile Val Ile Gly
              10              15              20

cag gca tgt gaa ttc gac tac tcc ggc acc cag gct tgc cgc gtg ctg 211
Gln Ala Cys Glu Phe Asp Tyr Ser Gly Thr Gln Ala Cys Arg Val Leu
              25              30              35

aag gaa gag gga ctg cgc gtc acc ctc atc aac tcc aac cca gca acg 259
Lys Glu Glu Gly Leu Arg Val Thr Leu Ile Asn Ser Asn Pro Ala Thr
              40              45              50

atc atg acc gac cca gaa atg gct gac cac acc tac gtg gag cca atc 307
Ile Met Thr Asp Pro Glu Met Ala Asp His Thr Tyr Val Glu Pro Ile
              55              60              65

gag ccg gaa tac atc gac aag att ttc gct aag gaa atc gag cag ggc 355
Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala Lys Glu Ile Glu Gln Gly
              70              75              80              85

cac cca atc gac gcc gtc ctg gca acc ctt ggt ggc cag act gca ctt 403
His Pro Ile Asp Ala Val Leu Ala Thr Leu Gly Gly Gln Thr Ala Leu
              90              95              100

aac gca gct atc cag ctg gat cgc ctc ggc atc ctg gaa aag tac ggc 451
Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly Ile Leu Glu Lys Tyr Gly
              105              110              115

gtt gaa ctc atc ggt gca gac atc gat gcc att gag cgc ggc gaa gat 499
Val Glu Leu Ile Gly Ala Asp Ile Asp Ala Ile Glu Arg Gly Glu Asp
              120              125              130

cgc cag aag ttc aag gat att gtc acc acc atc ggt ggc gaa tcc gcg 547
Arg Gln Lys Phe Lys Asp Ile Val Thr Thr Ile Gly Gly Glu Ser Ala
              135              140              145

cgt tcc cgc gtc tgc cac aac atg gaa gaa gtc cac gag act gtc gca 595
Arg Ser Arg Val Cys His Asn Met Glu Glu Val His Glu Thr Val Ala
              150              155              160              165

gaa ctc ggc ctt cca gta gtc gtg cgt cca tcc ttc act atg ggt ggc 643
Glu Leu Gly Leu Pro Val Val Val Arg Pro Ser Phe Thr Met Gly Gly
              170              175              180

ctg ggc tcc ggt ctt gca tac aac acc gaa gac ctt gag cgc atc gct 691
Leu Gly Ser Gly Leu Ala Tyr Asn Thr Glu Asp Leu Glu Arg Ile Ala
              185              190              195

ggt ggc gga ctt gct gca tct cct gaa gca aac gtc ttg atc gaa gaa 739
Gly Gly Gly Leu Ala Ala Ser Pro Glu Ala Asn Val Leu Ile Glu Glu
              200              205              210

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145		150		155		160
Val Ala Gly Gly	Leu Val Asp Leu Ile	Pro Arg Pro Asp	Val Cys Phe			
	165	170	175			
Gly Gln His	Val Val Pro Gly Ala	Ala Gly Thr Val	Met Ser Met Pro			
	180	185	190			
Gly Gly Ala Leu	Ala Ala Cys Asp	Ser Ile Glu Ile	Arg Ile Gln Gly			
	195	200	205			
Arg Ser Ala His	Gly Ser Met Pro	His Asn Ser Ile	Asp Pro Thr Tyr			
	210	215	220			
Val Ala Ala Met	Ile Val Val Arg	Leu Gln Gly Ile	Val Gly Arg Glu			
	225	230	235	240		
Val Ser Pro Glu	Asp Phe Ala Val	Ile Ser Val Gly	Thr Leu Gln Ser			
	245	250	255			
Gly Asn Thr Asn	Asn Thr Ile Pro	Ala Ser Ala Arg	Leu Val Leu Asn			
	260	265	270			
Cys Arg Phe Tyr	Asn Asp Lys Val	Lys His Lys Val	Tyr Arg Ala Ile			
	275	280	285			
Glu Arg Val Val	Arg Gly Glu Cys	Leu Ala Ser Gly	Ile Glu Glu Glu			
	290	295	300			
Pro Val Ile Glu	Tyr Phe Ala His	Gly Asp Leu Thr	Asn Asn Thr Pro			
	305	310	315	320		
Val Val Phe Asp	Thr Val Arg Pro	Val Phe Asp Asp	Val Phe Gly Glu			
	325	330	335			
Asp Ser Ile Asp	Ala Tyr Arg Trp	Thr Ala Ser Glu	Asp Phe Pro Ser			
	340	345	350			
Ile Pro Lys Ala	Phe Asn Ser Pro	Tyr Leu Tyr Trp	Thr Ile Gly Val			
	355	360	365			
Thr Pro Arg Asp	Gln Trp Thr Glu	Ala Val Glu Arg	Asp Arg Val Ala			
	370	375	380			
Ser Asp Val Pro	Ala Asn His Met	Gly Asp Phe Leu	Pro Asp Tyr Ala			
	385	390	395	400		
Pro Thr Met Ser	Ala Ala Thr Arg	Ala Ala Ala Ala	Leu Leu Thr			
	405	410	415			
Tyr Leu Gly Thr	Asn					
	420					

&lt;210&gt; 367

&lt;211&gt; 3462

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

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 345 350 355

aac agc cct tac ctg tac tgg acg att ggt gtc acg ccg cgc gat cag  
 1219

Asn Ser Pro Tyr Leu Tyr Trp Thr Ile Gly Val Thr Pro Arg Asp Gln  
 360 365 370

tgg aca gaa gcc gta gaa aga gac cgc gtg gca tcg gat gtg cca gcc  
 1267

Trp Thr Glu Ala Val Glu Arg Asp Arg Val Ala Ser Asp Val Pro Ala  
 375 380 385

aat cac atg gga gat ttc ctc cct gat tat gcg ccg acg atg tcc gct  
 1315

Asn His Met Gly Asp Phe Leu Pro Asp Tyr Ala Pro Thr Met Ser Ala  
 390 395 400 405

gcc acc cgc gca gcc gca gcc gcg ctg ctg acc tac ttg gga act aac  
 1363

Ala Thr Arg Ala Ala Ala Ala Ala Leu Leu Thr Tyr Leu Gly Thr Asn  
 410 415 420

taatcatcta gttttctgcg acg  
 1386

<210> 366

<211> 421

<212> PRT

<213> Corynebacterium glutamicum

<400> 366

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Trp Gln Glu Ala Ala Tyr Gln Asp Phe His Glu His Pro Glu Leu Ser  
 20 25 30

Gly Phe Glu Ser Glu Thr Ala Asp Arg Ile Gln Lys Tyr Leu Glu Arg  
 35 40 45

Phe Asp Cys Glu Val Ile Pro Asn Val Gly Gly Tyr Gly Ile Leu Ala  
 50 55 60

Val Phe Arg Asn Gly Ser Thr Asp Pro Gly Ala Pro Val Ala Leu Met  
 65 70 75 80

Arg Ala Asp Phe Asp Gly Leu Pro Val Lys Glu Ile Thr Gly Val Pro  
 85 90 95

Phe Ala Ser Thr Arg Met Arg Pro His Asp Gly Ala Asn Val His Val  
 100 105 110

Met His Ala Cys Gly His Asp Val His Val Thr Ala Leu Leu Gly Ala  
 115 120 125

Cys Ala Ile Leu Asp Glu Arg Arg Asp Ala Trp Glu Gly Thr Phe Ile  
 130 135 140

Ala Leu Phe Gln Pro Ser Glu Glu Asn Ser Gln Gly Ala Asn Lys Met

cac gat gtc cac gtc acc gcg ctg ctt ggt gcg tgt gcc att tta gat	499
His Asp Val His Val Thr Ala Leu Leu Gly Ala Cys Ala Ile Leu Asp	
120 125 130	
gag cgt cgc gat gca tgg gaa ggc acg ttc atc gcg ttg ttc cag cca	547
Glu Arg Arg Asp Ala Trp Glu Gly Thr Phe Ile Ala Leu Phe Gln Pro	
135 140 145	
tcg gag gaa aac tcc caa ggc gct aac aag atg gtc gcc ggc ggt tta	595
Ser Glu Glu Asn Ser Gln Gly Ala Asn Lys Met Val Ala Gly Gly Leu	
150 155 160 165	
gtt gat ctg atc cca cgc cct gat gtg tgc ttt ggc cag cat gta gtc	643
Val Asp Leu Ile Pro Arg Pro Asp Val Cys Phe Gly Gln His Val Val	
170 175 180	
ccc ggt gct gca gga acc gtg atg agc atg cct ggc ggt gct ctc gct	691
Pro Gly Ala Ala Gly Thr Val Met Ser Met Pro Gly Gly Ala Leu Ala	
185 190 195	
gcc tgc gat tcc att gaa atc cgc att cag ggt cgc agc gcc cat ggt	739
Ala Cys Asp Ser Ile Glu Ile Arg Ile Gln Gly Arg Ser Ala His Gly	
200 205 210	
tcc atg cct cat aat tcc atc gat ccc act tat gtt gca gcg atg att	787
Ser Met Pro His Asn Ser Ile Asp Pro Thr Tyr Val Ala Ala Met Ile	
215 220 225	
gtc gtg cga ctc caa gga atc gtg ggc cgc gag gtt tct cca gag gat	835
Val Val Arg Leu Gln Gly Ile Val Gly Arg Glu Val Ser Pro Glu Asp	
230 235 240 245	
ttc gcc gtt att tct gtg ggc acc ctc cag tgc ggc aac acc aac aac	883
Phe Ala Val Ile Ser Val Gly Thr Leu Gln Ser Gly Asn Thr Asn Asn	
250 255 260	
acc att cca gca agt gct cgt ttg gtg ttg aac tgc cgt ttc tac aac	931
Thr Ile Pro Ala Ser Ala Arg Leu Val Leu Asn Cys Arg Phe Tyr Asn	
265 270 275	
gac aaa gtc aag cac aag gtc tac cga gcc atc gaa cgt gtt gtc cgt	979
Asp Lys Val Lys His Lys Val Tyr Arg Ala Ile Glu Arg Val Val Arg	
280 285 290	
ggt gaa tgc ctt gct tcc ggt att gag gaa gaa cct gtc att gag tac	
1027	
Gly Glu Cys Leu Ala Ser Gly Ile Glu Glu Glu Pro Val Ile Glu Tyr	
295 300 305	
ttc gcc cac ggt gat ctc acc aac aac acc cct gtt gtc ttc gat act	
1075	
Phe Ala His Gly Asp Leu Thr Asn Asn Thr Pro Val Val Phe Asp Thr	
310 315 320 325	
gtg cgc cct gtc ttc gac gat gtt ttc ggc gag gat tct att gac gct	
1123	
Val Arg Pro Val Phe Asp Asp Val Phe Gly Glu Asp Ser Ile Asp Ala	
330 335 340	
tac cgg tgg act gcg tcg gag gat ttc ccc tcc att cct aag gca ttc	
1171	

Asn Pro Asn Gly Ser Arg Gly Met Gly Ala Glu Asp Phe Ser Tyr Phe  
 325 330 335

Leu Glu Lys Arg Pro Gly Ala Tyr Leu Phe Val Gly Asn Gly Asp Ser  
 340 345 350

Ala Gly Leu His Asn Pro Ala Tyr Asn Phe Asn Asp Glu Ala Ala Pro  
 355 360 365

Tyr Gly Ala Ser Phe Leu Ala Arg Met Ala Glu Arg Pro Leu Pro Leu  
 370 375 380

Lys Gly  
 385

<210> 365

<211> 1386

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1363)

<223> RXS02101

<400> 365

gccatggaat gctccgttga acgcaacagc cttaaataca atccccctcct ataagccaag 60

agtttttagtg tcgctgcgca ggtactctac tatctaatacc atg agc cgc att tca 115  
 Met Ser Arg Ile Ser  
 1 5

gaa ctt cta aac aat cat ggt gtt gat ctg tcg tgg caa gag gcc gca 163  
 Glu Leu Leu Asn Asn His Gly Val Asp Leu Ser Trp Gln Glu Ala Ala  
 10 15 20

tat cag gat ttc cac gaa cat cct gag ctc tcc ggc ttc gaa tca gag 211  
 Tyr Gln Asp Phe His Glu His Pro Glu Leu Ser Gly Phe Glu Ser Glu  
 25 30 35

acc gca gat cgc att cag aaa tac ctc gag cgt ttt gat tgt gag gtg 259  
 Thr Ala Asp Arg Ile Gln Lys Tyr Leu Glu Arg Phe Asp Cys Glu Val  
 40 45 50

att cca aat gtt ggc ggt tac ggc att ctg gcc gtg ttc cga aat ggg 307  
 Ile Pro Asn Val Gly Gly Tyr Gly Ile Leu Ala Val Phe Arg Asn Gly  
 55 60 65

tcg aca gat cct ggt gcc cct gtt gcg tta atg cgc gca gat ttc gat 355  
 Ser Thr Asp Pro Gly Ala Pro Val Ala Leu Met Arg Ala Asp Phe Asp  
 70 75 80 85

ggc ctt ccc gtc aag gaa atc acc gga gtt ccg ttt gct tcc act cgt 403  
 Gly Leu Pro Val Lys Ile Thr Gly Val Pro Phe Ala Ser Thr Arg  
 90 95 100

atg cgt ccg cat gat ggg gca aat gtc cat gtc atg cac gca tgc ggc 451  
 Met Arg Pro His Asp Gly Ala Asn Val His Val Met His Ala Cys Gly  
 105 110 115

&lt;400&gt; 364

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Met Pro Val Ile Asn Ser Ile Ala Ser Phe Ser Asp Glu Met Thr Arg
 1           5           10           15

Trp Arg Arg His Leu His Gln Asn Pro Glu Ile Ser Phe Asp Cys Val
          20           25           30

Glu Thr Ala Ala Phe Val Ala Glu Gln Leu Arg Ser Phe Gly Val Asp
          35           40           45

Glu Ile His Thr Gly Ile Ala Lys Thr Gly Ile Ile Ala Leu Ile His
 50           55           60

Gly Arg Glu Ala Gly Pro Val Val Gly Leu Arg Ala Asp Met Asp Ala
 65           70           75           80

Leu Pro Leu Thr Glu Ile Thr Gly Val Asp Tyr Ala Ser Thr Thr Pro
          85           90           95

Gly Lys Met His Ala Cys Gly His Asp Gly His Thr Thr Met Leu Leu
          100          105          110

Gly Ala Ala Lys Tyr Leu Ala Glu Thr Arg Asn Phe Ala Gly Thr Val
          115          120          125

Ala Leu Ile Phe Gln Pro Ala Glu Glu Asn Gly Gly Gly Ala Gly Val
          130          135          140

Met Val Asp Glu Gly Val Leu Asp Arg Phe Ala Ile Ala Glu Val Tyr
          145          150          155          160

Ala Leu His Asn Gln Pro Gly Leu Pro Leu Gly His Phe Met Thr Thr
          165          170          175

Ala Gly Pro Ile Met Ala Ala Val Asp Thr Phe Asp Ile Asn Ile Thr
          180          185          190

Gly Arg Gly Gly His Gly Ala Lys Pro His Gln Thr Arg Asp Pro Ile
          195          200          205

Val Ala Ala Val Gly Ile Val Gln Ala Phe Gln Thr Ile Val Ser Arg
          210          215          220

Asn His Asn Pro Val Glu Asp Leu Val Val Ser Val Thr Gln Ile His
          225          230          235          240

Thr Gly Ser Ala Asp Asn Ile Ile Pro Glu Thr Ala Tyr Ile Asn Gly
          245          250          255

Thr Val Arg Thr Phe Asn Lys Asp Val Gln Ala Met Val Ile Thr Arg
          260          265          270

Met Glu Glu Ile Val Ala Gly Gln Ala Ala Ala Tyr Gly Val Glu Ala
          275          280          285

Thr Leu Thr Tyr Asn Arg Asn Tyr Pro Ala Thr Ile Asn Asp Ala Ala
          290          295          300

Lys Ala Ala Ile Ala Ala Glu Val Ala Gly Glu Val Gly Leu Gly Val
          305          310          315          320

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200	205	210	
att gtc caa gcg ttt caa acg ata gtc agc cgg aat cac aat ccg gtc Ile Val Gln Ala Phe Gln Thr Ile Val Ser Arg Asn His Asn Pro Val 215 220 225			787
gag gac ctt gtc gtg tcg gtc acg caa atc cac acc ggc agc gcc gat Glu Asp Leu Val Val Ser Val Thr Gln Ile His Thr Gly Ser Ala Asp 230 235 240 245			835
aat atc atc ccc gaa acc gcc tat atc aac ggc act gtc cgc acc ttc Asn Ile Ile Pro Glu Thr Ala Tyr Ile Asn Gly Thr Val Arg Thr Phe 250 255 260			883
aac aaa gac gtg cag gcc atg gtc atc acg cgg atg gaa gaa atc gtc Asn Lys Asp Val Gln Ala Met Val Ile Thr Arg Met Glu Glu Ile Val 265 270 275			931
gcg ggc caa gct gca gcc tat ggg gtc gag gcg acg ctg acc tac aac Ala Gly Gln Ala Ala Ala Tyr Gly Val Glu Ala Thr Leu Thr Tyr Asn 280 285 290			979
cgc aac tat ccc gcc acc att aac gac gcc gcc aaa gcc gcc atc gct 1027 Arg Asn Tyr Pro Ala Thr Ile Asn Asp Ala Ala Lys Ala Ala Ile Ala 295 300 305			
gcc gaa gtc gcg ggc gag gtc ggc ctc ggg gtc aac ccg aac ggc tcg 1075 Ala Glu Val Ala Gly Glu Val Gly Leu Gly Val Asn Pro Asn Gly Ser 310 315 320 325			
cgc ggg atg ggg gcc gag gat ttc tcg tat ttc ctc gaa aag cgc ccg 1123 Arg Gly Met Gly Ala Glu Asp Phe Ser Tyr Phe Leu Glu Lys Arg Pro 330 335 340			
ggt gcc tac ctg ttc gtc ggt aat ggc gac agc gcg ggc ctt cac aac 1171 Gly Ala Tyr Leu Phe Val Gly Asn Gly Asp Ser Ala Gly Leu His Asn 345 350 355			
ccc gcc tat aat ttc aac gac gag gcc gcg ccc tac ggc gca tcg ttc 1219 Pro Ala Tyr Asn Phe Asn Asp Glu Ala Ala Pro Tyr Gly Ala Ser Phe 360 365 370			
ttg gcc cgc atg gca gaa cgc ccc ttg ccg tta aag ggc tgatccatgg 1268 Leu Ala Arg Met Ala Glu Arg Pro Leu Pro Leu Lys Gly 375 380 385			
cgctcgaaga tgc 1281			

&lt;210&gt; 364

&lt;211&gt; 386

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;221&gt; CDS

&lt;222&gt; (101)..(1258)

&lt;223&gt; RXS02001

&lt;400&gt; 363

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gatagtcag	catagaccgt	gctttatcga	agggtgaaccc	atg	ccc	gtt	atc	aat	115
				Met	Pro	Val	Ile	Asn	
				1				5	

agt	atc	gcc	agt	ttt	tcc	gac	gag	atg	acc	cgc	tgg	cgg	cgt	cac	ctg	163
Ser	Ile	Ala	Ser	Phe	Ser	Asp	Glu	Met	Thr	Arg	Trp	Arg	Arg	His	Leu	
			10						15					20		

cat	caa	aac	ccc	gaa	atc	agc	ttt	gat	tgt	gtg	gaa	act	gcg	gcc	ttc	211
His	Gln	Asn	Pro	Glu	Ile	Ser	Phe	Asp	Cys	Val	Glu	Thr	Ala	Ala	Phe	
			25					30					35			

gtg	gcc	gag	cag	ctg	cgc	agc	ttc	ggg	gtg	gat	gaa	att	cac	acc	ggc	259
Val	Ala	Glu	Gln	Leu	Arg	Ser	Phe	Gly	Val	Asp	Glu	Ile	His	Thr	Gly	
		40					45					50				

atc	gcg	aaa	acc	ggc	atc	atc	gcc	ctg	att	cac	ggg	cgc	gag	gct	ggc	307
Ile	Ala	Lys	Thr	Gly	Ile	Ile	Ala	Leu	Ile	His	Gly	Arg	Glu	Ala	Gly	
	55					60					65					

ccc	gtc	gtc	ggc	ctg	cgc	gcc	gat	atg	gac	gcg	ctg	ccg	ctg	acc	gag	355
Pro	Val	Val	Gly	Leu	Arg	Ala	Asp	Met	Asp	Ala	Leu	Pro	Leu	Thr	Glu	
	70				75					80					85	

att	acc	ggc	gtc	gac	tat	gcc	tcg	acc	acc	ccc	gga	aaa	atg	cac	gcc	403
Ile	Thr	Gly	Val	Asp	Tyr	Ala	Ser	Thr	Thr	Pro	Gly	Lys	Met	His	Ala	
			90						95					100		

tgc	ggc	cac	gac	ggc	cac	acg	acc	atg	ctg	ctg	ggc	gcc	gcc	aaa	tat	451
Cys	Gly	His	Asp	Gly	His	Thr	Thr	Met	Leu	Leu	Gly	Ala	Ala	Lys	Tyr	
			105					110				115				

ctg	gcc	gag	acg	cgc	aat	ttc	gca	ggc	acc	gtc	gcg	ctg	atc	ttc	cag	499
Leu	Ala	Glu	Thr	Arg	Asn	Phe	Ala	Gly	Thr	Val	Ala	Leu	Ile	Phe	Gln	
		120					125					130				

cct	gcg	gaa	gaa	aac	ggc	ggc	ggc	gcg	ggc	gtt	atg	gtc	gat	gaa	ggc	547
Pro	Ala	Glu	Glu	Asn	Gly	Gly	Gly	Ala	Gly	Val	Met	Val	Asp	Glu	Gly	
	135					140					145					

gtc	ctc	gac	cgc	ttt	gcc	atc	gcc	gaa	gtc	tac	gcc	ctg	cac	aac	cag	595
Val	Leu	Asp	Arg	Phe	Ala	Ile	Ala	Glu	Val	Tyr	Ala	Leu	His	Asn	Gln	
	150				155					160					165	

ccc	ggc	ctg	ccg	ctt	ggc	cat	ttt	atg	acg	aca	gcc	ggc	ccg	atc	atg	643
Pro	Gly	Leu	Pro	Leu	Gly	His	Phe	Met	Thr	Thr	Ala	Gly	Pro	Ile	Met	
			170						175					180		

gcc	gct	gtc	gac	acg	ttc	gac	atc	aac	att	acc	gga	cgc	ggc	ggc	cac	691
Ala	Ala	Val	Asp	Thr	Phe	Asp	Ile	Asn	Ile	Thr	Gly	Arg	Gly	Gly	His	
			185					190					195			

ggc	gcc	aaa	ccg	cac	caa	acc	cgc	gac	ccc	atc	gtc	gca	gcc	gtc	gga	739
Gly	Ala	Lys	Pro	His	Gln	Thr	Arg	Asp	Pro	Ile	Val	Ala	Ala	Val	Gly	

130

135

140

Gly Lys Asp Leu Val Thr Glu Gly Ser Gly Gly Ser Ile Pro Leu Cys  
 145 150 155 160

Thr Glu Leu Ile Glu Val Asn Pro  
 165

&lt;210&gt; 361

&lt;211&gt; 246

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(223)

&lt;223&gt; RXS00907

&lt;400&gt; 361

cctgagcgct gcgtacgagg gcaaggatct tgtaaccgaa ggcagcggcg gatccattcc 60

actgtgtacc gaactgattg aggtcaaccc ataagcagaa ttg gca ctc tac ggt 115  
 Leu Ala Leu Tyr Gly  
 1 5

gtg gaa gaa ccc ctc acc gtt atc cac tcc gct aat gaa tct gtt gac 163  
 Val Glu Glu Pro Leu Thr Val Ile His Ser Ala Asn Glu Ser Val Asp  
 10 15 20

ccc aat gag att cgc gat atc gcc acc gca gaa gca ttg ttc ctg ctc 211  
 Pro Asn Glu Ile Arg Asp Ile Ala Thr Ala Glu Ala Leu Phe Leu Leu  
 25 30 35

aac tac acc aag tagacccaaa agcaggcggtt aac 246  
 Asn Tyr Thr Lys  
 40

&lt;210&gt; 362

&lt;211&gt; 41

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 362

Leu Ala Leu Tyr Gly Val Glu Glu Pro Leu Thr Val Ile His Ser Ala  
 1 5 10 15

Asn Glu Ser Val Asp Pro Asn Glu Ile Arg Asp Ile Ala Thr Ala Glu  
 20 25 30

Ala Leu Phe Leu Leu Asn Tyr Thr Lys  
 35 40

&lt;210&gt; 363

&lt;211&gt; 1281

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;



ctc aac gca gtg ccc gca acg gcg tcc gcc aag cta aac ctt cgc gtg 355  
 Leu Asn Ala Val Pro Ala Thr Ala Ser Ala Lys Leu Asn Leu Arg Val  
 70 75 80 85

cca gca ggc ctg gaa gca aac gat gtg gcc gag aag ctg aag cag cac 403  
 Pro Ala Gly Leu Glu Ala Asn Asp Val Ala Glu Lys Leu Lys Gln His  
 90 95 100

ctg atc aat cac aca cct tgg ggc gca aag atc acg gtg gag atc gat 451  
 Leu Ile Asn His Thr Pro Trp Gly Ala Lys Ile Thr Val Glu Ile Asp  
 105 110 115

gac att aac caa ccg ttc tcc acc gat att acc ggc cct gca atg tcc 499  
 Asp Ile Asn Gln Pro Phe Ser Thr Asp Ile Thr Gly Pro Ala Met Ser  
 120 125 130

acc ctg gcg tcc tgc ctg agc gct gcg tac gag ggc aag gat ctt gtc 547  
 Thr Leu Ala Ser Cys Leu Ser Ala Ala Tyr Glu Gly Lys Asp Leu Val  
 135 140 145

acc gaa ggc agc ggc gga tcc att cca ctg tgt acc gaa ctg att gag 595  
 Thr Glu Gly Ser Gly Gly Ser Ile Pro Leu Cys Thr Glu Leu Ile Glu  
 150 155 160 165

gtc aac cca taagcagaat tggcactcta cgg 627  
 Val Asn Pro

&lt;210&gt; 360

&lt;211&gt; 168

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 360

Met Asn Thr Asp Ala Pro Leu Ser Thr Ala Val Asn Thr Thr Ala Asn  
 1 5 10 15

Trp Lys Gly Glu Pro Tyr Asp Pro Glu Thr Phe Arg Ser Asp Ala Gly  
 20 25 30

Ile Leu Asp Gly Val Asp Ile Met Gly Asp Gly Asp Asn Pro Ala Ser  
 35 40 45

Met Leu Trp Ser Arg Pro Ala Ile Ser Ile Thr Gly Phe Thr Ser Thr  
 50 55 60

Pro Val Ala Glu Ala Leu Asn Ala Val Pro Ala Thr Ala Ser Ala Lys  
 65 70 75 80

Leu Asn Leu Arg Val Pro Ala Gly Leu Glu Ala Asn Asp Val Ala Glu  
 85 90 95

Lys Leu Lys Gln His Leu Ile Asn His Thr Pro Trp Gly Ala Lys Ile  
 100 105 110

Thr Val Glu Ile Asp Asp Ile Asn Gln Pro Phe Ser Thr Asp Ile Thr  
 115 120 125

Gly Pro Ala Met Ser Thr Leu Ala Ser Cys Leu Ser Ala Ala Tyr Glu

Asp Cys Lys Gly Asn Leu Val Met His Leu Ala Ala Leu Arg Ala Val  
 130 135 140

Glu Ala Ser Gly Asp Thr Thr Leu Asn Leu Thr Tyr Val Val Glu Gly  
 145 150 155 160

Ser Glu Glu Met Gly Gly Gly Ala Leu Ser Ala Leu Ile Lys Asp Lys  
 165 170 175

Pro Glu Leu Phe Asp Ala Asp Val Ile Leu Ile Ala Asp Ser Gly Asn  
 180 185 190

Ala Ser Val Gly Thr Pro Thr Leu Thr Thr Thr Leu Arg Gly Gly Gly  
 195 200 205

Gln Val Thr Val Thr Val Asp Thr Leu Glu Gly Ala Val His Ser Gly  
 210 215 220

Gln Asn Gly Gly Ala Ala Pro Asp Ala Val Ala Ala Leu Val Arg Val  
 225 230 235 240

Leu Asp Thr Leu Arg Asp Glu His Gly Arg Thr Val Ile Asp Gly Cys  
 245 250 255

Gln His His Arg Lys Leu Glu Gly Arg Ala Leu  
 260 265

<210> 359

<211> 627

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(604)

<223> RXS00906

<400> 359

accgtggaca cccttgaagg cgctgttcac tccggccaga acgggtggcgc tgccccagat 60

gctgttgctg ctctcgtgcg cgttctggat actttgcgcg atg aac acg gac gca 115  
 Met Asn Thr Asp Ala  
 1 5

ccg tta tcg acg gct gtc aac acc acc gca aac tgg aag ggc gag cct 163  
 Pro Leu Ser Thr Ala Val Asn Thr Thr Ala Asn Trp Lys Gly Glu Pro  
 10 15 20

tat gat cca gag act ttc cgc agc gat gcc ggc atc ctc gac ggt gta 211  
 Tyr Asp Pro Glu Thr Phe Arg Ser Asp Ala Gly Ile Leu Asp Gly Val  
 25 30 35

gac atc atg ggc gac ggc gac aac cca gca agc atg ctg tgg tcc agg 259  
 Asp Ile Met Gly Asp Gly Asp Asn Pro Ala Ser Met Leu Trp Ser Arg  
 40 45 50

cct gca atc tcc atc acc gga ttc act tcc acc cca gtg gca gaa gca 307  
 Pro Ala Ile Ser Ile Thr Gly Phe Thr Ser Thr Pro Val Ala Glu Ala  
 55 60 65

Pro Ala Asp Glu Glu Trp Ser Ile Glu Lys Leu Asp Gly Lys Arg Ile  
 100 105 110  
 Ala Thr Ser Tyr Pro Asn Leu Val Arg Asp Asp Leu Ala Ala Arg Gly  
 115 120 125  
 Leu Ser Ala Glu Val Leu Arg Leu Asp Gly Ala Val Glu Val Ser Ile  
 130 135 140  
 Lys Leu Gly Val Ala Asp Ala Ile Ala Asp Val Val Ser Thr Gly Arg  
 145 150 155 160  
 Thr Leu Arg Gln Gln Gly Leu Ala Pro Phe Gly Glu Val Leu Cys Thr  
 165 170 175  
 Ser Glu Ala Val Ile Val Gly Arg Lys Asp Glu Lys Val Thr Pro Glu  
 180 185 190  
 Gln Gln Ile Leu Leu Arg Arg Ile Gln Gly Ile Leu His Ala Gln Asn  
 195 200 205  
 Phe Leu Met Leu Asp Tyr Asn Val Asp Arg Asp Asn Leu Asp Ala Ala  
 210 215 220  
 Thr Ala Val Thr Pro Gly Leu Ser Gly Pro Thr Val Ser Pro Leu Ala  
 225 230 235 240  
 Arg Asp Asn Trp Val Ala Val Arg Ala Met Val Pro Arg Arg Ser Ala  
 245 250 255  
 Asn Ala Ile Met Asp Lys Leu Ala Gly Leu Gly Ala Glu Ala Ile Leu  
 260 265 270  
 Ala Ser Glu Ile Arg Ile Ala Arg Ile  
 275 280

&lt;210&gt; 377

&lt;211&gt; 393

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(370)

&lt;223&gt; RXA02195

&lt;400&gt; 377

tcgagccggc aggtgtcgca aaataaaacc aggtggggga gtgaaattat tcgactaata 60

tcctccccca aacacacatt gataactgtt gtgtggaaga atg tac cga gtg aag 115  
 Met Tyr Arg Val Lys  
 1 5

aca ttt gac tcg ctg tac gaa gaa ctt ctt aac cgt gct cag acc cgc 163  
 Thr Phe Asp Ser Leu Tyr Glu Glu Leu Leu Asn Arg Ala Gln Thr Arg  
 10 15 20

cct gaa ggg tct gga acc gtg gcc gcc ttg gat aaa ggc atc cat cat 211  
 Pro Glu Gly Ser Gly Thr Val Ala Ala Leu Asp Lys Gly Ile His His

gat gcc atc gcc gat gtt gta tcc acc ggc cgc acg ctg cgt cag caa 595  
 Asp Ala Ile Ala Asp Val Val Ser Thr Gly Arg Thr Leu Arg Gln Gln  
 150 155 160 165  
 ggt ctt gca cct ttc ggc gag gtt ctg tgc acc tct gag gct gtc att 643  
 Gly Leu Ala Pro Phe Gly Glu Val Leu Cys Thr Ser Glu Ala Val Ile  
 170 175 180  
 gtt ggc cgc aag gat gaa aag gtc acc cca gag cag cag atc ctg ctt 691  
 Val Gly Arg Lys Asp Glu Lys Val Thr Pro Glu Gln Gln Ile Leu Leu  
 185 190 195  
 cgc cgc atc cag gga att ttg cac gcg cag aac ttc ctc atg ctg gat 739  
 Arg Arg Ile Gln Gly Ile Leu His Ala Gln Asn Phe Leu Met Leu Asp  
 200 205 210  
 tac aac gtc gac cgc gac aac ctg gac gct gcc act gca gta acc cca 787  
 Tyr Asn Val Asp Arg Asp Asn Leu Asp Ala Ala Thr Ala Val Thr Pro  
 215 220 225  
 ggc tta tcc ggc cca acg gta tcc cca ctg gca cgc gac aac tgg gtt 835  
 Gly Leu Ser Gly Pro Thr Val Ser Pro Leu Ala Arg Asp Asn Trp Val  
 230 235 240 245  
 gct gta cgc gcc atg gtg cca cgc agg tca gct aac gcc atc atg gat 883  
 Ala Val Arg Ala Met Val Pro Arg Arg Ser Ala Asn Ala Ile Met Asp  
 250 255 260  
 aag ctt gct gga ctc ggc gct gaa gcc atc ctg gct tct gaa atc cgc 931  
 Lys Leu Ala Gly Leu Gly Ala Glu Ala Ile Leu Ala Ser Glu Ile Arg  
 265 270 275  
 atc gcc cgc atc tagttttaac taccctcgaa aat 966  
 Ile Ala Arg Ile  
 280

&lt;210&gt; 376

&lt;211&gt; 281

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 376

Met Leu Lys Ile Ala Val Pro Asn Lys Gly Ser Leu Ser Glu Arg Ala  
 1 5 10 15  
 Met Glu Ile Leu Ala Glu Ala Gly Tyr Ala Gly Arg Gly Asp Ser Lys  
 20 25 30  
 Ser Leu Asn Val Phe Asp Glu Ala Asn Asn Val Glu Phe Phe Phe Leu  
 35 40 45  
 Arg Pro Lys Asp Ile Ala Ile Tyr Val Ala Gly Gly Gln Leu Asp Leu  
 50 55 60  
 Gly Ile Thr Gly Arg Asp Leu Ala Arg Asp Ser Gln Ala Asp Val His  
 65 70 75 80  
 Glu Val Leu Ser Leu Gly Phe Gly Ser Ser Thr Phe Arg Tyr Ala Ala  
 85 90 95

100	105	110	
Met Gln Pro Thr Leu Asp Arg Gly Val Glu Ala Leu Val Val Ala Ala			
115	120	125	
Ser Ala Trp Leu Val Lys			
130			
<210> 375			
<211> 966			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (101)..(943)			
<223> RXA02194			
<400> 375			
gaaatctccc agctcattta ttggacccag gtcacatcatgg ttgctcgcg cctgaagcca 60			
gaagatatct acaagaacct gtaggagttt taaagcaatc atg ttg aaa atc gct 115			
		Met Leu Lys Ile Ala	
		1 5	
gtc cca aac aaa ggc tcg ctg tcc gag cgc gcc atg gaa atc ctc gcc 163			
Val Pro Asn Lys	Gly Ser Leu Ser Glu Arg Ala Met Glu Ile Leu Ala		
10	15	20	
gaa gca ggc tac gca ggc cgt gga gat tcc aaa tcc ctc aac gtt ttt 211			
Glu Ala Gly Tyr Ala Gly Arg Gly Asp Ser Lys Ser Leu Asn Val Phe			
25	30	35	
gat gaa gca aac aac gtt gaa ttc ttc ttc ctt cgc cct aaa gat atc 259			
Asp Glu Ala Asn Asn Val Glu Phe Phe Phe Leu Arg Pro Lys Asp Ile			
40	45	50	
gcc atc tac gtt gct ggt ggc cag ctc gat ttg ggt atc acc ggc cgc 307			
Ala Ile Tyr Val Ala Gly Gly Gln Leu Asp Leu Gly Ile Thr Gly Arg			
55	60	65	
gac ctt gct cgc gat tcc cag gct gat gtc cac gaa gtt ctt tcc ctc 355			
Asp Leu Ala Arg Asp Ser Gln Ala Asp Val His Glu Val Leu Ser Leu			
70	75	80	85
ggc ttc ggt tcc tcc act ttc cgt tac gca gca cca gct gat gaa gag 403			
Gly Phe Gly Ser Ser Thr Phe Arg Tyr Ala Ala Pro Ala Asp Glu Glu			
90	95	100	
tgg agc atc gaa aag ctc gac ggc aag cgc atc gct acc tct tac ccc 451			
Trp Ser Ile Glu Lys Leu Asp Gly Lys Arg Ile Ala Thr Ser Tyr Pro			
105	110	115	
aac ctt gtt cgc gat gac ctc gca gca cgt ggg ctt tcc gct gag gtg 499			
Asn Leu Val Arg Asp Asp Leu Ala Ala Arg Gly Leu Ser Ala Glu Val			
120	125	130	
ctc cgc ctc gac ggt gca gta gag gta tcc atc aag ctt ggt gtc gca 547			
Leu Arg Leu Asp Gly Ala Val Glu Val Ser Ile Lys Leu Gly Val Ala			
135	140	145	

Glu Gly Pro Val Val Ala Leu Arg Gly Asp Ile Asp Ala Leu Pro Met  
                                   10                                  15                                  20  
 gcg gag cga tcc ggc aaa gaa tac gca gca acc gga gtg aca cag gtg 211  
 Ala Glu Arg Ser Gly Lys Glu Tyr Ala Ala Thr Gly Val Thr Gln Val  
                                   25                                  30                                  35  
 gat aac acc acc ggt caa gaa act ccg gtg gcg cat acc tgt ggc cac 259  
 Asp Asn Thr Thr Gly Gln Glu Thr Pro Val Ala His Thr Cys Gly His  
                                   40                                  45                                  50  
 gat gtg cat att tca tca ctg ttg ggt gcg gtg cag gcg ttc aat tct 307  
 Asp Val His Ile Ser Ser Leu Leu Gly Ala Val Gln Ala Phe Asn Ser  
                                   55                                  60                                  65  
 cat cgg gaa ttg tgg aac gga acg ttg atg gcc gtt ttc cag cca gcg 355  
 His Arg Glu Leu Trp Asn Gly Thr Leu Met Ala Val Phe Gln Pro Ala  
                                   70                                  75                                  80                                  85  
 gaa gag acg gca gct ggt gcg agg atg atg gcg gat cag gac aac gcg 403  
 Glu Glu Thr Ala Ala Gly Ala Arg Met Met Ala Asp Gln Asp Asn Ala  
                                   90                                  95                                  100  
 ccg gga aat cac tct cca gcg ttc gcg cca gat atg cag cca act ctt 451  
 Pro Gly Asn His Ser Pro Ala Phe Ala Pro Asp Met Gln Pro Thr Leu  
                                   105                                  110                                  115  
 gat cgt ggt gtg gaa gcg ctg gtt gta gct gct tct gcg tgg cta gta 499  
 Asp Arg Gly Val Glu Ala Leu Val Val Ala Ala Ser Ala Trp Leu Val  
                                   120                                  125                                  130  
 aaa taattggcta atgaatcctt ttc 525  
 Lys

<210> 374  
 <211> 134  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 374  
 Val Ile Ser Asn Gly Glu Gly Pro Val Val Ala Leu Arg Gly Asp Ile  
                                   1                                  5                                  10                                  15  
 Asp Ala Leu Pro Met Ala Glu Arg Ser Gly Lys Glu Tyr Ala Ala Thr  
                                   20                                  25                                  30  
 Gly Val Thr Gln Val Asp Asn Thr Thr Gly Gln Glu Thr Pro Val Ala  
                                   35                                  40                                  45  
 His Thr Cys Gly His Asp Val His Ile Ser Ser Leu Leu Gly Ala Val  
                                   50                                  55                                  60  
 Gln Ala Phe Asn Ser His Arg Glu Leu Trp Asn Gly Thr Leu Met Ala  
                                   65                                  70                                  75                                  80  
 Val Phe Gln Pro Ala Glu Glu Thr Ala Ala Gly Ala Arg Met Met Ala  
                                   85                                  90                                  95  
 Asp Gln Asp Asn Ala Pro Gly Asn His Ser Pro Ala Phe Ala Pro Asp

Arg Arg Ile Ala Ala Ala Asp Leu Lys Val Ala Lys Asp Asp Ile Trp  
 210 215 220  
 Gln Gly Phe Val Gln Ala His Arg Phe Asp Pro Glu Thr Glu Gln Ala  
 225 230 235 240  
 Leu Leu Ser Gly Thr Ser Pro Glu Ala Tyr Ala Glu Phe Gly Gly Leu  
 245 250 255  
 Ser Arg Phe Ala His Ala Val Ser His Leu Thr Ile Ala Gln Thr Val  
 260 265 270  
 Val Arg Ala Gly Gln Ala Ile Asn Val Leu Pro Ser His Ala Tyr Leu  
 275 280 285  
 Glu Leu Asp Ile Arg Thr Leu Pro Gly Gln Thr Asn Asp Tyr Val Asp  
 290 295 300  
 Asp Thr Leu Arg Ala Ala Leu Gly Asp Leu Ala Asp Glu Val Glu Ile  
 305 310 315 320  
 Glu His Leu Ile Ser Glu Glu Ala Thr Val Ser Pro Thr Asp Ser Arg  
 325 330 335  
 Leu Tyr Asn Thr Leu Glu Lys Val Leu Gly Asp Phe Phe Pro Asp Ala  
 340 345 350  
 Pro Val Val Pro Ile Ile Ser Ser Gly Gly Ser Asp Leu Arg Phe Gly  
 355 360 365  
 Arg Arg Leu Gly Gly Val Gly Tyr Gly Phe Ala Val His Ala Arg Glu  
 370 375 380  
 Arg Thr Leu Ala Glu Ala Met Gly Gln Leu His Ser His Asp Glu Ala  
 385 390 395 400  
 Leu Tyr Leu Glu Asp Leu Glu Leu Thr Val Arg Gly Tyr Asp Ser Val  
 405 410 415  
 Val Arg Glu Phe Leu Gly  
 420

<210> 373  
 <211> 525  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(502)  
 <223> RXS02937

<400> 373  
 gctaccgcga agaactgtac tagttcttcc atcagcaccc gcagttgtct ttgcaagagt 60  
 tcgaaacatc caacgcattg gtgacaccgg tgttgctcgcg gtg atc agc aat ggg 115  
 Val Ile Ser Asn Gly  
 1 5  
 gaa ggt ccg gtt gtt gcg ctt cgt ggc gac att gat gcg ttg ccc atg 163

gca atg ggg caa ctt cac tcc cat gac gag gcg ctg tac ctg gaa gat  
 1315  
 Ala Met Gly Gln Leu His Ser His Asp Glu Ala Leu Tyr Leu Glu Asp  
 390 395 400 405  
 ctt gaa ctg act gtt cgg ggt tat gac tcc gtc gtg cgt gaa ttc cta  
 1363  
 Leu Glu Leu Thr Val Arg Gly Tyr Asp Ser Val Val Arg Glu Phe Leu  
 410 415 420  
 ggc taaaaacatg aagcaggagt ctt  
 1389  
 Gly

<210> 372  
 <211> 422  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 372  
 Val Asn Asp Leu Thr Pro Asp Ser Gly Gln Glu Ile Arg Asn Ala Glu  
 1 5 10 15  
 Ser Leu Glu Arg Phe Phe Glu Gly Thr Pro Asn Val Lys Ile Thr Lys  
 20 25 30  
 Leu Glu Pro His Pro Gly Arg Thr Ser Ile Ile Val Thr Val Pro Gly  
 35 40 45  
 Ser Asp Pro Asp Ala Glu Pro Leu Thr Leu Leu Gly His Thr Asp Val  
 50 55 60  
 Val Pro Val Asp Leu Pro Lys Trp Thr Lys Asp Pro Phe Gly Ala Glu  
 65 70 75 80  
 Ile Ser Asp Gly Gln Ile Trp Gly Arg Gly Ser Val Asp Met Leu Phe  
 85 90 95  
 Ile Thr Ala Thr Gln Ala Ala Val Thr Arg Gln Val Ala Arg Glu Gly  
 100 105 110  
 Gly Leu Arg Gly Thr Leu Thr Phe Val Gly Val Ala Asp Glu Glu Ala  
 115 120 125  
 Arg Gly Gly Leu Gly Ala Lys Trp Leu Ser Glu Glu His Gln Asn Leu  
 130 135 140  
 Phe Ser Trp Lys Asn Cys Leu Ser Glu Ser Gly Gly Ser His Leu Pro  
 145 150 155 160  
 Val His Asp Gly Ser Asp Ala Val Val Ile Asn Val Gly Glu Lys Gly  
 165 170 175  
 Ala Ala Gln Arg Arg Ile His Val Asn Gly Asp Ala Gly His Gly Ser  
 180 185 190  
 Ile Pro Phe Asp Arg Asp Ser Ala Ile Val Lys Ile Gly Glu Val Ala  
 195 200 205



Asp	Ala	Val	Val	Ile	Asn	Val	Gly	Glu	Lys	Gly	Ala	Ala	Gln	Arg	Arg		
				170					175					180			
att	cac	gtc	aat	ggc	gat	gct	ggg	cat	ggg	tcc	att	cct	ttc	gac	cgt	691	
Ile	His	Val	Asn	Gly	Asp	Ala	Gly	His	Gly	Ser	Ile	Pro	Phe	Asp	Arg		
			185					190					195				
gac	agc	gct	att	gtc	aag	atc	ggg	gaa	gtc	gcc	cgc	cga	atc	gct	gcc	739	
Asp	Ser	Ala	Ile	Val	Lys	Ile	Gly	Glu	Val	Ala	Arg	Arg	Ile	Ala	Ala		
		200					205					210					
gcc	gat	ctg	aag	gta	gcc	aag	gac	gat	atc	tgg	caa	ggc	ttc	gtc	caa	787	
Ala	Asp	Leu	Lys	Val	Ala	Lys	Asp	Asp	Ile	Trp	Gln	Gly	Phe	Val	Gln		
	215					220					225						
gcg	cac	cgt	ttc	gac	cca	gaa	acg	gag	cag	gcg	ctt	ctt	agc	ggg	acc	835	
Ala	His	Arg	Phe	Asp	Pro	Glu	Thr	Glu	Gln	Ala	Leu	Leu	Ser	Gly	Thr		
230					235					240					245		
tcc	cct	gag	gcc	tac	gca	gag	ttc	ggc	gga	ctc	tcc	cgc	ttc	gcc	cac	883	
Ser	Pro	Glu	Ala	Tyr	Ala	Glu	Phe	Gly	Gly	Leu	Ser	Arg	Phe	Ala	His		
				250					255					260			
gcg	gtg	tct	cat	ctc	acg	atc	gcc	caa	act	gtg	gtt	cgt	gca	ggg	caa	931	
Ala	Val	Ser	His	Leu	Thr	Ile	Ala	Gln	Thr	Val	Val	Arg	Ala	Gly	Gln		
			265				270						275				
gcc	atc	aat	gta	ttg	cca	tcg	cat	gcg	tac	ttg	gaa	ctg	gat	atc	cgt	979	
Ala	Ile	Asn	Val	Leu	Pro	Ser	His	Ala	Tyr	Leu	Glu	Leu	Asp	Ile	Arg		
		280					285					290					
acc	ctt	cca	ggc	caa	acc	aat	gac	tat	gtt	gat	gac	acc	ctg	cgt	gct		
1027																	
Thr	Leu	Pro	Gly	Gln	Thr	Asn	Asp	Tyr	Val	Asp	Asp	Thr	Leu	Arg	Ala		
	295					300					305						
gct	ctg	ggc	gat	ctt	gcc	gat	gaa	gta	gaa	atc	gaa	cac	ctc	atc	tct		
1075																	
Ala	Leu	Gly	Asp	Leu	Ala	Asp	Glu	Val	Glu	Ile	Glu	His	Leu	Ile	Ser		
310					315				320					325			
gaa	gaa	gca	acg	gtg	agc	cca	act	gat	tcc	agg	ttg	tat	aac	acc	ttg		
1123																	
Glu	Glu	Ala	Thr	Val	Ser	Pro	Thr	Asp	Ser	Arg	Leu	Tyr	Asn	Thr	Leu		
			330						335					340			
gaa	aaa	gtt	ctt	ggg	gat	ttc	ttc	ccc	gat	gcg	cct	gtg	gtc	cca	att		
1171																	
Glu	Lys	Val	Leu	Gly	Asp	Phe	Phe	Pro	Asp	Ala	Pro	Val	Val	Pro	Ile		
			345					350					355				
att	tcc	tct	ggg	ggc	tct	gac	ctg	cgc	ttt	ggg	cgt	cga	cta	ggc	ggg		
1219																	
Ile	Ser	Ser	Gly	Gly	Ser	Asp	Leu	Arg	Phe	Gly	Arg	Arg	Leu	Gly	Gly		
		360					365					370					
gtt	ggg	tat	ggg	ttt	gca	gtt	cat	gca	cgt	gaa	cga	act	ttg	gcg	gaa		
1267																	
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Pro Asp Ser Gly Gln Glu Ile Arg Asn Ala Glu Ser Leu Glu Arg Phe  
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Phe Glu Gly Thr Pro Asn Val Lys Ile Thr Lys Leu Glu Pro His Pro  
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Gly Arg Thr Ser Ile Ile Val Thr Val Pro Gly Ser Asp Pro Asp Ala  
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Glu Pro Leu Thr Leu Leu Gly His Thr Asp Val Val Pro Val Asp Leu  
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Pro Lys Trp Thr Lys Asp Pro Phe Gly Ala Glu Ile Ser Asp Gly Gln  
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ctg aca ttc gtt ggc gtt gct gat gag gaa gcc cgc ggc gga ctc gga 499  
Leu Thr Phe Val Gly Val Ala Asp Glu Glu Ala Arg Gly Gly Leu Gly  
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Ala Lys Trp Leu Ser Glu Glu His Gln Asn Leu Phe Ser Trp Lys Asn  
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Cys Leu Ser Glu Ser Gly Gly Ser His Leu Pro Val His Asp Gly Ser  
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Cys Asp Gly Asp Glu Val Tyr Leu Ala Gly Val Met Glu His Ile Glu  
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 980 985 990  
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Ser Ser Ile Asp Pro Trp Phe Leu Ala Glu Leu Glu Ala Leu Val Gln  
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 465 470 475 480  
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 485 490 495  
 Phe Glu Ala Lys Thr Pro Tyr His Tyr Ser Ala Tyr Glu Leu Asp Pro  
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 595 600 605  
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 Lys Ala Gly Val Pro Val Ile Gly Thr Ser Pro Glu Ala Ile Asp Met  
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 Ala Glu Asp Arg Gly Glu Phe Gly Ala Leu Leu Asn Arg Glu Gln Leu  
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 675 680 685  
 Leu Gly Gly Arg Gly Met Glu Ile Val Tyr Asp Glu Ala Ser Leu Glu  
 690 695 700  
 Asp Tyr Ile Asn Arg Ala Thr Glu Leu Ser Ser Asp His Pro Val Leu  
 705 710 715 720  
 Val Asp Arg Phe Leu Asp Asn Ala Ile Glu Ile Asp Val Asp Ala Leu  
 725 730 735

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Ile	Gly	Gly	Glu	Ser	Ala	Arg	Ser	Arg	Val	Cys	His	Asn	Met	Glu	Glu		
			100					105					110				
Val	His	Glu	Thr	Val	Ala	Glu	Leu	Gly	Leu	Pro	Val	Val	Val	Arg	Pro		
		115					120					125					
Ser	Phe	Thr	Met	Gly	Gly	Leu	Gly	Ser	Gly	Leu	Ala	Tyr	Asn	Thr	Glu		
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Asp	Leu	Glu	Arg	Ile	Ala	Gly	Gly	Gly	Leu	Ala	Ala	Ser	Pro	Glu	Ala		
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Asn	Val	Leu	Ile	Glu	Glu	Ser	Ile	Leu	Gly	Trp	Lys	Glu	Phe	Glu	Leu		
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Glu	Leu	Met	Arg	Asp	Thr	Ala	Asp	Asn	Val	Val	Val	Ile	Cys	Ser	Ile		
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Gln	Gly	Ile	Ala	Ile	Ile	Arg	Glu	Val	Gly	Val	Asp	Thr	Gly	Gly	Cys		
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Asn	Ile	Gln	Phe	Ala	Ile	Asn	Pro	Val	Asp	Gly	Arg	Ile	Ile	Thr	Ile		
				245					250					255			
Glu	Met	Asn	Pro	Arg	Val	Ser	Arg	Ser	Ser	Ala	Leu	Ala	Ser	Lys	Ala		
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Thr	Gly	Phe	Pro	Ile	Ala	Lys	Met	Ala	Ala	Lys	Leu	Ala	Ile	Gly	Tyr		
		275					280					285					
Thr	Leu	Asp	Glu	Ile	Thr	Asn	Asp	Ile	Thr	Gly	Glu	Thr	Pro	Ala	Ala		
		290					295					300					
Phe	Glu	Pro	Thr	Ile	Asp	Tyr	Val	Val	Val	Lys	Ala	Pro	Arg	Phe	Ala		
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Phe	Glu	Lys	Phe	Val	Gly	Ala	Asp	Asp	Thr	Leu	Thr	Thr	Thr	Met	Lys		
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Ser	Val	Gly	Glu	Val	Met	Ser	Leu	Gly	Arg	Asn	Tyr	Ile	Ala	Ala	Leu		
		340						345					350				
Asn	Lys	Ala	Leu	Arg	Ser	Leu	Glu	Thr	Lys	Gln	Gln	Gly	Phe	Trp	Thr		
		355					360					365					
Lys	Pro	Asp	Glu	Phe	Phe	Ala	Gly	Glu	Arg	Ala	Thr	Asp	Lys	Ala	Ala		
		370					375					380					
Val	Leu	Glu	Asp	Leu	Lys	Arg	Pro	Thr	Glu	Gly	Arg	Leu	Tyr	Asp	Val		
		385					390					395					
Glu	Leu	Ala	Met	Arg	Leu	Gly	Ala	Ser	Val	Glu	Glu	Leu	Tyr	Glu	Ala		
				405					410					415			

acc gca ggc atg ctg cgc cgc aac ggc att gag tgt gaa gtt gtg ctc  
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Thr Ala Gly Met Leu Arg Arg Asn Gly Ile Glu Cys Glu Val Val Leu  
965 970 975

aag gct tcc gac atc cgc gaa ggt gta gag ggc aag tcc atc gtg gat  
2976

Lys Ala Ser Asp Ile Arg Glu Gly Val Glu Gly Lys Ser Ile Val Asp  
980 985 990

cgt atc cgc gaa ggc gaa gtt gac ctc atc ctc aac acc cca gct ggt  
3024

Arg Ile Arg Glu Gly Glu Val Asp Leu Ile Leu Asn Thr Pro Ala Gly  
995 1000 1005

tct gct ggc gct cgc cac gat ggc tac gat atc cgc gca gca gca gtg  
3072

Ser Ala Gly Ala Arg His Asp Gly Tyr Asp Ile Arg Ala Ala Ala Val  
1010 1015 1020

acc gtg ggt gtt ccg ctg atc acc act gtt cag ggt gtc acc gca gct  
3120

Thr Val Gly Val Pro Leu Ile Thr Thr Val Gln Gly Val Thr Ala Ala  
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gtc cag ggc ata gag gcc ctg cgt gag ggc gtt gtc agc gtc cgc gcg  
3168

Val Gln Gly Ile Glu Ala Leu Arg Glu Gly Val Val Ser Val Arg Ala  
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ctg cag gaa ctc gac cac gca gtc aag gct taagccctat gacattcggc  
3218

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3221

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35 40 45

Gly Gly Gln Thr Ala Leu Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly  
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Ile Leu Glu Lys Tyr Gly Val Glu Leu Ile Gly Ala Asp Ile Asp Ala  
65 70 75 80

Ile Glu Arg Gly Glu Asp Arg Gln Lys Phe Lys Asp Ile Val Thr Thr

act ttg ggc gca cag gac atc gag aag gtc cgc gaa gca acc aag aag  
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 Thr Leu Gly Ala Gln Asp Ile Glu Lys Val Arg Glu Ala Thr Lys Lys  
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ctg gct ctg ggc atc ggt gta cag ggc ctg atg aac gtc cag tac gca  
 2400  
 Leu Ala Leu Gly Ile Gly Val Gln Gly Leu Met Asn Val Gln Tyr Ala  
       785                      790                      795                      800

ctc aag gac gac atc ctc tac gtc atc gag gca aac cca cgt gca tcc  
 2448  
 Leu Lys Asp Asp Ile Leu Tyr Val Ile Glu Ala Asn Pro Arg Ala Ser  
                       805                      810                      815

cgc acc gtg ccg ttc gtc tcc aag gca acg ggc gtc aac ctg gcc aag  
 2496  
 Arg Thr Val Pro Phe Val Ser Lys Ala Thr Gly Val Asn Leu Ala Lys  
                       820                      825                      830

gca gca tcc cgt atc gca gtg ggc gcc acc atc aag gat ctc caa gat  
 2544  
 Ala Ala Ser Arg Ile Ala Val Gly Ala Thr Ile Lys Asp Leu Gln Asp  
                       835                      840                      845

gag ggc atg att cct acc gag tac gac ggc ggc tcc ttg cca ctg gac  
 2592  
 Glu Gly Met Ile Pro Thr Glu Tyr Asp Gly Gly Ser Leu Pro Leu Asp  
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gct cca atc gct gtg aag gaa gca gtg ttg ccg ttc aac cgc ttc cgt  
 2640  
 Ala Pro Ile Ala Val Lys Glu Ala Val Leu Pro Phe Asn Arg Phe Arg  
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cgc cca gat gga aag acc ctg gac acc ctg ctt tcc cca gag atg aag  
 2688  
 Arg Pro Asp Gly Lys Thr Leu Asp Thr Leu Leu Ser Pro Glu Met Lys  
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tcc act ggc gag gtc atg ggc ttg gcc aac aac ttc ggc gct gca tat  
 2736  
 Ser Thr Gly Glu Val Met Gly Leu Ala Asn Asn Phe Gly Ala Ala Tyr  
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gca aag gct gaa gct ggc gcg ttt ggt gca ttg cca acc gaa ggc acc  
 2784  
 Ala Lys Ala Glu Ala Gly Ala Phe Gly Ala Leu Pro Thr Glu Gly Thr  
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 Val Phe Val Thr Val Ala Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro  
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 Ile Gln Arg Leu Ala Leu Met Gly Tyr Lys Ile Leu Ala Thr Glu Gly  
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565 570 575  
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 1776  
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 580 585 590  
 gag gtc tac cac gct gag gcg cag tcc ggc acc gtc gca ggt gtt atc  
 1824  
 Glu Val Tyr His Ala Glu Ala Gln Ser Gly Thr Val Ala Gly Val Ile  
 595 600 605  
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 1872  
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 1920  
 Lys Ala Gly Val Pro Val Ile Gly Thr Ser Pro Glu Ala Ile Asp Met  
 625 630 635 640  
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 1968  
 Ala Glu Asp Arg Gly Glu Phe Gly Ala Leu Leu Asn Arg Glu Gln Leu  
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 675 680 685  
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 2112  
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 2160  
 Asp Tyr Ile Asn Arg Ala Thr Glu Leu Ser Ser Asp His Pro Val Leu  
 705 710 715 720  
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 2256  
 Cys Asp Gly Asp Glu Val Tyr Leu Ala Gly Val Met Glu His Ile Glu  
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 2304  
 Glu Ala Gly Ile His Ser Gly Asp Ser Ala Cys Ala Leu Pro Pro Met  
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Lys Pro Asp Glu Phe Phe Ala Gly Glu Arg Ala Thr Asp Lys Ala Ala  
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 1344  
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 1488  
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 1536  
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 1584  
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 545 550 555 560  
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 Asn Val Leu Ile Glu Glu Ser Ile Leu Gly Trp Lys Glu Phe Glu Leu  
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gag ctc atg cgc gat acc gca gac aac gtt gtg gtt atc tgc tcc att 576  
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 180 185 190

gaa aac gtc gac gca ctg ggc gtg cac acc ggc gac tct gtc acc gtg 624  
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 275 280 285

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 305 310 315 320

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 340 345 350

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 1104  
 Asn Lys Ala Leu Arg Ser Leu Glu Thr Lys Gln Gln Gly Phe Trp Thr  
 355 360 365

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 Thr Tyr Val Glu Pro Ile Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala  
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aag gaa atc gag cag ggc cac cca atc gac gcc gtc ctg gca acc ctt 144  
 Lys Glu Ile Glu Gln Gly His Pro Ile Asp Ala Val Leu Ala Thr Leu  
 35 40 45

ggc ggc cag act gca ctt aac gca gct atc cag ctg gat cgc ctc ggc 192  
 Gly Gly Gln Thr Ala Leu Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly  
 50 55 60

atc ctg gaa aag tac ggc gtt gaa ctc atc ggt gca gac atc gat gcc 240  
 Ile Leu Glu Lys Tyr Gly Val Glu Leu Ile Gly Ala Asp Ile Asp Ala  
 65 70 75 80

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 Ile Glu Arg Gly Glu Asp Arg Gln Lys Phe Lys Asp Ile Val Thr Thr  
 85 90 95

atc ggt ggc gaa tcc gcg cgt tcc cgc gtc tgc cac aac atg gaa gaa 336  
 Ile Gly Gly Glu Ser Ala Arg Ser Arg Val Cys His Asn Met Glu Glu  
 100 105 110

gtc cac gag act gtc gca gaa ctc ggc ctt cca gta gtc gtg cgt cca 384  
 Val His Glu Thr Val Ala Glu Leu Gly Leu Pro Val Val Val Arg Pro  
 115 120 125

tcc ttc act atg ggt ggc ctg ggc tcc ggt ctt gca tac aac acc gaa 432  
 Ser Phe Thr Met Gly Gly Leu Gly Ser Gly Leu Ala Tyr Asn Thr Glu  
 130 135 140

725	730	735
Gly Gly Arg Gly Met Glu Ile Val Tyr Asp Glu Ala Ser Leu Glu Asp 740 745 750		
Tyr Ile Asn Arg Ala Thr Glu Leu Ser Ser Asp His Pro Val Leu Val 755 760 765		
Asp Arg Phe Leu Asp Asn Ala Ile Glu Ile Asp Val Asp Ala Leu Cys 770 775 780		
Asp Gly Asp Glu Val Tyr Leu Ala Gly Val Met Glu His Ile Glu Glu 785 790 795 800		
Ala Gly Ile His Ser Gly Asp Ser Ala Cys Ala Leu Pro Pro Met Thr 805 810 815		
Leu Gly Ala Gln Asp Ile Glu Lys Val Arg Glu Ala Thr Lys Lys Leu 820 825 830		
Ala Leu Gly Ile Gly Val Gln Gly Leu Met Asn Val Gln Tyr Ala Leu 835 840 845		
Lys Asp Asp Ile Leu Tyr Val Ile Glu Ala Asn Pro Arg Ala Ser Arg 850 855 860		
Thr Val Pro Phe Val Ser Lys Ala Thr Gly Val Asn Leu Ala Lys Ala 865 870 875 880		
Ala Ser Arg Ile Ala Val Gly Ala Thr Ile Lys Asp Leu Gln Asp Glu 885 890 895		
Gly Met Ile Pro Thr Glu Tyr Asp Gly Gly Ser Leu Pro Leu Asp Ala 900 905 910		
Pro Ile Ala Val Lys Glu Ala Val Leu Pro Phe Asn Arg Phe Arg Arg 915 920 925		
Pro Asp Gly Lys Thr Leu Asp Thr Leu Leu Ser Pro Glu Met Lys Ser 930 935 940		
Thr Gly Glu Val Met Gly Leu Ala Asn Asn Phe Gly Ala Ala Tyr Ala 945 950 955 960		
Lys Ala Glu Ala Gly Ala Phe Gly Ala Leu Pro Thr Glu Gly Thr Val 965 970 975		
Phe Val Thr Val Ala Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro Ile 980 985 990		
Gln Arg Leu Ala Leu Met Gly Tyr Lys Ile Leu Ala Thr Glu Gly Thr 995 1000 1005		
Ala Gly Met Leu Arg Arg Asn Gly Ile Glu Cys Glu Val Val Leu Lys 1010 1015 1020		
Ala Ser Asp Ile Arg Glu Gly Val Glu Gly Lys Ser Ile Val Asp Arg 1025 1030 1035 1040		
Ile Arg Glu Gly Glu Val Asp Leu Ile Leu Asn Thr Pro Ala Gly Ser 1045 1050 1055		

Lys Ala Leu Arg Ser Leu Glu Thr Lys Gln Gln Gly Phe Trp Thr Lys  
 405 410 415  
 Pro Asp Glu Phe Phe Ala Gly Glu Arg Ala Thr Asp Lys Ala Ala Val  
 420 425 430  
 Leu Glu Asp Leu Lys Arg Pro Thr Glu Gly Arg Leu Tyr Asp Val Glu  
 435 440 445  
 Leu Ala Met Arg Leu Gly Ala Ser Val Glu Glu Leu Tyr Glu Ala Ser  
 450 455 460  
 Ser Ile Asp Pro Trp Phe Leu Ala Glu Leu Glu Ala Leu Val Gln Phe  
 465 470 475 480  
 Arg Gln Lys Leu Val Asp Ala Pro Phe Leu Asn Glu Asp Leu Leu Arg  
 485 490 495  
 Glu Ala Lys Phe Met Gly Leu Ser Asp Leu Gln Ile Ala Ala Leu Arg  
 500 505 510  
 Pro Glu Phe Ala Gly Glu Asp Gly Val Arg Thr Leu Arg Leu Ser Leu  
 515 520 525  
 Gly Ile Arg Pro Val Phe Lys Thr Val Asp Thr Cys Ala Ala Glu Phe  
 530 535 540  
 Glu Ala Lys Thr Pro Tyr His Tyr Ser Ala Tyr Glu Leu Asp Pro Ala  
 545 550 555 560  
 Ala Glu Ser Glu Val Ala Pro Gln Thr Glu Arg Glu Lys Val Leu Ile  
 565 570 575  
 Leu Gly Ser Gly Pro Asn Arg Ile Gly Gln Gly Ile Glu Phe Asp Tyr  
 580 585 590  
 Ser Cys Val His Ala Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu Thr  
 595 600 605  
 Val Met Val Asn Cys Asn Pro Glu Thr Val Ser Thr Asp Tyr Asp Thr  
 610 615 620  
 Ala Asp Arg Leu Tyr Phe Glu Pro Leu Thr Phe Glu Asp Val Met Glu  
 625 630 635 640  
 Val Tyr His Ala Glu Ala Gln Ser Gly Thr Val Ala Gly Val Ile Val  
 645 650 655  
 Gln Leu Gly Gly Gln Thr Pro Leu Gly Leu Ala Asp Arg Leu Lys Lys  
 660 665 670  
 Ala Gly Val Pro Val Ile Gly Thr Ser Pro Glu Ala Ile Asp Met Ala  
 675 680 685  
 Glu Asp Arg Gly Glu Phe Gly Ala Leu Leu Asn Arg Glu Gln Leu Pro  
 690 695 700  
 Ala Pro Ala Phe Gly Thr Ala Thr Ser Phe Glu Glu Ala Arg Thr Val  
 705 710 715 720  
 Ala Asp Glu Ile Ser Tyr Pro Val Leu Val Arg Pro Ser Tyr Val Leu

Glu Ile Glu Gln Gly His Pro Ile Asp Ala Val Leu Ala Thr Leu Gly  
 85 90 95  
 Gly Gln Thr Ala Leu Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly Ile  
 100 105 110  
 Leu Glu Lys Tyr Gly Val Glu Leu Ile Gly Ala Asp Ile Asp Ala Ile  
 115 120 125  
 Glu Arg Gly Glu Asp Arg Gln Lys Phe Lys Asp Ile Val Thr Thr Ile  
 130 135 140  
 Gly Gly Glu Ser Ala Arg Ser Arg Val Cys His Asn Met Glu Glu Val  
 145 150 155 160  
 His Glu Thr Val Ala Glu Leu Gly Leu Pro Val Val Val Arg Pro Ser  
 165 170 175  
 Phe Thr Met Gly Gly Leu Gly Ser Gly Leu Ala Tyr Asn Thr Glu Asp  
 180 185 190  
 Leu Glu Arg Ile Ala Gly Gly Gly Leu Ala Ala Ser Pro Glu Ala Asn  
 195 200 205  
 Val Leu Ile Glu Glu Ser Ile Leu Gly Trp Lys Glu Phe Glu Leu Glu  
 210 215 220  
 Leu Met Arg Asp Thr Ala Asp Asn Val Val Val Ile Cys Ser Ile Glu  
 225 230 235 240  
 Asn Val Asp Ala Leu Gly Val His Thr Gly Asp Ser Val Thr Val Ala  
 245 250 255  
 Pro Ala Leu Thr Leu Thr Asp Arg Glu Phe Gln Lys Met Arg Asp Gln  
 260 265 270  
 Gly Ile Ala Ile Ile Arg Glu Val Gly Val Asp Thr Gly Gly Cys Asn  
 275 280 285  
 Ile Gln Phe Ala Ile Asn Pro Val Asp Gly Arg Ile Ile Thr Ile Glu  
 290 295 300  
 Met Asn Pro Arg Val Ser Arg Ser Ser Ala Leu Ala Ser Lys Ala Thr  
 305 310 315 320  
 Gly Phe Pro Ile Ala Lys Met Ala Ala Lys Leu Ala Ile Gly Tyr Thr  
 325 330 335  
 Leu Asp Glu Ile Thr Asn Asp Ile Thr Gly Glu Thr Pro Ala Ala Phe  
 340 345 350  
 Glu Pro Thr Ile Asp Tyr Val Val Val Lys Ala Pro Arg Phe Ala Phe  
 355 360 365  
 Glu Lys Phe Val Gly Ala Asp Asp Thr Leu Thr Thr Thr Met Lys Ser  
 370 375 380  
 Val Gly Glu Val Met Ser Leu Gly Arg Asn Tyr Ile Ala Ala Leu Asn  
 385 390 395 400

atg ggc tac aag atc ctc gcc acc gaa ggc acc gca ggc atg ctg cgc  
3139

Met Gly Tyr Lys Ile Leu Ala Thr Glu Gly Thr Ala Gly Met Leu Arg  
1000 1005 1010

cgc aac ggc att gag tgt gaa gtt gtg ctc aag gct tcc gac atc cgc  
3187

Arg Asn Gly Ile Glu Cys Glu Val Val Leu Lys Ala Ser Asp Ile Arg  
1015 1020 1025

gaa ggt gta gag ggc aag tcc atc gtg gat cgt atc cgc gaa ggc gaa  
3235

Glu Gly Val Glu Gly Lys Ser Ile Val Asp Arg Ile Arg Glu Gly Glu  
1030 1035 1040 1045

gtt gac ctc atc ctc aac acc cca gct ggt tct gct ggc gct cgc cac  
3283

Val Asp Leu Ile Leu Asn Thr Pro Ala Gly Ser Ala Gly Ala Arg His  
1050 1055 1060

gat ggc tac gat atc cgc gca gca gca gtg acc gtg ggt gtt ccg ctg  
3331

Asp Gly Tyr Asp Ile Arg Ala Ala Val Thr Val Gly Val Pro Leu  
1065 1070 1075

atc acc act gtt cag ggt gtc acc gca gct gtc cag ggc ata gag gcc  
3379

Ile Thr Thr Val Gln Gly Val Thr Ala Ala Val Gln Gly Ile Glu Ala  
1080 1085 1090

ctg cgt gag ggc gtt gtc agc gtc cgc gcg ctg cag gaa ctc gac cac  
3427

Leu Arg Glu Gly Val Val Ser Val Arg Ala Leu Gln Glu Leu Asp His  
1095 1100 1105

gca gtc aag gct taagccctat gacattcggc gag  
3462

Ala Val Lys Ala  
1110

<210> 368

<211> 1113

<212> PRT

<213> Corynebacterium glutamicum

<400> 368

Met Pro Lys Arg Ser Asp Ile Asn His Val Leu Val Ile Gly Ser Gly  
1 5 10 15

Pro Ile Val Ile Gly Gln Ala Cys Glu Phe Asp Tyr Ser Gly Thr Gln  
20 25 30

Ala Cys Arg Val Leu Lys Glu Glu Gly Leu Arg Val Thr Leu Ile Asn  
35 40 45

Ser Asn Pro Ala Thr Ile Met Thr Asp Pro Glu Met Ala Asp His Thr  
50 55 60

Tyr Val Glu Pro Ile Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala Lys  
65 70 75 80

ggt gac tcc gca tgt gca ctt cct cca atg act ttg ggc gca cag gac  
 2563  
 Gly Asp Ser Ala Cys Ala Leu Pro Pro Met Thr Leu Gly Ala Gln Asp  
 810 815 820  
 atc gag aag gtc cgc gaa gca acc aag aag ctg gct ctg ggc atc ggt  
 2611  
 Ile Glu Lys Val Arg Glu Ala Thr Lys Lys Leu Ala Leu Gly Ile Gly  
 825 830 835  
 gta cag ggc ctg atg aac gtc cag tac gca ctc aag gac gac atc ctc  
 2659  
 Val Gln Gly Leu Met Asn Val Gln Tyr Ala Leu Lys Asp Asp Ile Leu  
 840 845 850  
 tac gtc atc gag gca aac cca cgt gca tcc cgc acc gtg ccg ttc gtc  
 2707  
 Tyr Val Ile Glu Ala Asn Pro Arg Ala Ser Arg Thr Val Pro Phe Val  
 855 860 865  
 tcc aag gca acg ggc gtc aac ctg gcc aag gca gca tcc cgt atc gca  
 2755  
 Ser Lys Ala Thr Gly Val Asn Leu Ala Lys Ala Ala Ser Arg Ile Ala  
 870 875 880 885  
 gtg ggc gcc acc atc aag gat ctc caa gat gag ggc atg att cct acc  
 2803  
 Val Gly Ala Thr Ile Lys Asp Leu Gln Asp Glu Gly Met Ile Pro Thr  
 890 895 900  
 gag tac gac ggc ggc tcc ttg cca ctg gac gct cca atc gct gtg aag  
 2851  
 Glu Tyr Asp Gly Gly Ser Leu Pro Leu Asp Ala Pro Ile Ala Val Lys  
 905 910 915  
 gaa gca gtg ttg ccg ttc aac cgc ttc cgt cgc cca gat gga aag acc  
 2899  
 Glu Ala Val Leu Pro Phe Asn Arg Phe Arg Arg Pro Asp Gly Lys Thr  
 920 925 930  
 ctg gac acc ctg ctt tcc cca gag atg aag tcc act ggc gag gtc atg  
 2947  
 Leu Asp Thr Leu Leu Ser Pro Glu Met Lys Ser Thr Gly Glu Val Met  
 935 940 945  
 ggc ttg gcc aac aac ttc ggc gct gca tat gca aag gct gaa gct ggc  
 2995  
 Gly Leu Ala Asn Asn Phe Gly Ala Ala Tyr Ala Lys Ala Glu Ala Gly  
 950 955 960 965  
 gcg ttt ggt gca ttg cca acc gaa ggc acc gtc ttc gtg acc gtg gct  
 3043  
 Ala Phe Gly Ala Leu Pro Thr Glu Gly Thr Val Phe Val Thr Val Ala  
 970 975 980  
 aac cgc gac aag cgc acc ctg atc ctg cca atc cag cgc ctg gcg ttg  
 3091  
 Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro Ile Gln Arg Leu Ala Leu  
 985 990 995



gac cct cac cac atc acc gaa gca gag tac aag gct gtt gcc cgt gcg 643  
 Asp Pro His His Ile Thr Glu Ala Glu Tyr Lys Ala Val Ala Arg Ala  
                   170                  175                  180

ctg cgc ggt gcc gta gag atg gat cct cgt caa aca gga atc cca tcc 691  
 Leu Arg Gly Ala Val Glu Met Asp Pro Arg Gln Thr Gly Ile Pro Ser  
                   185                  190                  195

act aag gga gcg ctc tagacatgaa ctcttctccc atc 729  
 Thr Lys Gly Ala Leu  
                   200

<210> 394

<211> 202

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 394

Met Thr Val Ala Pro Arg Ile Gly Thr Ala Thr Arg Thr Thr Ser Glu  
       1                  5                  10                  15

Ser Asp Ile Thr Val Glu Ile Asn Leu Asp Gly Thr Gly Lys Val Asp  
                   20                  25                  30

Ile Asp Thr Gly Leu Pro Phe Phe Asp His Met Leu Thr Ala Phe Gly  
                   35                  40                  45

Val His Gly Ser Phe Asp Leu Lys Val His Ala Lys Gly Asp Ile Glu  
       50                  55                  60

Ile Asp Ala His His Thr Val Glu Asp Thr Ala Ile Val Leu Gly Gln  
       65                  70                  75                  80

Ala Leu Leu Asp Ala Ile Gly Asp Lys Lys Gly Ile Arg Arg Phe Ala  
                   85                  90                  95

Ser Cys Gln Leu Pro Met Asp Glu Ala Leu Val Glu Ser Val Val Asp  
                   100                  105                  110

Ile Ser Gly Arg Pro Tyr Phe Val Ile Ser Gly Glu Pro Asp His Met  
                   115                  120                  125

Ile Thr Ser Val Ile Gly Gly His Tyr Ala Thr Val Ile Asn Glu His  
                   130                  135                  140

Phe Phe Glu Thr Leu Ala Leu Asn Ser Arg Ile Thr Leu His Val Ile  
       145                  150                  155                  160

Cys His Tyr Gly Arg Asp Pro His His Ile Thr Glu Ala Glu Tyr Lys  
                   165                  170                  175

Ala Val Ala Arg Ala Leu Arg Gly Ala Val Glu Met Asp Pro Arg Gln  
                   180                  185                  190

Thr Gly Ile Pro Ser Thr Lys Gly Ala Leu  
                   195                  200

<210> 395

Thr Gly Ile Pro Ser Thr Lys Gly Ala Leu  
 195 200

<210> 393

<211> 729

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(706)

<223> FRXA01104

<400> 393

cacttgcgca ctaccattgg tgtgcctgag gaaaatgatg cgtttttgga cgcagctgca 60  
 gagatcatca agctgaacct gtaagagaga agaatttttc atg act gtc gca cca 115  
 Met Thr Val Ala Pro  
 1 5  
 aga att ggt acc gca acc cgc acc acc agc gaa tcc gac atc acc gtc 163  
 Arg Ile Gly Thr Ala Thr Arg Thr Thr Ser Glu Ser Asp Ile Thr Val  
 10 15 20  
 gag atc aac ctg gac ggc acc ggc aaa gta gat atc gat acc ggc ctg 211  
 Glu Ile Asn Leu Asp Gly Thr Gly Lys Val Asp Ile Asp Thr Gly Leu  
 25 30 35  
 cca ttt ttc gac cac atg ctc act gca ttc ggc gtg cac ggc agt ttt 259  
 Pro Phe Phe Asp His Met Leu Thr Ala Phe Gly Val His Gly Ser Phe  
 40 45 50  
 gat ctg aaa gtc cat gcc aag ggc gac atc gag atc gac gca cac cac 307  
 Asp Leu Lys Val His Ala Lys Gly Asp Ile Glu Ile Asp Ala His His  
 55 60 65  
 acc gtg gaa gat acc gcc atc gtg ctc ggc caa gca ctc ctt gac gct 355  
 Thr Val Glu Asp Thr Ala Ile Val Leu Gly Gln Ala Leu Leu Asp Ala  
 70 75 80 85  
 att ggc gac aag aaa ggc atc cgc cgt ttc gca tcc tgc cag ctg ccc 403  
 Ile Gly Asp Lys Lys Gly Ile Arg Arg Phe Ala Ser Cys Gln Leu Pro  
 90 95 100  
 atg gat gag gca tta gtg gag tcc gtg gtg gat atc tcc ggt cgc cca 451  
 Met Asp Glu Ala Leu Val Glu Ser Val Val Asp Ile Ser Gly Arg Pro  
 105 110 115  
 tac ttc gtg atc tcc ggc gaa cca gac cac atg atc acc tcc gtg atc 499  
 Tyr Phe Val Ile Ser Gly Glu Pro Asp His Met Ile Thr Ser Val Ile  
 120 125 130  
 ggt gga cac tac gca acc gtg atc aac gag cac ttc ttt gaa acc ctc 547  
 Gly Gly His Tyr Ala Thr Val Ile Asn Glu His Phe Phe Glu Thr Leu  
 135 140 145  
 gcg ctc aac tcc cga atc acc ctc cac gtg atc tgc cac tac ggc cgc 595  
 Ala Leu Asn Ser Arg Ile Thr Leu His Val Ile Cys His Tyr Gly Arg  
 150 155 160 165

Gly Gly His Tyr Ala Thr Val Ile Asn Glu His Phe Phe Glu Thr Leu  
 135 140 145  
 gcg ctc aac tcc cga atc acc ctc cac gtg atc tgc cac tac ggc cgc 595  
 Ala Leu Asn Ser Arg Ile Thr Leu His Val Ile Cys His Tyr Gly Arg  
 150 155 160 165  
 gac cct cac cac atc acc gaa gca gag tac aag gct gtt gcc cgt gcg 643  
 Asp Pro His His Ile Thr Glu Ala Glu Tyr Lys Ala Val Ala Arg Ala  
 170 175 180  
 ctg cgc ggt gcc gta gag atg gat cct cgt caa aca gga atc cca tcc 691  
 Leu Arg Gly Ala Val Glu Met Asp Pro Arg Gln Thr Gly Ile Pro Ser  
 185 190 195  
 act aag gga gcg ctc tagacatgaa ctcttctccc atc 729  
 Thr Lys Gly Ala Leu  
 200

&lt;210&gt; 392

&lt;211&gt; 202

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 392

Met Thr Val Ala Pro Arg Ile Gly Thr Ala Thr Arg Thr Thr Ser Glu  
 1 5 10 15  
 Ser Asp Ile Thr Val Glu Ile Asn Leu Asp Gly Thr Gly Lys Val Asp  
 20 25 30  
 Ile Asp Thr Gly Leu Pro Phe Phe Asp His Met Leu Thr Ala Phe Gly  
 35 40 45  
 Val His Gly Ser Phe Asp Leu Lys Val His Ala Lys Gly Asp Ile Glu  
 50 55 60  
 Ile Asp Ala His His Thr Val Glu Asp Thr Ala Ile Val Leu Gly Gln  
 65 70 75 80  
 Ala Leu Leu Asp Ala Ile Gly Asp Lys Lys Gly Ile Arg Arg Phe Ala  
 85 90 95  
 Ser Cys Gln Leu Pro Met Asp Glu Ala Leu Val Glu Ser Val Val Asp  
 100 105 110  
 Ile Ser Gly Arg Pro Tyr Phe Val Ile Ser Gly Glu Pro Asp His Met  
 115 120 125  
 Ile Thr Ser Val Ile Gly Gly His Tyr Ala Thr Val Ile Asn Glu His  
 130 135 140  
 Phe Phe Glu Thr Leu Ala Leu Asn Ser Arg Ile Thr Leu His Val Ile  
 145 150 155 160  
 Cys His Tyr Gly Arg Asp Pro His His Ile Thr Glu Ala Glu Tyr Lys  
 165 170 175  
 Ala Val Ala Arg Ala Leu Arg Gly Ala Val Glu Met Asp Pro Arg Gln  
 180 185 190

Gly Ala Asn Ala Val Leu Ala Ala Thr Ile Phe His Phe Arg Glu Val  
 225 230 235 240

Thr Ile Ala Glu Val Lys Gly Ala Ile Lys Asp Ala Gly Phe Glu Val  
 245 250 255

Arg Lys

<210> 391

<211> 729

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(706)

<223> RXN01104

<400> 391

cacttgcgca ctaccattgg tgtgcctgag gaaaatgatg cgtttttggga cgcagctgca 60  
 gagatcatca agctgaacct gtaagagaga agaatttttc atg act gtc gca cca 115  
 Met Thr Val Ala Pro  
 1 5  
 aga att ggt acc gca acc cgc acc acc agc gaa tcc gac atc acc gtc 163  
 Arg Ile Gly Thr Ala Thr Arg Thr Thr Ser Glu Ser Asp Ile Thr Val  
 10 15 20  
 gag atc aac ctg gac ggc acc ggc aaa gta gat atc gat acc ggc ctg 211  
 Glu Ile Asn Leu Asp Gly Thr Gly Lys Val Asp Ile Asp Thr Gly Leu  
 25 30 35  
 cca ttt ttc gac cac atg ctc act gca ttc ggc gtg cac ggc agt ttt 259  
 Pro Phe Phe Asp His Met Leu Thr Ala Phe Gly Val His Gly Ser Phe  
 40 45 50  
 gat ctg aaa gtc cat gcc aag ggc gac atc gag atc gac gca cac cac 307  
 Asp Leu Lys Val His Ala Lys Gly Asp Ile Glu Ile Asp Ala His His  
 55 60 65  
 acc gtg gaa gat acc gcc atc gtg ctc ggc caa gca ctc ctt gac gct 355  
 Thr Val Glu Asp Thr Ala Ile Val Leu Gly Gln Ala Leu Leu Asp Ala  
 70 75 80 85  
 att ggc gac aag aaa ggc atc cgc cgt ttc gca tcc tgc cag ctg ccc 403  
 Ile Gly Asp Lys Lys Gly Ile Arg Arg Phe Ala Ser Cys Gln Leu Pro  
 90 95 100  
 atg gat gag gca tta gtg gag tcc gtg gtg gat atc tcc ggt cgc cca 451  
 Met Asp Glu Ala Leu Val Glu Ser Val Val Asp Ile Ser Gly Arg Pro  
 105 110 115  
 tac ttc gtg atc tcc ggc gaa cca gac cac atg atc acc tcc gtg atc 499  
 Tyr Phe Val Ile Ser Gly Glu Pro Asp His Met Ile Thr Ser Val Ile  
 120 125 130  
 ggt gga cac tac gca acc gtg atc aac gag cac ttc ttt gaa acc ctc 547

Lys Ala Glu His Phe Pro Pro Ala Val Ala Ala Gly Ala Asn Ala Val  
 215 220 225  
 ctt gcc gcg acc att ttc cac ttc cgc gaa gta acc atc gcc gaa gta 835  
 Leu Ala Ala Thr Ile Phe His Phe Arg Glu Val Thr Ile Ala Glu Val  
 230 235 240 245  
 aag gga gcc att aaa gat gca gga ttt gag gtg cgg aaa tgagtgacaa 884  
 Lys Gly Ala Ile Lys Asp Ala Gly Phe Glu Val Arg Lys  
 250 255  
 tccacaagag tat 897

<210> 390  
 <211> 258  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 390  
 Met Gly Val Ala Ile Arg Val Ile Pro Cys Leu Asp Val Asp Asn Gly  
 1 5 10 15  
 Arg Val Val Lys Gly Val Asn Phe Glu Asn Leu Arg Asp Ala Gly Asp  
 20 25 30  
 Pro Val Glu Leu Ala Lys Arg Tyr Asp Glu Glu Gly Ala Asp Glu Leu  
 35 40 45  
 Thr Phe Leu Asp Val Thr Ala Ser Lys His Gly Arg Gly Thr Met Leu  
 50 55 60  
 Asp Val Val Arg Arg Thr Ala Asp Gln Val Phe Ile Pro Leu Thr Val  
 65 70 75 80  
 Gly Gly Gly Val Arg Ser Glu Glu Asp Val Asp Gln Leu Leu Arg Ala  
 85 90 95  
 Gly Ala Asp Lys Val Ser Val Asn Thr Ser Ala Ile Ala Arg Pro Glu  
 100 105 110  
 Leu Leu Ser Glu Leu Ser Lys Arg Phe Gly Ala Gln Cys Ile Val Leu  
 115 120 125  
 Ser Val Asp Ala Arg Arg Val Pro Glu Gly Gly Thr Pro Gln Pro Ser  
 130 135 140  
 Gly Phe Glu Val Thr Thr His Gly Gly Ser Lys Ser Ala Glu Leu Asp  
 145 150 155 160  
 Ala Ile Glu Trp Ala Lys Arg Gly Glu Glu Leu Gly Val Gly Glu Ile  
 165 170 175  
 Leu Leu Asn Ser Met Asp Gly Asp Gly Thr Lys Asn Gly Phe Asp Leu  
 180 185 190  
 Glu Leu Leu Glu Lys Val Arg Ala Ala Val Ser Ile Pro Val Ile Ala  
 195 200 205  
 Ser Gly Gly Ala Gly Lys Ala Glu His Phe Pro Pro Ala Val Ala Ala  
 210 215 220

578

Gln Ala Ser Phe Ile Arg Ala Pro Ile Val Thr Ala Phe Gly Pro Thr  
 135 140 145

gta gaa gcg atc gct gct ctc aac ggt ggg gag gtg gtt ggt gta cgc 595  
 Val Glu Ala Ile Ala Ala Leu Asn Gly Gly Glu Val Val Gly Val Arg  
 150 155 160 165

caa ggc 601  
 Gln Gly

<210> 388  
 <211> 167  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 388  
 Val Ile Val Gly Val Leu Ala Leu Gln Gly Gly Val Glu Glu His Leu  
 1 5 10 15

Thr Ala Leu Glu Ala Leu Gly Ala Thr Thr Arg Lys Val Arg Val Pro  
 20 25 30

Lys Asp Leu Asp Gly Leu Glu Gly Ile Val Ile Pro Gly Gly Glu Ser  
 35 40 45

Thr Val Leu Asp Lys Leu Ala Arg Thr Phe Asp Val Val Glu Pro Leu  
 50 55 60

Ala Asn Leu Ile Arg Asp Gly Leu Pro Val Phe Ala Thr Cys Ala Gly  
 65 70 75 80

Leu Ile Tyr Leu Ala Lys His Leu Asp Asn Pro Ala Arg Gly Gln Gln  
 85 90 95

Thr Leu Ala Val Val Asp Val Val Val Arg Arg Asn Ala Phe Gly Ala  
 100 105 110

Gln Arg Glu Ser Phe Asp Thr Thr Val Asp Val Ser Phe Asp Gly Ala  
 115 120 125

Thr Phe Pro Gly Val Gln Ala Ser Phe Ile Arg Ala Pro Ile Val Thr  
 130 135 140

Ala Phe Gly Pro Thr Val Glu Ala Ile Ala Ala Leu Asn Gly Gly Glu  
 145 150 155 160

Val Val Gly Val Arg Gln Gly  
 165

<210> 389  
 <211> 897  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(874)  
 <223> RXA01098

Val Val Gly Val Arg Gln Gly Asn Ile Ile Ala Leu Ser Phe His Pro  
 165 170 175

Glu Glu Thr Gly Asp Tyr Arg Ile His Gln Ala Trp Leu Asp Leu Val  
 180 185 190

Arg Lys His Ala Glu Leu Ala Ile  
 195 200

<210> 387

<211> 601

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(601)

<223> FRXA01657

<400> 387

cctccgcat tgccgacgta tcccgcggcc tgggtgaagc catggtgggc atcaacgtat 60  
 ccgacgttcc agcaccacac cgactcgccg agcgcggctg gtg atc gtt gga gtt 115  
 Val Ile Val Gly Val  
 1 5  
 tta gct ctc cag ggc ggg gtg gaa gaa cac ctc acc gcc ttg gaa gct 163  
 Leu Ala Leu Gln Gly Gly Val Glu Glu His Leu Thr Ala Leu Glu Ala  
 10 15 20  
 ctc gga gcg acg acc cga aaa gta cgt gtg cca aag gac ctt gat ggt 211  
 Leu Gly Ala Thr Thr Arg Lys Val Arg Val Pro Lys Asp Leu Asp Gly  
 25 30 35  
 ctc gaa ggc atc gtc atc ccc ggc ggg gaa tcc acc gtg ttg gac aaa 259  
 Leu Glu Gly Ile Val Ile Pro Gly Gly Glu Ser Thr Val Leu Asp Lys  
 40 45 50  
 ctg gct cgg aca ttc gac gtg gta gaa cct cta gcg aat ctc att cgc 307  
 Leu Ala Arg Thr Phe Asp Val Val Glu Pro Leu Ala Asn Leu Ile Arg  
 55 60 65  
 gac ggc cta ccc gtt ttc gct acc tgc gct ggc ctg atc tat ctg gcg 355  
 Asp Gly Leu Pro Val Phe Ala Thr Cys Ala Gly Leu Ile Tyr Leu Ala  
 70 75 80 85  
 aaa cac ctc gac aac cca gca agg gga caa caa acc ttg gcg gta gtg 403  
 Lys His Leu Asp Asn Pro Ala Arg Gly Gln Gln Thr Leu Ala Val Val  
 90 95 100  
 gac gtg gtg gtg cgt cga aac gca ttt ggc gcc caa gcg gaa tcc ttc 451  
 Asp Val Val Val Arg Arg Asn Ala Phe Gly Ala Gln Arg Glu Ser Phe  
 105 110 115  
 gac acc acc gtg gat gtt tcc ttc gac ggt gca aca ttc ccc gga gtg 499  
 Asp Thr Thr Val Asp Val Ser Phe Asp Gly Ala Thr Phe Pro Gly Val  
 120 125 130  
 cag gcc tcg ttt atc cga gct ccc atc gtc act gct ttt ggt cct acg 547



gac acc acc gtg gat gtt tcc ttc gac ggt gca aca ttc ccc gga gtg 499  
 Asp Thr Thr Val Asp Val Ser Phe Asp Gly Ala Thr Phe Pro Gly Val  
           120                          125                          130

cag gcc tcg ttt atc cga gct ccc atc gtc act gct ttt ggt cct acg 547  
 Gln Ala Ser Phe Ile Arg Ala Pro Ile Val Thr Ala Phe Gly Pro Thr  
           135                          140                          145

gta gaa gcg atc gct gct ctc aac ggt ggg gag gtg gtt ggt gta cgc 595  
 Val Glu Ala Ile Ala Ala Leu Asn Gly Gly Glu Val Val Gly Val Arg  
           150                          155                          160                          165

caa ggc aac atc atc gcg ctg tct ttc cat ccc gaa gaa acc ggc gat 643  
 Gln Gly Asn Ile Ile Ala Leu Ser Phe His Pro Glu Glu Thr Gly Asp  
                           170                          175                          180

tac cgc atc cac caa gcc tgg ctg gac ctg gtg aga aaa cac gct gaa 691  
 Tyr Arg Ile His Gln Ala Trp Leu Asp Leu Val Arg Lys His Ala Glu  
                           185                          190                          195

ctg gcg att tgatgttttc ggtagcgctc tgt 723  
 Leu Ala Ile  
           200

<210> 386

<211> 200

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 386

Val Ile Val Gly Val Leu Ala Leu Gln Gly Gly Val Glu Glu His Leu  
   1                          5                          10                          15

Thr Ala Leu Glu Ala Leu Gly Ala Thr Thr Arg Lys Val Arg Val Pro  
           20                          25                          30

Lys Asp Leu Asp Gly Leu Glu Gly Ile Val Ile Pro Gly Gly Glu Ser  
           35                          40                          45

Thr Val Leu Asp Lys Leu Ala Arg Thr Phe Asp Val Val Glu Pro Leu  
           50                          55                          60

Ala Asn Leu Ile Arg Asp Gly Leu Pro Val Phe Ala Thr Cys Ala Gly  
           65                          70                          75                          80

Leu Ile Tyr Leu Ala Lys His Leu Asp Asn Pro Ala Arg Gly Gln Gln  
                           85                          90                          95

Thr Leu Ala Val Val Asp Val Val Val Arg Arg Asn Ala Phe Gly Ala  
           100                          105                          110

Gln Arg Glu Ser Phe Asp Thr Thr Val Asp Val Ser Phe Asp Gly Ala  
           115                          120                          125

Thr Phe Pro Gly Val Gln Ala Ser Phe Ile Arg Ala Pro Ile Val Thr  
           130                          135                          140

Ala Phe Gly Pro Thr Val Glu Ala Ile Ala Ala Leu Asn Gly Gly Glu  
           145                          150                          155                          160

Phe Val His Ser Tyr Gly Val Arg Lys Trp Thr Leu Glu Thr Asp Asp  
 145 150 155 160  
 Leu Thr Thr Pro Pro Glu Val Val Trp Ala Lys His Glu Asn Asp Arg  
 165 170 175  
 Phe Val Ala Ala Val Glu Asn Gly Thr Leu Trp Ala Thr Gln Phe His  
 180 185 190  
 Pro Glu Lys Ser Gly Asp Ala Gly Ala Gln Leu Leu Arg Asn Trp Ile  
 195 200 205  
 Asn Tyr Ile  
 210

<210> 385  
 <211> 723  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(700)  
 <223> RXN01657

<400> 385  
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 ccgacgttcc agcaccacac cgactcgccg agcgcggctg gtg atc gtt gga gtt 115  
 Val Ile Val Gly Val  
 1 5  
 tta gct ctc cag ggc ggg gtg gaa gaa cac ctc acc gcc ttg gaa gct 163  
 Leu Ala Leu Gln Gly Val Glu Glu His Leu Thr Ala Leu Glu Ala  
 10 15 20  
 ctc gga gcg acg acc cga aaa gta cgt gtg cca aag gac ctt gat ggt 211  
 Leu Gly Ala Thr Thr Arg Lys Val Arg Val Pro Lys Asp Leu Asp Gly  
 25 30 35  
 ctc gaa ggc atc gtc atc ccc ggc ggg gaa tcc acc gtg ttg gac aaa 259  
 Leu Glu Gly Ile Val Ile Pro Gly Gly Glu Ser Thr Val Leu Asp Lys  
 40 45 50  
 ctg gct cgg aca ttc gac gtg gta gaa cct cta gcg aat ctc att cgc 307  
 Leu Ala Arg Thr Phe Asp Val Val Glu Pro Leu Ala Asn Leu Ile Arg  
 55 60 65  
 gac ggc cta ccc gtt ttc gct acc tgc gct ggc ctg atc tat ctg gcg 355  
 Asp Gly Leu Pro Val Phe Ala Thr Cys Ala Gly Leu Ile Tyr Leu Ala  
 70 75 80 85  
 aaa cac ctc gac aac cca gca agg gga caa caa acc ttg gcg gta gtg 403  
 Lys His Leu Asp Asn Pro Ala Arg Gly Gln Gln Thr Leu Ala Val Val  
 90 95 100  
 gac gtg gtg gtg cgt cga aac gca ttt ggc gcc caa cgc gaa tcc ttc 451  
 Asp Val Val Val Arg Arg Asn Ala Phe Gly Ala Gln Arg Glu Ser Phe  
 105 110 115

105	110	115	
cct cac atg ggg tgg aac aca ctt gaa atg cct acc aac tca cca atg			499
Pro His Met Gly Trp Asn Thr Leu Glu Met Pro Thr Asn Ser Pro Met			
120	125	130	
ttt gag gga att tca cct gat gag cgt ttc tac ttc gtg cac tcc tat			547
Phe Glu Gly Ile Ser Pro Asp Glu Arg Phe Tyr Phe Val His Ser Tyr			
135	140	145	
ggt gtg cgc aag tgg acg ttg gaa acc gac gat ctg acc acg cct cca			595
Gly Val Arg Lys Trp Thr Leu Glu Thr Asp Asp Leu Thr Thr Pro Pro			
150	155	160	165
gag gtt gtg tgg gcg aag cac gaa aat gat cgt ttt gtg gca gct gtg			643
Glu Val Val Trp Ala Lys His Glu Asn Asp Arg Phe Val Ala Ala Val			
170	175		180
gaa aac ggc acg ctg tgg gct act caa ttc cac cca gaa aaa tca ggt			691
Glu Asn Gly Thr Leu Trp Ala Thr Gln Phe His Pro Glu Lys Ser Gly			
185	190		195
gac gca ggc gca cag cta ctg cga aac tgg atc aac tac atc			733
Asp Ala Gly Ala Gln Leu Leu Arg Asn Trp Ile Asn Tyr Ile			
200	205	210	
taacagatag gatcaatatt cat			756

&lt;210&gt; 384

&lt;211&gt; 211

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 384

Met Thr Lys Thr Val Ala Leu Leu Asp Tyr Gly Ser Gly Asn Leu Arg			
1	5	10	15
Ser Ala Gln Arg Ala Leu Glu Arg Ala Gly Ala Glu Val Ile Val Ser			
20	25		30
Ser Asp Pro Glu Val Cys Thr Asn Ala Asp Gly Leu Leu Val Pro Gly			
35	40		45
Val Gly Ala Phe Asp Ala Cys Met Lys Gly Leu Lys Asn Val Phe Gly			
50	55		60
His Arg Ile Ile Gly Gln Arg Leu Ala Gly Gly Arg Pro Val Met Gly			
65	70	75	80
Ile Cys Val Gly Met Gln Ile Leu Phe Asp Glu Gly Asp Glu His Gly			
85	90		95
Ile Lys Ser Ala Gly Cys Gly Glu Trp Pro Gly Lys Val Glu Arg Leu			
100	105		110
Gln Ala Glu Ile Leu Pro His Met Gly Trp Asn Thr Leu Glu Met Pro			
115	120		125
Thr Asn Ser Pro Met Phe Glu Gly Ile Ser Pro Asp Glu Arg Phe Tyr			
130	135		140

165 170 175  
 Leu Ser Gly Pro Asn Val Glu Leu Leu Arg Glu Val Ala Ala Ala Thr  
 180 185 190  
 Asp Ala Pro Ile Val Ala Ser Gly Gly Ile Ser Val Leu Glu Asp Val  
 195 200 205  
 Leu Glu Leu Ala Lys Tyr Gln Asp Glu Gly Ile Asp Ser Val Ile Ile  
 210 215 220  
 Gly Lys Ala Leu Tyr Glu His Lys Phe Thr Leu Glu Glu Ala Leu Ala  
 225 230 235 240  
 Ala Val Glu Lys Leu Gly  
 245  
  
 <210> 383  
 <211> 756  
 <212> DNA  
 <213> Corynebacterium glutamicum  
  
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 <221> CDS  
 <222> (101)..(733)  
 <223> RXA01101  
  
 <400> 383  
 atcgcagcta ggccagtgtg gtggatataa aacccttttg gggagaaaga aactcgactg 60  
 cggttcttga tcctgaaagc acgtgacata aactatcggc atg acc aaa act gtc 115  
 Met Thr Lys Thr Val  
 1 5  
 gcc ctt ctc gac tac gga tct gga aac ctt cgt tct gct caa cgc gca 163  
 Ala Leu Leu Asp Tyr Gly Ser Gly Asn Leu Arg Ser Ala Gln Arg Ala  
 10 15 20  
 cta gag cgt gcc ggt gca gaa gtt atc gtg agc tcc gat cca gaa gtt 211  
 Leu Glu Arg Ala Gly Ala Glu Val Ile Val Ser Ser Asp Pro Glu Val  
 25 30 35  
 tgc acc aac gct gat ggc ctc cta gtt cct gga gtg ggc gca ttt gat 259  
 Cys Thr Asn Ala Asp Gly Leu Leu Val Pro Gly Val Gly Ala Phe Asp  
 40 45 50  
 gcc tgc atg aag ggt ttg aaa aac gtc ttc gga cat cgc att atc gga 307  
 Ala Cys Met Lys Gly Leu Lys Asn Val Phe Gly His Arg Ile Ile Gly  
 55 60 65  
 cag cgt ctt gct ggt gga cgt cca gtg atg ggt att tgt gtg ggc atg 355  
 Gln Arg Leu Ala Gly Gly Arg Pro Val Met Gly Ile Cys Val Gly Met  
 70 75 80 85  
 cag atc ctg ttc gat gaa ggc gat gag cac ggc att aag tca gct ggt 403  
 Gln Ile Leu Phe Asp Glu Gly Asp Glu His Gly Ile Lys Ser Ala Gly  
 90 95 100  
 tgc ggc gag tgg cct ggc aaa gtg gaa cgc ctc caa gcg gag atc ctg 451  
 Cys Gly Glu Trp Pro Gly Lys Val Glu Arg Leu Gln Ala Glu Ile Leu

Phe Val Val Thr Asp Val Ser Lys Asp Gly Thr Leu Ser Gly Pro Asn  
 170 175 180  
 gtt gag ctg ctg cgt gag gtt gct gca gct aca gac gca cct atc gtg 691  
 Val Glu Leu Leu Arg Glu Val Ala Ala Ala Thr Asp Ala Pro Ile Val  
 185 190 195  
 gca tct ggt gga att tct gtt ttg gaa gat gtt ttg gaa cta gcc aag 739  
 Ala Ser Gly Gly Ile Ser Val Leu Glu Asp Val Leu Glu Leu Ala Lys  
 200 205 210  
 tac cag gat gag ggc att gat tcc gtc atc att ggc aag gca ctt tat 787  
 Tyr Gln Asp Glu Gly Ile Asp Ser Val Ile Ile Gly Lys Ala Leu Tyr  
 215 220 225  
 gag cac aag ttc acc ctc gaa gag gct ttg gct gca gta gaa aag ctc 835  
 Glu His Lys Phe Thr Leu Glu Glu Ala Leu Ala Val Glu Lys Leu  
 230 235 240 245  
 ggt taatacatgg atgctcgtgg gat 861  
 Gly

&lt;210&gt; 382

&lt;211&gt; 246

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 382

Met Thr Phe Thr Ile Leu Pro Ala Val Asp Val Val Asn Gly Gln Ala  
 1 5 10 15  
 Val Arg Leu Asp Gln Gly Glu Ala Gly Thr Glu Lys Ser Tyr Gly Thr  
 20 25 30  
 Pro Leu Glu Ser Ala Leu Lys Trp Gln Glu Gln Gly Ala Lys Trp Leu  
 35 40 45  
 His Phe Val Asp Leu Asp Ala Ala Phe Asn Arg Gly Ser Asn His Glu  
 50 55 60  
 Met Met Ala Glu Ile Val Gly Lys Leu Asp Val Asp Val Glu Leu Thr  
 65 70 75 80  
 Gly Gly Ile Arg Asp Asp Glu Ser Leu Glu Arg Ala Leu Ala Thr Gly  
 85 90 95  
 Ala Arg Arg Val Asn Ile Gly Thr Ala Ala Leu Glu Lys Pro Glu Trp  
 100 105 110  
 Ile Ala Ser Ala Ile Gln Arg Tyr Gly Glu Lys Ile Ala Val Asp Ile  
 115 120 125  
 Ala Val Arg Leu Glu Asp Gly Glu Trp Arg Thr Arg Gly Asn Gly Trp  
 130 135 140  
 Val Ser Asp Gly Gly Asp Leu Trp Glu Val Leu Glu Arg Leu Asp Ser  
 145 150 155 160  
 Gln Gly Cys Ala Arg Phe Val Val Thr Asp Val Ser Lys Asp Gly Thr

115

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<210> 381
<211> 861
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(838)  
<223> RXA01100
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<400> 381

gctgtgggct actcaattcc acccagaaaa atcaggtgac gcaggcgcac agctactgcg	60
aaactggatc aactacatct aacagatagg atcaatatcc atg acc ttc act att	115
	Met Thr Phe Thr Ile
	1 5
ctt cct gca gtc gat gta gtt aac gga caa gca gtt cgc cta gat cag	163
Leu Pro Ala Val Asp Val Val Asn Gly Gln Ala Val Arg Leu Asp Gln	
	10 15 20
ggc gag gcc ggc act gaa aag tct tat ggc acc cct ttg gaa tcc gca	211
Gly Glu Ala Gly Thr Glu Lys Ser Tyr Gly Thr Pro Leu Glu Ser Ala	
	25 30 35
ctg aag tgg cag gag cag ggt gca aag tgg ttg cac ttt gtg gac ctg	259
Leu Lys Trp Gln Glu Gln Gly Ala Lys Trp Leu His Phe Val Asp Leu	
	40 45 50
gac gca gcg ttc aac cgt ggt tcc aac cat gag atg atg gcg gaa att	307
Asp Ala Ala Phe Asn Arg Gly Ser Asn His Glu Met Met Ala Glu Ile	
	55 60 65
gtc ggc aag ctc gat gtt gat gtg gag ctc act ggc ggt atc cgt gat	355
Val Gly Lys Leu Asp Val Asp Val Glu Leu Thr Gly Gly Ile Arg Asp	
	70 75 80 85
gat gag tct ctg gag cgc gcg ctg gca acc ggt gca cgt cgt gta aac	403
Asp Glu Ser Leu Glu Arg Ala Leu Ala Thr Gly Ala Arg Arg Val Asn	
	90 95 100
att ggt acc gct gct ctg gag aag cca gag tgg att gct tct gcg att	451
Ile Gly Thr Ala Ala Leu Glu Lys Pro Glu Trp Ile Ala Ser Ala Ile	
	105 110 115
caa cgc tat ggc gag aag att gct gtc gat atc gct gtg cgt ttg gaa	499
Gln Arg Tyr Gly Glu Lys Ile Ala Val Asp Ile Ala Val Arg Leu Glu	
	120 125 130
gat ggt gaa tgg cgc acc cgt gga aac ggt tgg gtc tcc gat ggt ggc	547
Asp Gly Glu Trp Arg Thr Arg Gly Asn Gly Trp Val Ser Asp Gly Gly	
	135 140 145
gat ctg tgg gaa gtt ctc gag cgt ttg gat tcc caa ggt tgt gca cgt	595
Asp Leu Trp Glu Val Leu Glu Arg Leu Asp Ser Gln Gly Cys Ala Arg	
	150 155 160 165
ttc gtg gtt acc gat gtg tcc aag gac ggc acc ttg agt ggt cca aat	643

caa gag tat gag ctg gat tgg gac gtc gaa aag cga tta aag ctt aac 163  
 Gln Glu Tyr Glu Leu Asp Trp Asp Val Glu Lys Arg Leu Lys Leu Asn  
                     10                    15                    20

gac gcc ggc ctg gtg ccg gca atc gtc cag gcc gac ggg acc aac gag 211  
 Asp Ala Gly Leu Val Pro Ala Ile Val Gln Ala Asp Gly Thr Asn Glu  
                     25                    30                    35

gtc ctc atg atg gcc tgg atg gat acc cac gcg cta gcc tat act ttg 259  
 Val Leu Met Met Ala Trp Met Asp Thr His Ala Leu Ala Tyr Thr Leu  
                     40                    45                    50

gcg acc cgc cgt gga acc tat ttt tct agg tcc cgc aac gag tac tgg 307  
 Ala Thr Arg Arg Gly Thr Tyr Phe Ser Arg Ser Arg Asn Glu Tyr Trp  
                     55                    60                    65

atc aag ggc ctg acc tct gga aac gtc caa gaa gtc acc gga ctt gcc 355  
 Ile Lys Gly Leu Thr Ser Gly Asn Val Gln Glu Val Thr Gly Leu Ala  
                     70                    75                    80                    85

ctc gac tgc gac ggc gac acc gtc ctt ctg acc gtg aaa caa acc ggc 403  
 Leu Asp Cys Asp Gly Asp Thr Val Leu Leu Thr Val Lys Gln Thr Gly  
                     90                    95                    100

ggt gcg tgc cac act ggt gcc cac aca tgt ttc gac aat gac gtt ttg 451  
 Gly Ala Cys His Thr Gly Ala His Thr Cys Phe Asp Asn Asp Val Leu  
                     105                    110                    115

ctg taaaagcaac aacgattaag gaa 477  
 Leu

&lt;210&gt; 380

&lt;211&gt; 118

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 380

Met Ser Asp Asn Pro Gln Glu Tyr Glu Leu Asp Trp Asp Val Glu Lys  
   1                    5                    10                    15

Arg Leu Lys Leu Asn Asp Ala Gly Leu Val Pro Ala Ile Val Gln Ala  
                     20                    25                    30

Asp Gly Thr Asn Glu Val Leu Met Met Ala Trp Met Asp Thr His Ala  
                     35                    40                    45

Leu Ala Tyr Thr Leu Ala Thr Arg Arg Gly Thr Tyr Phe Ser Arg Ser  
                     50                    55                    60

Arg Asn Glu Tyr Trp Ile Lys Gly Leu Thr Ser Gly Asn Val Gln Glu  
                     65                    70                    75                    80

Val Thr Gly Leu Ala Leu Asp Cys Asp Gly Asp Thr Val Leu Leu Thr  
                     85                    90                    95

Val Lys Gln Thr Gly Gly Ala Cys His Thr Gly Ala His Thr Cys Phe  
                     100                    105                    110

Asp Asn Asp Val Leu Leu

25	30	35	
cta ggt aag aag gtc atc gaa gaa gcc gga gag gtc tgg att gca gcc			259
Leu Gly Lys Lys Val Ile Glu Glu Ala Gly Glu Val Trp Ile Ala Ala			
40	45	50	
gag tat gag acc gat gaa gag cta gcc gga gaa atc tcc cag ctc att			307
Glu Tyr Glu Thr Asp Glu Glu Leu Ala Gly Glu Ile Ser Gln Leu Ile			
55	60	65	
tat tgg acc cag gtc atc atg gtt gct cgc ggc ctg aag cca gaa gat			355
Tyr Trp Thr Gln Val Ile Met Val Ala Arg Gly Leu Lys Pro Glu Asp			
70	75	80	85
atc tac aag aac ctg taggagtttt aaagcaatca tgt			393
Ile Tyr Lys Asn Leu			
90			

&lt;210&gt; 378

&lt;211&gt; 90

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 378

Met Tyr Arg Val Lys Thr Phe Asp Ser Leu Tyr Glu Glu Leu Leu Asn	
1	15
5	10

Arg Ala Gln Thr Arg Pro Glu Gly Ser Gly Thr Val Ala Ala Leu Asp	
20	30
25	

Lys Gly Ile His His Leu Gly Lys Lys Val Ile Glu Glu Ala Gly Glu	
35	45
40	

Val Trp Ile Ala Ala Glu Tyr Glu Thr Asp Glu Glu Leu Ala Gly Glu	
50	60
55	

Ile Ser Gln Leu Ile Tyr Trp Thr Gln Val Ile Met Val Ala Arg Gly	
65	80
70	75

Leu Lys Pro Glu Asp Ile Tyr Lys Asn Leu	
85	90

&lt;210&gt; 379

&lt;211&gt; 477

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(454)

&lt;223&gt; RXA01097

&lt;400&gt; 379

gcgccaacgc agtgcttgcc gcgaccattt tccacttccg cgaagtaacc atcgccgaag	60
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taaagggagc cattaaagat gcaggatttg aggtgcggaa atg agt gac aat cca	115
Met Ser Asp Asn Pro	
1	5



Lys Gly Asp Leu Ser Glu Asp Asp Val Leu Met Ala Val Leu Glu Ala  
 145 150 155 160  
 Gly Ala Glu Glu Val Asn Asp Asn Gly Asp Leu Phe Glu Val Thr Cys  
 165 170 175  
 Ala Pro Thr Asp Ile Gln Ala Val Arg Asp Ala Leu Val Glu Ala Gly  
 180 185 190  
 Ile Glu Val Glu Asp Ser Glu Ser Asp Phe Arg Ala Ser Val Gln Val  
 195 200 205  
 Pro Leu Asp Ala Asp Gly Ala Arg Lys Ile Phe Lys Leu Val Asp Ala  
 210 215 220  
 Leu Glu Asp Ser Asp Asp Val Gln Asn Val Tyr Thr Asn Ile Asp Leu  
 225 230 235 240  
 Ser Asp Glu Val Leu Thr Glu Leu Glu Asn Asp  
 245 250

<210> 405  
 <211> 547  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(547)  
 <223> RXC01096

<400> 405  
 accgtgaaac aaaccggcgg tgcgtgccac actggtgccc acacatgttt cgacaatgac 60

gttttgctgt aaaagcaaca acgattaagg aagaaatctt atg aag cca cgc gtg 115  
 Met Lys Pro Arg Val  
 1 5

ctg tca gca tta ggc att gga gct ggc gcc ctg gtt gtc tgg atc agc 163  
 Leu Ser Ala Leu Gly Ile Gly Ala Gly Ala Leu Val Val Trp Ile Ser  
 10 15 20

tca cgc atg aac tgg gta acc atc gag gct ttc gac gat aaa tca ggt 211  
 Ser Arg Met Asn Trp Val Thr Ile Glu Ala Phe Asp Asp Lys Ser Gly  
 25 30 35

agt gtc acc caa tct att gtg ggt gca acc tgg tct aca gaa atc atg 259  
 Ser Val Thr Gln Ser Ile Val Gly Ala Thr Trp Ser Thr Glu Ile Met  
 40 45 50

gcg ctt gca ctt gct ttg ctc gct gcc ttc gcc gcc gcg ttg gtg ctc 307  
 Ala Leu Ala Leu Ala Leu Leu Ala Ala Phe Ala Ala Ala Leu Val Leu  
 55 60 65

aag cgc atg ggt cgg cgc atc att ggt ggt att tcg gcg ctg atc gcg 355  
 Lys Arg Met Gly Arg Arg Ile Ile Gly Gly Ile Ser Ala Leu Ile Ala  
 70 75 80 85

gtg ggt gcc agc ctg tct cca ctc gcg ctt ctc acc caa gac cca gac 403  
 Val Gly Ala Ser Leu Ser Pro Leu Ala Leu Leu Thr Gln Asp Pro Asp

Glu Asp Asp Val Leu Met Ala Val Leu Glu Ala Gly Ala Glu Glu Val  
 150 155 160 165  
 aac gac aac ggc gat ctg ttc gag gtt acc tgc gca cca act gac att 643  
 Asn Asp Asn Gly Asp Leu Phe Glu Val Thr Cys Ala Pro Thr Asp Ile  
 170 175 180  
 cag gct gtt cgc gac gca ctc gtg gaa gct ggc att gaa gta gaa gat 691  
 Gln Ala Val Arg Asp Ala Leu Val Glu Ala Gly Ile Glu Val Glu Asp  
 185 190 195  
 tct gaa tca gac ttc cgg gca tct gtt cag gtc ccc ctg gac gct gac 739  
 Ser Glu Ser Asp Phe Arg Ala Ser Val Gln Val Pro Leu Asp Ala Asp  
 200 205 210  
 ggt gca cgc aag atc ttc aag ctt gtg gac gcg ttg gaa gat tcc gac 787  
 Gly Ala Arg Lys Ile Phe Lys Leu Val Asp Ala Leu Glu Asp Ser Asp  
 215 220 225  
 gat gtg caa aac gtc tac acc aac atc gac ttg agc gat gag gtt ttg 835  
 Asp Val Gln Asn Val Tyr Thr Asn Ile Asp Leu Ser Asp Glu Val Leu  
 230 235 240 245  
 aca gag ctg gaa aac gac tagttcgtat tttccgcact ccg 876  
 Thr Glu Leu Glu Asn Asp  
 250

&lt;210&gt; 404

&lt;211&gt; 251

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 404

Met Ser Gly His Ser Lys Trp Ala Thr Thr Lys His Lys Lys Ala Ala  
 1 5 10 15  
 Asn Asp Ala Lys Arg Gly Lys Glu Phe Ala Lys Leu Ile Lys Asn Ile  
 20 25 30  
 Glu Val Ala Ala Arg Thr Gly Gly Gly Asp Pro Ser Ala Asn Pro Thr  
 35 40 45  
 Leu Asp Asp Met Ile Lys Lys Ala Lys Lys Ala Ser Val Pro Asn Asp  
 50 55 60  
 Asn Ile Glu Arg Ala Arg Lys Arg Gly Ser Gly Glu Glu Ala Gly Gly  
 65 70 75 80  
 Ala Asp Trp Met Asn Ile Met Tyr Glu Gly Tyr Gly Pro Asn Gly Val  
 85 90 95  
 Ala Met Leu Ile Glu Cys Leu Thr Asp Asn Arg Asn Arg Ala Ala Thr  
 100 105 110  
 Glu Val Arg Thr Ala Met Thr Lys Asn Gly Gly Asn Leu Gly Glu Ser  
 115 120 125  
 Gly Ser Val Ser Tyr Met Phe Thr Arg Thr Gly Val Val Thr Val Gln  
 130 135 140

Ala Asn Ala Glu Asp Leu Pro Ala His Gly Glu Ala Ile Arg Ala Arg  
 420 425 430

Phe Glu Asn Leu Pro Thr Thr Asp Glu Ala  
 435 440

<210> 403

<211> 876

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(853)

<223> RXC00930

<400> 403

acggcgcacc acacatttgg tgggtgtattg agctatctctt gggctgcgtg agaaaccatt 60

ttccggtgga tgatggaagc tagacgacga aagggagcat atg tct ggc cac tca 115  
 Met Ser Gly His Ser  
 1 5

aaa tgg gcg act acc aag cac aag aag gct gct aac gac gcc aag cga 163  
 Lys Trp Ala Thr Thr Lys His Lys Lys Ala Ala Asn Asp Ala Lys Arg  
 10 15 20

ggc aag gaa ttt gcc aag ctg atc aag aac atc gaa gtt gcg gca cgt 211  
 Gly Lys Glu Phe Ala Lys Leu Ile Lys Asn Ile Glu Val Ala Ala Arg  
 25 30 35

aca ggc ggt gga gat ccg tct gcg aac cca acg ctt gat gac atg atc 259  
 Thr Gly Gly Gly Asp Pro Ser Ala Asn Pro Thr Leu Asp Asp Met Ile  
 40 45 50

aag aaa gcc aag aag gct tct gtg ccg aac gat aac atc gaa cgt gca 307  
 Lys Lys Ala Lys Lys Ala Ser Val Pro Asn Asp Asn Ile Glu Arg Ala  
 55 60 65

cgc aag cgt ggc tcc ggc gaa gaa gct ggt ggc gct gac tgg atg aac 355  
 Arg Lys Arg Gly Ser Gly Glu Glu Ala Gly Gly Ala Asp Trp Met Asn  
 70 75 80 85

atc atg tac gag gga tac ggc ccc aac ggc gtt gcc atg ctt atc gag 403  
 Ile Met Tyr Glu Gly Tyr Gly Pro Asn Gly Val Ala Met Leu Ile Glu  
 90 95 100

tgt ctg acc gac aac cgt aac cgc gca gct acc gaa gtt cgc acc gca 451  
 Cys Leu Thr Asp Asn Arg Asn Arg Ala Ala Thr Glu Val Arg Thr Ala  
 105 110 115

atg acc aaa aac ggt ggc aac ttg ggc gag tcc ggt tcc gtg tcc tac 499  
 Met Thr Lys Asn Gly Gly Asn Leu Gly Glu Ser Gly Ser Val Ser Tyr  
 120 125 130

atg ttc acc cgc acc ggt gtc gtc acc gta caa aag ggc gat ctt agt 547  
 Met Phe Thr Arg Thr Gly Val Val Thr Val Gln Lys Gly Asp Leu Ser  
 135 140 145

gaa gat gac gtg ctc atg gct gtt ctt gaa gct ggt gct gaa gaa gtc 595

Val His Ala Glu Gln Lys Pro Ser Glu His Thr Thr Glu Leu Ser Pro  
 100 105 110  
 Gly Gly Thr Val Thr Glu Arg Phe Met Pro Ile Asp Arg Val Gly Leu  
 115 120 125  
 Tyr Val Pro Gly Gly Asn Ala Val Tyr Pro Ser Ser Val Ile Met Asn  
 130 135 140  
 Thr Val Pro Ala Gln Glu Ala Gly Val Asn Ser Leu Val Val Ala Ser  
 145 150 155 160  
 Pro Pro Gln Ala Glu His Gly Gly Trp Pro His Pro Thr Ile Leu Ala  
 165 170 175  
 Ala Cys Ser Ile Leu Gly Val Asp Glu Val Trp Ala Val Gly Gly Gly  
 180 185 190  
 Gln Ala Val Ala Leu Leu Ala Tyr Gly Asp Asp Ala Ala Gly Leu Glu  
 195 200 205  
 Pro Val Asp Met Ile Thr Gly Pro Gly Asn Ile Phe Val Thr Ala Ala  
 210 215 220  
 Lys Arg Leu Val Arg Gly Val Val Gly Thr Asp Ser Glu Ala Gly Pro  
 225 230 235 240  
 Thr Glu Ile Ala Val Leu Ala Asp Ala Ser Ala Asn Ala Val Asn Val  
 245 250 255  
 Ala Tyr Asp Leu Ile Ser Gln Ala Glu His Asp Val Met Ala Ala Ser  
 260 265 270  
 Val Leu Ile Thr Asp Ser Glu Gln Leu Ala Lys Asp Val Asn Arg Glu  
 275 280 285  
 Ile Glu Ala Arg Tyr Ser Ile Thr Arg Asn Ala Glu Arg Val Ala Glu  
 290 295 300  
 Ala Leu Arg Gly Ala Gln Ser Gly Ile Val Leu Val Asp Asp Ile Ser  
 305 310 315 320  
 Val Gly Ile Gln Val Ala Asp Gln Tyr Ala Ala Glu His Leu Glu Ile  
 325 330 335  
 His Thr Glu Asn Ala Arg Ala Val Ala Glu Gln Ile Thr Asn Ala Gly  
 340 345 350  
 Ala Ile Phe Val Gly Asp Phe Ser Pro Val Pro Leu Gly Asp Tyr Ser  
 355 360 365  
 Ala Gly Ser Asn His Val Leu Pro Thr Ser Gly Ser Ala Arg Phe Ser  
 370 375 380  
 Ala Gly Leu Ser Thr His Thr Phe Leu Arg Pro Val Asn Leu Ile Glu  
 385 390 395 400  
 Tyr Asp Glu Ala Ala Leu Lys Asp Val Ser Gln Val Val Ile Asn Phe  
 405 410 415

330 335 340  
 cgc gcc gta gca gag cag atc acc aac gcg ggt gcg atc ttc gtg ggc  
 1171  
 Arg Ala Val Ala Glu Gln Ile Thr Asn Ala Gly Ala Ile Phe Val Gly  
 345 350 355  
 gat ttc tca cca gta cca ctg ggt gat tac tcc gca gga tcc aac cac  
 1219  
 Asp Phe Ser Pro Val Pro Leu Gly Asp Tyr Ser Ala Gly Ser Asn His  
 360 365 370  
 gtg ctg cca acc tct gga tcc gct cgt ttc tcc gca ggt cta tcc acg  
 1267  
 Val Leu Pro Thr Ser Gly Ser Ala Arg Phe Ser Ala Gly Leu Ser Thr  
 375 380 385  
 cac acg ttc ctt cgc cca gtc aac ctc att gaa tac gat gag gct gct  
 1315  
 His Thr Phe Leu Arg Pro Val Asn Leu Ile Glu Tyr Asp Glu Ala Ala  
 390 395 400 405  
 ctg aag gac gtc tcg cag gtt gtc atc aac ttt gcc aac gcc gaa gat  
 1363  
 Leu Lys Asp Val Ser Gln Val Val Ile Asn Phe Ala Asn Ala Glu Asp  
 410 415 420  
 ctt cca gcg cac ggc gaa gca atc cgt gca cgc ttt gaa aac ctc ccc  
 1411  
 Leu Pro Ala His Gly Glu Ala Ile Arg Ala Arg Phe Glu Asn Leu Pro  
 425 430 435  
 acc acc gac gag gcc taagaaaaat gacaaaaatt act  
 1449  
 Thr Thr Asp Glu Ala  
 440

<210> 402  
 <211> 442  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 402  
 Met Leu Asn Val Thr Asp Leu Arg Gly Gln Thr Pro Ser Lys Ser Asp  
 1 5 10 15  
 Ile Arg Arg Ala Leu Pro Arg Gly Gly Thr Asp Val Trp Ser Val Leu  
 20 25 30  
 Pro Ile Val Gln Pro Val Val Glu Asp Val Gln Asn Arg Gly Ala Glu  
 35 40 45  
 Ala Ala Leu Asp Tyr Gly Glu Lys Phe Asp His Ile Arg Pro Ala Ser  
 50 55 60  
 Val Arg Val Pro Ala Glu Val Ile Ala Ala Ala Glu Asn Thr Leu Asp  
 65 70 75 80  
 Pro Leu Val Arg Glu Ser Ile Glu Glu Ser Ile Arg Arg Val Arg Lys  
 85 90 95

aag cca tcc gag cac acc act gaa ctt tca cca ggt ggc acc gtc act 451  
 Lys Pro Ser Glu His Thr Thr Glu Leu Ser Pro Gly Gly Thr Val Thr  
 105 110 115

gag cgt ttc atg ccg att gat cgc gtg gga ctg tac gtt cca ggc ggc 499  
 Glu Arg Phe Met Pro Ile Asp Arg Val Gly Leu Tyr Val Pro Gly Gly  
 120 125 130

aat gcg gtg tac cca tca agc gtg att atg aat act gtc cca gct caa 547  
 Asn Ala Val Tyr Pro Ser Ser Val Ile Met Asn Thr Val Pro Ala Gln  
 135 140 145

gag gct ggt gtg aac tcc ctt gtg gtt gcg tcg cct cct cag gct gag 595  
 Glu Ala Gly Val Asn Ser Leu Val Val Ala Ser Pro Pro Gln Ala Glu  
 150 155 160 165

cac ggt ggc tgg cct cac ccc acc att ttg gcg gcg tgt tcc atc ttg 643  
 His Gly Gly Trp Pro His Pro Thr Ile Leu Ala Ala Cys Ser Ile Leu  
 170 175 180

ggt gtt gat gag gtg tgg gct gtc ggc ggc ggt cag gcc gtg gcg ttg 691  
 Gly Val Asp Glu Val Trp Ala Val Gly Gly Gly Gln Ala Val Ala Leu  
 185 190 195

ctg gct tat ggt gat gac gct gca ggt ctc gag cct gtg gat atg atc 739  
 Leu Ala Tyr Gly Asp Asp Ala Ala Gly Leu Glu Pro Val Asp Met Ile  
 200 205 210

act gga cct ggc aat atc ttt gtc acc gct gcg aag cgc ctg gtc agg 787  
 Thr Gly Pro Gly Asn Ile Phe Val Thr Ala Ala Lys Arg Leu Val Arg  
 215 220 225

gga gtg gta ggt act gat tct gag gct ggc cct aca gaa atc gct gtg 835  
 Gly Val Val Gly Thr Asp Ser Glu Ala Gly Pro Thr Glu Ile Ala Val  
 230 235 240 245

ctt gct gat gcc tct gcc aac gcc gtc aac gtt gcc tac gat ctg atc 883  
 Leu Ala Asp Ala Ser Ala Asn Ala Val Asn Val Ala Tyr Asp Leu Ile  
 250 255 260

agc caa gca gaa cac gat gtc atg gct gcg tcc gtg ctc atc act gac 931  
 Ser Gln Ala Glu His Asp Val Met Ala Ala Ser Val Leu Ile Thr Asp  
 265 270 275

tcc gag cag ctt gcc aag gac gta aac agg gaa atc gag gcg cgt tac 979  
 Ser Glu Gln Leu Ala Lys Asp Val Asn Arg Glu Ile Glu Ala Arg Tyr  
 280 285 290

tca atc acg cgc aac gcc gag cgc gtc gca gaa gct ttg cgc ggg gcc  
 1027  
 Ser Ile Thr Arg Asn Ala Glu Arg Val Ala Glu Ala Leu Arg Gly Ala  
 295 300 305

cag agt ggc atc gtg ctt gtc gac gac att tcc gtg ggt atc caa gta  
 1075  
 Gln Ser Gly Ile Val Leu Val Asp Asp Ile Ser Val Gly Ile Gln Val  
 310 315 320 325

gcc gat caa tac gca gcg gaa cac ctg gaa atc cac act gag aac gcg  
 1123  
 Ala Asp Gln Tyr Ala Ala Glu His Leu Glu Ile His Thr Glu Asn Ala

His Ser Ala Asp Thr Leu Gly Thr Val Glu Lys Leu Ser Val Glu Arg  
 275 280 285  
 Val Arg Val Ala Ala Arg Leu Glu Glu Leu Gly Tyr Ala Val Val Pro  
 290 295 300  
 Ser Glu Ser Asn Phe Val Phe Phe Gly Asp Phe Ser Asp Gln His Ala  
 305 310 315 320  
 Ala Trp Gln Ala Phe Leu Asp Arg Gly Val Leu Ile Arg Asp Val Gly  
 325 330 335  
 Ile Ala Gly His Leu Arg Thr Thr Ile Gly Val Pro Glu Glu Asn Asp  
 340 345 350  
 Ala Phe Leu Asp Ala Ala Ala Glu Ile Ile Lys Leu Asn Leu  
 355 360 365

&lt;210&gt; 401

&lt;211&gt; 1449

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1426)

&lt;223&gt; RXA01106

&lt;400&gt; 401

ggtaaaccatg cgggcttaag aacttggtgtt gaggccgctt ggattcgggc accgagctcg 60

aagaatttcg attcaacctt ttaagggaga acttttcgcc atg ttg aat gtc act 115  
 Met Leu Asn Val Thr  
 1 5

gac ctg cga ggt caa aca cca tcc aag agc gac atc cga cgt gct ttg 163  
 Asp Leu Arg Gly Gln Thr Pro Ser Lys Ser Asp Ile Arg Arg Ala Leu  
 10 15 20

cca cgt ggt ggc act gac gtg tgg tct gtg ctt ccc ata gtg cag cct 211  
 Pro Arg Gly Gly Thr Asp Val Trp Ser Val Leu Pro Ile Val Gln Pro  
 25 30 35

gtt gta gaa gat gtc caa aac cgc ggc gct gaa gct gct ttg gat tac 259  
 Val Val Glu Asp Val Gln Asn Arg Gly Ala Glu Ala Ala Leu Asp Tyr  
 40 45 50

ggc gag aag ttc gac cat att cgc ccc gcc tcg gtg cgg gtg cca gct 307  
 Gly Glu Lys Phe Asp His Ile Arg Pro Ala Ser Val Arg Val Pro Ala  
 55 60 65

gag gtt att gct gca gca gaa aac acc tta gat ccg ttg gtg cgt gaa 355  
 Glu Val Ile Ala Ala Ala Glu Asn Thr Leu Asp Pro Leu Val Arg Glu  
 70 75 80 85

tcg att gaa gag tcg att cgt cgc gtc cgc aag gtt cac gct gag caa 403  
 Ser Ile Glu Glu Ser Ile Arg Arg Val Arg Lys Val His Ala Glu Gln  
 90 95 100

tga  
1221

<210> 400  
<211> 366  
<212> PRT  
<213> *Corynebacterium glutamicum*

<400> 400

Met Thr Lys Ile Thr Leu Ser Asp Leu Pro Leu Arg Glu Glu Leu Arg  
1 5 10 15  
Gly Glu His Ala Tyr Gly Ala Pro Gln Leu Asn Val Asp Ile Arg Leu  
20 25 30  
Asn Thr Asn Glu Asn Pro Tyr Pro Pro Ser Glu Ala Leu Val Ala Asp  
35 40 45  
Leu Val Ala Thr Val Asp Lys Ile Ala Thr Glu Leu Asn Arg Tyr Pro  
50 55 60  
Glu Arg Asp Ala Val Glu Leu Arg Asp Glu Leu Ala Ala Tyr Ile Thr  
65 70 75 80  
Lys Gln Thr Gly Val Ala Val Thr Arg Asp Asn Leu Trp Ala Ala Asn  
85 90 95  
Gly Ser Asn Glu Ile Leu Gln Gln Leu Leu Gln Ala Phe Gly Gly Pro  
100 105 110  
Gly Arg Thr Ala Leu Gly Phe Gln Pro Ser Tyr Ser Met His Pro Ile  
115 120 125  
Leu Ala Lys Gly Thr His Thr Glu Phe Ile Ala Val Ser Arg Gly Ala  
130 135 140  
Asp Phe Arg Ile Asp Met Asp Val Ala Leu Glu Glu Ile Arg Ala Lys  
145 150 155 160  
Gln Pro Asp Ile Val Phe Val Thr Thr Pro Asn Asn Pro Thr Gly Asp  
165 170 175  
Val Thr Ser Leu Asp Asp Val Glu Arg Ile Ile Asn Val Ala Pro Gly  
180 185 190  
Ile Val Ile Val Asp Glu Ala Tyr Ala Glu Phe Ser Pro Ser Pro Ser  
195 200 205  
Ala Thr Thr Leu Leu Glu Lys Tyr Pro Thr Lys Leu Val Val Ser Arg  
210 215 220  
Thr Met Ser Lys Ala Phe Asp Phe Ala Gly Gly Arg Leu Gly Tyr Phe  
225 230 235 240  
Val Ala Asn Pro Ala Phe Ile Asp Ala Val Met Leu Val Arg Leu Pro  
245 250 255  
Tyr His Leu Ser Ala Leu Ser Gln Ala Ala Ala Ile Val Ala Leu Arg  
260 265 270



atg gat gtg gcg ctg gaa gaa att cgt gca aag cag cct gac att gtt 595  
 Met Asp Val Ala Leu Glu Glu Ile Arg Ala Lys Gln Pro Asp Ile Val  
 150 155 160 165

ttt gtc acc acc ccg aac aac ccg acc ggt gat gtg acc tcg ctg gac 643  
 Phe Val Thr Thr Pro Asn Asn Pro Thr Gly Asp Val Thr Ser Leu Asp  
 170 175 180

gat gtt gag cgc atc atc aac gtt gcc cca ggc atc gtg atc gtg gat 691  
 Asp Val Glu Arg Ile Ile Asn Val Ala Pro Gly Ile Val Ile Val Asp  
 185 190 195

gaa gct tat gcg gaa ttc tcc cca tca cct tca gca acc act ctt ctg 739  
 Glu Ala Tyr Ala Glu Phe Ser Pro Ser Pro Ser Ala Thr Thr Leu Leu  
 200 205 210

gag aag tac cca acc aag ctg gtg gtg tcc cgc acc atg agt aag gct 787  
 Glu Lys Tyr Pro Thr Lys Leu Val Val Ser Arg Thr Met Ser Lys Ala  
 215 220 225

ttt gat ttc gca ggt gga cgc ctc ggc tac ttc gtg gcc aac cca gcg 835  
 Phe Asp Phe Ala Gly Gly Arg Leu Gly Tyr Phe Val Ala Asn Pro Ala  
 230 235 240 245

ttt atc gac gcc gtg atg cta gtc cgc ctt ccg tat cat ctt tca gcg 883  
 Phe Ile Asp Ala Val Met Leu Val Arg Leu Pro Tyr His Leu Ser Ala  
 250 255 260

ctg agc caa gca gcc gca atc gta gcg ctg cgt cac tcc gct gac acg 931  
 Leu Ser Gln Ala Ala Ala Ile Val Ala Leu Arg His Ser Ala Asp Thr  
 265 270 275

ctg gga acc gtc gaa aag ctc tct gta gag cgt gtt cgc gtg gca gca 979  
 Leu Gly Thr Val Glu Lys Leu Ser Val Glu Arg Val Arg Val Ala Ala  
 280 285 290

cgc ttg gag gaa ctg ggc tac gct gtg gtt cca agt gag tcc aac ttt  
 1027  
 Arg Leu Glu Glu Leu Gly Tyr Ala Val Val Pro Ser Glu Ser Asn Phe  
 295 300 305

gtg ttc ttt gga gat ttc tcc gat cag cac gcg gca tgg cag gca ttt  
 1075  
 Val Phe Phe Gly Asp Phe Ser Asp Gln His Ala Ala Trp Gln Ala Phe  
 310 315 320 325

ttg gat agg gga gtg ctc atc cgc gat gtg gga atc gct ggg cac ttg  
 1123  
 Leu Asp Arg Gly Val Leu Ile Arg Asp Val Gly Ile Ala Gly His Leu  
 330 335 340

cgc act acc att ggt gtg cct gag gaa aat gat gcg ttt ttg gac gca  
 1171  
 Arg Thr Thr Ile Gly Val Pro Glu Glu Asn Asp Ala Phe Leu Asp Ala  
 345 350 355

gct gca gag atc atc aag ctg aac ctg taagagagaa gaatttttca  
 1218  
 Ala Ala Glu Ile Ile Lys Leu Asn Leu  
 360 365

130 135 140

Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu  
145 150 155 160

Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly  
165 170

<210> 399  
<211> 1221  
<212> DNA  
<213> *Corynebacterium glutamicum*

<220>  
<221> CDS  
<222> (101)..(1198)  
<223> RXA01105

<400> 399  
ttgtcatcaa ctttgccaac gccgaagatc ttccagcgca cggcgaagca atccgtgcac 60  
gctttgaaaa cctccccacc accgacgagg cctaagaaaa atg acc aaa att act 115  
Met Thr Lys Ile Thr  
1 5

ttg agc gat ttg cca ttg cgt gaa gaa ctg cgc ggt gag cac gct tac 163  
Leu Ser Asp Leu Pro Leu Arg Glu Glu Leu Arg Gly Glu His Ala Tyr  
10 15 20

ggc gca ccc cag ctc aac gtt gat att cgc ctc aac acc aac gaa aac 211  
Gly Ala Pro Gln Leu Asn Val Asp Ile Arg Leu Asn Thr Asn Glu Asn  
25 30 35

cct tac cca ccg tca gag gca ttg gtc gct gac ttg gtt gcc acc gtg 259  
Pro Tyr Pro Pro Ser Glu Ala Leu Val Ala Asp Leu Val Ala Thr Val  
40 45 50

gat aag atc gcc acc gag ctg aac cgc tac cca gag cgc gat gct gtg 307  
Asp Lys Ile Ala Thr Glu Leu Asn Arg Tyr Pro Glu Arg Asp Ala Val  
55 60 65

gaa ctg cgt gat gag ttg gct gcg tac atc acc aag caa acc ggc gtg 355  
Glu Leu Arg Asp Glu Leu Ala Ala Tyr Ile Thr Lys Gln Thr Gly Val  
70 75 80 85

gct gtc acc agg gat aac ctg tgg gct gcc aat ggt tcc aat gaa att 403  
Ala Val Thr Arg Asp Asn Leu Trp Ala Ala Asn Gly Ser Asn Glu Ile  
90 95 100

ctg cag cag ctg ctg cag gct ttt ggt gga cct gga cgc acc gcg ttg 451  
Leu Gln Gln Leu Leu Gln Ala Phe Gly Gly Pro Gly Arg Thr Ala Leu  
105 110 115

gga ttc caa ccc agc tat tcc atg cac cca att ttg gct aaa ggc acc 499  
Gly Phe Gln Pro Ser Tyr Ser Met His Pro Ile Leu Ala Lys Gly Thr  
120 125 130

cac act gaa ttc att gcg gtg tcc cga ggt gct gat ttc cgc atc gat 547  
His Thr Glu Phe Ile Ala Val Ser Arg Gly Ala Asp Phe Arg Ile Asp  
135 140 145

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Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala
 65                      70                      75                      80

gct cag gcg gca gcg ctt gcg agt ttg aat tct gcc gat gag ttg atg      288
Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met
                      85                      90                      95

gaa cgg gtg gag gaa acc gtc gaa aag cgt gat gct gtg gtg tca gcg      336
Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala
                      100                      105                      110

ctt ggt gct gcg ccg acg cag gcc aat ttc gtc tgg ctg ccg ggc gag      384
Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu
                      115                      120                      125

ggc gcc gct gag ttg gcg gct aaa ttg gcc gag cac ggc atc gtg att      432
Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile
                      130                      135                      140

cgc gcg ttc ccc gag ggt gcg cgc att tcg gtg acc aac gcc gag gaa      480
Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu
                      145                      150                      155                      160

act gac aag ctg ctg cgc gcg tgg gag gcc atc aat gct ggg      522
Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly
                      165                      170

tagtcttttg cgttttgcgg tgc      545

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&lt;210&gt; 398

&lt;211&gt; 174

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 398

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Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu Ala Tyr
 1                      5                      10                      15

Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile
                      20                      25                      30

His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr
                      35                      40                      45

Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile
                      50                      55                      60

Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala
 65                      70                      75                      80

Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met
                      85                      90                      95

Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala
                      100                      105                      110

Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu
                      115                      120                      125

Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile

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130                      135                      140  
 Glu Ile His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys  
 145                      150                      155                      160  
 Ala Tyr Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala  
                     165                      170                      175  
 Glu Ile Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn  
                     180                      185                      190  
 Ser Ala Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu  
                     195                      200                      205  
 Leu Met Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val  
                     210                      215                      220  
 Ser Ala Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro  
 225                      230                      235                      240  
 Gly Glu Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile  
                     245                      250                      255  
 Val Ile Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala  
                     260                      265                      270  
 Glu Glu Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly  
                     275                      280                      285

&lt;210&gt; 397

&lt;211&gt; 545

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(522)

&lt;223&gt; FRXA00446

&lt;400&gt; 397

atg gaa aag gtt cca aac gat gtc gtt gtt ggg ctg gat gag gct tat    48  
 Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu Ala Tyr  
   1                    5                    10                    15  
 ttt gag ttc aac cgc gcg gac gac acc cca gtt gcc act gag gaa atc    96  
 Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile  
                     20                    25                    30  
 cac cgc cac gac aac gtg att ggt ttg cgc acg ttc tcc aag gcg tat    144  
 His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr  
                     35                    40                    45  
 ggc ctg gcg ggc ttg cgt gtt ggt tac gcc ttc gga aac gca gag atc    192  
 Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile  
                     50                    55                    60  
 atc gca gcg atg aat aag gtg gct att cct ttc gcg gtg aat tca gca    240

Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala Ala Gln Ala  
 185 190 195

gca gcg ctt gcg agt ttg aat tct gcc gat gag ttg atg gaa cgg gtg 739  
 Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met Glu Arg Val  
 200 205 210

gag gaa acc gtc gaa aag cgt gat gct gtg gtg tca gcg ctt ggt gct 787  
 Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala Leu Gly Ala  
 215 220 225

gcg ccg acg cag gcc aat ttc gtc tgg ctg ccg ggc gag ggc gcc gct 835  
 Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu Gly Ala Ala  
 230 235 240 245

gag ttg gcg gct aaa ttg gcc gag cac ggc atc gtg att cgc gcg ttc 883  
 Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile Arg Ala Phe  
 250 255 260

ccc gag ggt gcg cgc att tcg gtg acc aac gcc gag gaa act gac aag 931  
 Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu Thr Asp Lys  
 265 270 275

ctg ctg cgc gcg tgg gag gcc atc aat gct ggg tagtctttgg cgttttgcgg 984  
 Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly  
 280 285

tgc 987

&lt;210&gt; 396

&lt;211&gt; 288

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 396

Met Gly Ala Val Glu Leu Arg Glu Ala Leu Ala Glu His Leu Glu Val  
 1 5 10 15

Glu Phe Asp Gln Val Thr Val Gly Cys Gly Ser Ser Ala Leu Cys Gln  
 20 25 30

Gln Leu Val Gln Ala Thr Cys Ala Gln Gly Asp Glu Val Ile Phe Pro  
 35 40 45

Trp Arg Ser Phe Glu Ala Tyr Pro Ile Phe Ala Gln Val Ala Gly Ala  
 50 55 60

Thr Pro Val Ala Ile Pro Leu Thr Ala Asp Gln Asn His Asp Leu Asp  
 65 70 75 80

Ala Met Ala Ala Ala Ile Thr Asp Lys Thr Arg Leu Ile Phe Ile Cys  
 85 90 95

Asn Pro Asn Asn Pro Ser Gly Thr Thr Ile Thr Gln Ala Gln Phe Asp  
 100 105 110

Asn Phe Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu  
 115 120 125

Ala Tyr Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu

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<220>
<221> CDS
<222> (101)..(964)
<223> RXN00446
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584

Val Gly Tyr Leu Arg Gly Asn Gly Asp Met Asp Asn Cys Ile Val Ile  
 450 455 460

Arg Ser Ala Phe Val Gln Asp Gly Val Ala Ala Val Gln Ala Gly Ala  
 465 470 475 480

Gly Val Val Arg Asp Ser Asn Pro Gln Ser Glu Ala Asp Glu Thr Leu  
 485 490 495

His Lys Ala Tyr Ala Val Leu Asn Ala Ile Ala Leu Ala Ala Gly Ser  
 500 505 510

Thr Leu Glu Val Ile Arg  
 515

&lt;210&gt; 421

&lt;211&gt; 1151

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1128)

&lt;223&gt; FRXA00957

&lt;400&gt; 421

gat ttc tta gaa acc ttt gaa acg ctc ccc gct gtc gag gag agc gtc	48
Asp Phe Leu Glu Thr Phe Glu Thr Leu Pro Ala Val Glu Glu Ser Val	
1 5 10 15	
aac act tac ccc gat tac cag ttc gtc ctc gcg gaa atc gtc ctg gac	96
Asn Thr Tyr Pro Asp Tyr Gln Phe Val Leu Ala Glu Ile Val Leu Asp	
20 25 30	
atc aat cac cag gac cag acc gcc aaa ctc gcc ggc gtc tcc aac gcc	144
Ile Asn His Gln Asp Gln Thr Ala Lys Leu Ala Gly Val Ser Asn Ala	
35 40 45	
cca ggc gag ctc gag gcc gag ctc aac aag ctt tca ttg ctt atc gac	192
Pro Gly Glu Leu Glu Ala Glu Leu Asn Lys Leu Ser Leu Leu Ile Asp	
50 55 60	
gcc gcc ctc ccc gca acc gaa cac gcc tac caa acc acc cct cac gac	240
Ala Ala Leu Pro Ala Thr Glu His Ala Tyr Gln Thr Thr Pro His Asp	
65 70 75 80	
ggc gac act ctt cgc gtt gtg gct gat att ccc gat gct cag ttc cgc	288
Gly Asp Thr Leu Arg Val Val Ala Asp Ile Pro Asp Ala Gln Phe Arg	
85 90 95	
acc cag atc aat gag ctg aaa gaa aac att tac aac ggt gac atc tac	336
Thr Gln Ile Asn Glu Leu Lys Glu Asn Ile Tyr Asn Gly Asp Ile Tyr	
100 105 110	
caa gtt gtc ccg gcg cgc act ttc acc gca cca tgt cct gat gca ttc	384
Gln Val Val Pro Ala Arg Thr Phe Thr Ala Pro Cys Pro Asp Ala Phe	
115 120 125	
gct gct tat ctg cag ctg cgt gcc acc aac ccg tcg ccg tac atg ttc	432
Ala Ala Tyr Leu Gln Leu Arg Ala Thr Asn Pro Ser Pro Tyr Met Phe	

Ser Asp Ala Ser Leu Pro Leu Leu Met Gly Gly Phe Ala Phe Asp Phe  
 130 135 140  
 Leu Glu Thr Phe Glu Thr Leu Pro Ala Val Glu Glu Ser Val Asn Thr  
 145 150 155 160  
 Tyr Pro Asp Tyr Gln Phe Val Leu Ala Glu Ile Val Leu Asp Ile Asn  
 165 170 175  
 His Gln Asp Gln Thr Ala Lys Leu Ala Gly Val Ser Asn Ala Pro Gly  
 180 185 190  
 Glu Leu Glu Ala Glu Leu Asn Lys Leu Ser Leu Leu Ile Asp Ala Ala  
 195 200 205  
 Leu Pro Ala Thr Glu His Ala Tyr Gln Thr Thr Pro His Asp Gly Asp  
 210 215 220  
 Thr Leu Arg Val Val Ala Asp Ile Pro Asp Ala Gln Phe Arg Thr Gln  
 225 230 235 240  
 Ile Asn Glu Leu Lys Glu Asn Ile Tyr Asn Gly Asp Ile Tyr Gln Val  
 245 250 255  
 Val Pro Ala Arg Thr Phe Thr Ala Pro Cys Pro Asp Ala Phe Ala Ala  
 260 265 270  
 Tyr Leu Gln Leu Arg Ala Thr Asn Pro Ser Pro Tyr Met Phe Tyr Ile  
 275 280 285  
 Arg Gly Leu Asn Glu Gly Arg Ser Tyr Glu Leu Phe Gly Ala Ser Pro  
 290 295 300  
 Glu Ser Asn Leu Lys Phe Thr Ala Ala Asn Arg Glu Leu Gln Leu Tyr  
 305 310 315 320  
 Pro Ile Ala Gly Thr Arg Pro Arg Gly Leu Asn Pro Asp Gly Ser Ile  
 325 330 335  
 Asn Asp Glu Leu Asp Ile Arg Asn Glu Leu Asp Met Arg Thr Asp Ala  
 340 345 350  
 Lys Glu Ile Ala Glu His Thr Met Leu Val Asp Leu Ala Arg Asn Asp  
 355 360 365  
 Leu Ala Arg Val Ser Val Pro Ala Ser Arg Arg Val Ala Asp Leu Leu  
 370 375 380  
 Gln Val Asp Arg Tyr Ser Arg Val Met His Leu Val Ser Arg Val Thr  
 385 390 395 400  
 Ala Thr Leu Asp Pro Glu Leu Asp Ala Leu Asp Ala Tyr Arg Ala Cys  
 405 410 415  
 Met Asn Met Gly Thr Leu Thr Gly Ala Pro Lys Leu Arg Ala Met Glu  
 420 425 430  
 Leu Leu Arg Gly Val Glu Lys Arg Arg Arg Gly Ser Tyr Gly Gly Ala  
 435 440 445



gaa aag cgc agg cgt ggt tct tat ggt ggg gca gtg ggg tac ctg cgc  
1459

Glu Lys Arg Arg Arg Gly Ser Tyr Gly Gly Ala Val Gly Tyr Leu Arg  
440 445 450

ggc aat ggc gat atg gat aat tgc att gtt att cgt tcg gcg ttt gtc  
1507

Gly Asn Gly Asp Met Asp Asn Cys Ile Val Ile Arg Ser Ala Phe Val  
455 460 465

cag gat ggt gtg gct gct gtg cag gct ggt gct ggt gtg gtc cgc gat  
1555

Gln Asp Gly Val Ala Ala Val Gln Ala Gly Ala Gly Val Val Arg Asp  
470 475 480 485

tct aat cct caa tct gaa gcc gat gag acg ttg cac aag gcg tat gcc  
1603

Ser Asn Pro Gln Ser Glu Ala Asp Glu Thr Leu His Lys Ala Tyr Ala  
490 495 500

gtg ttg aat gcc att gcg ctt gct gct ggt tcc act ttg gag gtc atc  
1651

Val Leu Asn Ala Ile Ala Leu Ala Ala Gly Ser Thr Leu Glu Val Ile  
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1677

Arg

<210> 420

<211> 518

<212> PRT

<213> Corynebacterium glutamicum

<400> 420

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20 25 30

Ala Ala Leu Leu Glu Ser Ala Asp Ile Thr Thr Lys Asn Gly Ile Ser  
35 40 45

Ser Leu Ala Val Leu Lys Ser Ser Val Arg Ile Thr Cys Thr Gly Asn  
50 55 60

Thr Val Val Thr Gln Pro Leu Thr Asp Ser Gly Arg Ala Val Val Ala  
65 70 75 80

Arg Leu Thr Gln Gln Leu Gly Gln Tyr Asn Thr Ala Glu Asn Thr Phe  
85 90 95

Ser Phe Pro Ala Ser Asp Ala Val Asp Glu Arg Glu Arg Leu Thr Ala  
100 105 110

Pro Ser Thr Ile Glu Val Leu Arg Lys Leu Gln Phe Glu Ser Gly Tyr  
115 120 125

gct gat att ccc gat gct cag ttc cgc acc cag atc aat gag ctg aaa 835  
 Ala Asp Ile Pro Asp Ala Gln Phe Arg Thr Gln Ile Asn Glu Leu Lys  
 230 235 240 245

gaa aac att tac aac ggt gac atc tac caa gtt gtc ccg gcg cgc act 883  
 Glu Asn Ile Tyr Asn Gly Asp Ile Tyr Gln Val Val Pro Ala Arg Thr  
 250 255 260

ttc acc gca cca tgt cct gat gca ttc gct gct tat ctg cag ctg cgt 931  
 Phe Thr Ala Pro Cys Pro Asp Ala Phe Ala Ala Tyr Leu Gln Leu Arg  
 265 270 275

gcc acc aac ccg tcg ccg tac atg ttc tat atc cgt ggc ctc aac gaa 979  
 Ala Thr Asn Pro Ser Pro Tyr Met Phe Tyr Ile Arg Gly Leu Asn Glu  
 280 285 290

ggc cgc tcc tat gaa ctt ttt ggc gca tcc cct gag tcc aac ctc aag  
 1027  
 Gly Arg Ser Tyr Glu Leu Phe Gly Ala Ser Pro Glu Ser Asn Leu Lys  
 295 300 305

ttc acc gct gct aac cgt gag ctg cag ctg tac cca atc gca ggt acc  
 1075  
 Phe Thr Ala Ala Asn Arg Glu Leu Gln Leu Tyr Pro Ile Ala Gly Thr  
 310 315 320 325

cgc ccc cgt gga ctc aac cca gat ggc tcc atc aac gat gag cta gat  
 1123  
 Arg Pro Arg Gly Leu Asn Pro Asp Gly Ser Ile Asn Asp Glu Leu Asp  
 330 335 340

atc cgc aat gag ttg gat atg cgc act gat gcc aaa gag atc gcg gag  
 1171  
 Ile Arg Asn Glu Leu Asp Met Arg Thr Asp Ala Lys Glu Ile Ala Glu  
 345 350 355

cac acc atg ctt gtc gat ctc gcc cgc aac gac ctg gcc cgc gtc tcg  
 1219  
 His Thr Met Leu Val Asp Leu Ala Arg Asn Asp Leu Ala Arg Val Ser  
 360 365 370

gtc cca gcg tcg cgc cgg gtt gcg gat ctt ttg cag gtg gat cgc tat  
 1267  
 Val Pro Ala Ser Arg Arg Val Ala Asp Leu Leu Gln Val Asp Arg Tyr  
 375 380 385

tcc cgc gtg atg cac ttg gtg tcc cgt gtg acg gcg acg ttg gac cca  
 1315  
 Ser Arg Val Met His Leu Val Ser Arg Val Thr Ala Thr Leu Asp Pro  
 390 395 400 405

gag ctt gat gct ttg gac gcc tat cgg gcg tgc atg aat atg ggc acg  
 1363  
 Glu Leu Asp Ala Leu Asp Ala Tyr Arg Ala Cys Met Asn Met Gly Thr  
 410 415 420

ttg acc ggc gct ccg aag ttg cgc gct atg gag ctg ttg cgc ggc gtc  
 1411  
 Leu Thr Gly Ala Pro Lys Leu Arg Ala Met Glu Leu Leu Arg Gly Val  
 425 430 435

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aaggcttcag ccccaaatg atttcctcgg taggtgcccc atg agc acg aat ccc 115  
Met Ser Thr Asn Pro  
1 5  
cat gtt ttc tcc cta gat gtc cgc tat cac gag gat gct tct gca ttg 163  
His Val Phe Ser Leu Asp Val Arg Tyr His Glu Asp Ala Ser Ala Leu  
10 15 20  
ttt gcc cac ttg ggt ggc aca acc gca gat gat gca gcc ctg ttg gaa 211  
Phe Ala His Leu Gly Gly Thr Thr Ala Asp Asp Ala Ala Leu Leu Glu  
25 30 35  
agc gct gat atc acc acc aag aat ggt att tct tcc ctc gcg gtg ttg 259  
Ser Ala Asp Ile Thr Thr Lys Asn Gly Ile Ser Ser Leu Ala Val Leu  
40 45 50  
aag agt tcg gtg cgc att acg tgc acg ggc aac acg gtg gta acg cag 307  
Lys Ser Ser Val Arg Ile Thr Cys Thr Gly Asn Thr Val Val Thr Gln  
55 60 65  
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Pro Leu Thr Asp Ser Gly Arg Ala Val Val Ala Arg Leu Thr Gln Gln  
70 75 80 85  
ctt ggc cag tac aac acc gca gag aac acc ttt agc ttc ccc gcc tca 403  
Leu Gly Gln Tyr Asn Thr Ala Glu Asn Thr Phe Ser Phe Pro Ala Ser  
90 95 100  
gat gcg gtt gat gag cgc gag cgc ctc acc gca cca agc acc atc gaa 451  
Asp Ala Val Asp Glu Arg Glu Arg Leu Thr Ala Pro Ser Thr Ile Glu  
105 110 115  
gtg ctg cgc aag ttg cag ttc gag tcc ggt tac agc gac gcg tcc ctg 499  
Val Leu Arg Lys Leu Gln Phe Glu Ser Gly Tyr Ser Asp Ala Ser Leu  
120 125 130  
cca ctg ctc atg ggc ggt ttc gcg ttt gat ttc tta gaa acc ttt gaa 547  
Pro Leu Leu Met Gly Gly Phe Ala Phe Asp Phe Leu Glu Thr Phe Glu  
135 140 145  
acg ctc ccc gct gtc gag gag agc gtc aac act tac ccc gat tac cag 595  
Thr Leu Pro Ala Val Glu Glu Ser Val Asn Thr Tyr Pro Asp Tyr Gln  
150 155 160 165  
ttc gtc ctc gcg gaa atc gtc ctg gac atc aat cac cag gac cag acc 643  
Phe Val Leu Ala Glu Ile Val Leu Asp Ile Asn His Gln Asp Gln Thr  
170 175 180  
gcc aaa ctc gcc ggc gtc tcc aac gcc cca ggc gag ctc gag gcc gag 691  
Ala Lys Leu Ala Gly Val Ser Asn Ala Pro Gly Glu Leu Glu Ala Glu  
185 190 195  
ctc aac aag ctt tca ttg ctt atc gac gcc gcc ctc ccc gca acc gaa 739  
Leu Asn Lys Leu Ser Leu Leu Ile Asp Ala Ala Leu Pro Ala Thr Glu  
200 205 210  
cac gcc tac caa acc acc cct cac gac ggc gac act ctt cgc gtt gtg 787  
His Ala Tyr Gln Thr Thr Pro His Asp Gly Asp Thr Leu Arg Val Val  
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Ser Ser Asn Asp  
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<210> 418

<211> 196

<212> PRT

<213> Corynebacterium glutamicum

<400> 418

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Leu Leu Ser Pro Ala Arg Pro Glu Arg Gln Ile Met Gly Val Ala Asn  
35 40 45

Ala Asn His Gly Gln Leu Ile Ala Glu Val Phe Arg Glu Leu Gly Arg  
50 55 60

Thr Arg Ala Leu Val Val His Gly Ala Gly Thr Asp Glu Ile Ala Val  
65 70 75 80

His Gly Thr Thr Leu Val Trp Glu Leu Lys Glu Asp Gly Thr Ile Glu  
85 90 95

His Tyr Thr Ile Glu Pro Glu Asp Leu Gly Leu Gly Arg Tyr Thr Leu  
100 105 110

Glu Asp Leu Val Gly Gly Leu Gly Thr Glu Asn Ala Glu Ala Met Arg  
115 120 125

Ala Thr Phe Ala Gly Thr Gly Pro Asp Ala His Arg Asp Ala Leu Ala  
130 135 140

Ala Ser Ala Gly Ala Met Phe Tyr Leu Asn Gly Asp Val Asp Ser Leu  
145 150 155 160

Lys Asp Gly Ala Gln Lys Ala Leu Ser Leu Leu Ala Asp Gly Thr Thr  
165 170 175

Gln Ala Trp Leu Ala Lys His Glu Glu Ile Asp Tyr Ser Glu Lys Glu  
180 185 190

Ser Ser Asn Asp  
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<210> 419

<211> 1677

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(1654)

<223> RXN00957

<400> 419

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 gtt cgc cag gcg ctg aaa ttc ccc acc atc ttc aac acg ctt gga cca 96  
 Val Arg Gln Ala Leu Lys Phe Pro Thr Ile Phe Asn Thr Leu Gly Pro  
 20 25 30  
 ttg ctg tcc ccg gcg cgc ccg gag cgt cag atc atg ggc gtg gcc aat 144  
 Leu Leu Ser Pro Ala Arg Pro Glu Arg Gln Ile Met Gly Val Ala Asn  
 35 40 45  
 gcc aat cat gga cag ctc atc gcc gag gtc ttc cgc gag ttg ggc cgt 192  
 Ala Asn His Gly Gln Leu Ile Ala Glu Val Phe Arg Glu Leu Gly Arg  
 50 55 60  
 aca cgc gcg ctt gtt gtg cat ggc gca ggc acc gat gag atc gca gtc 240  
 Thr Arg Ala Leu Val Val His Gly Ala Gly Thr Asp Glu Ile Ala Val  
 65 70 75 80  
 cac ggc acc acc ttg gtg tgg gag ctt aaa gaa gac ggc acc atc gag 288  
 His Gly Thr Thr Leu Val Trp Glu Leu Lys Glu Asp Gly Thr Ile Glu  
 85 90 95  
 cat tac acc atc gag cct gag gac ctt ggc ctt ggc cgc tac acc ctt 336  
 His Tyr Thr Ile Glu Pro Glu Asp Leu Gly Leu Gly Arg Tyr Thr Leu  
 100 105 110  
 gag gat ctc gta ggt ggc ctc ggc act gag aac gcc gaa gct atg cgc 384  
 Glu Asp Leu Val Gly Gly Leu Gly Thr Glu Asn Ala Glu Ala Met Arg  
 115 120 125  
 gct act ttc gcg ggc acc ggc cct gat gca cac cgt gat gcg ttg gct 432  
 Ala Thr Phe Ala Gly Thr Gly Pro Asp Ala His Arg Asp Ala Leu Ala  
 130 135 140  
 gcg tcc gca ggt gcg atg ttc tac ctc aac ggc gat gtc gac tcc ttg 480  
 Ala Ser Ala Gly Ala Met Phe Tyr Leu Asn Gly Asp Val Asp Ser Leu  
 145 150 155 160  
 aaa gat ggt gca caa aag gcg ctt tcc ttg ctt gcc gac ggc acc acc 528  
 Lys Asp Gly Ala Gln Lys Ala Leu Ser Leu Leu Ala Asp Gly Thr Thr  
 165 170 175  
 cag gca tgg ttg gcc aag cac gaa gag atc gat tac tca gaa aag gag 576  
 Gln Ala Trp Leu Ala Lys His Glu Glu Ile Asp Tyr Ser Glu Lys Glu  
 180 185 190  
 tct tcc aat gac tagtaataat ctgcccacag tgt 611

atg ttc tac ctc aac ggc gat gtc gac tcc ttg aaa gat ggt gca caa 528  
Met Phe Tyr Leu Asn Gly Asp Val Asp Ser Leu Lys Asp Gly Ala Gln  
165 170 175

aag gcg ctt tcc ttg ctt gcc gac ggc acc acc cag gca tgg ttg gcc 576  
Lys Ala Leu Ser Leu Leu Ala Asp Gly Thr Thr Gln Ala Trp Leu Ala  
180 185 190

aag cac gaa gag atc gat tac tca gaa aag gag tct tcc aat gac 621  
Lys His Glu Glu Ile Asp Tyr Ser Glu Lys Glu Ser Ser Asn Asp  
195 200 205

tagtaataat ctgcccacag tgt 644

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<211> 207  
<212> PRT  
<213> Corynebacterium glutamicum

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Lys Phe Pro Thr Ile Phe Asn Thr Leu Gly Pro Leu Leu Ser Pro Ala  
35 40 45  
Arg Pro Glu Arg Gln Ile Met Gly Val Ala Asn Ala Asn His Gly Gln  
50 55 60  
Leu Ile Ala Glu Val Phe Arg Glu Leu Gly Arg Thr Arg Ala Leu Val  
65 70 75 80  
Val His Gly Ala Gly Thr Asp Glu Ile Ala Val His Gly Thr Thr Leu  
85 90 95  
Val Trp Glu Leu Lys Glu Asp Gly Thr Ile Glu His Tyr Thr Ile Glu  
100 105 110  
Pro Glu Asp Leu Gly Leu Gly Arg Tyr Thr Leu Glu Asp Leu Val Gly  
115 120 125  
Gly Leu Gly Thr Glu Asn Ala Glu Ala Met Arg Ala Thr Phe Ala Gly  
130 135 140  
Thr Gly Pro Asp Ala His Arg Asp Ala Leu Ala Ala Ser Ala Gly Ala  
145 150 155 160  
Met Phe Tyr Leu Asn Gly Asp Val Asp Ser Leu Lys Asp Gly Ala Gln  
165 170 175  
Lys Ala Leu Ser Leu Leu Ala Asp Gly Thr Thr Gln Ala Trp Leu Ala  
180 185 190  
Lys His Glu Glu Ile Asp Tyr Ser Glu Lys Glu Ser Ser Asn Asp  
195 200 205

Asn Pro Ala Glu Gly Asn Trp Leu Tyr Phe Val Thr Ile Asp Thr Asp  
 340 345 350

Gly Thr Thr Val Phe Asn Asp Thr Phe Glu Glu His Glu Ala Asp Ile  
 355 360 365

Glu Gln Ala Leu Asn Ser Gly Val Leu Asp Ser Asn Arg  
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<210> 415

<211> 644

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(621)

<223> RXN00954

<400> 415

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 1 5 10 15

gcg tac aac cct gcg att gcg cat gtg cag ccg gtt cgc cag gcg ctg 96  
 Ala Tyr Asn Pro Ala Ile Ala His Val Gln Pro Val Arg Gln Ala Leu  
 20 25 30

aaa ttc ccc acc atc ttc aac acg ctt gga cca ttg ctg tcc ccg gcg 144  
 Lys Phe Pro Thr Ile Phe Asn Thr Leu Gly Pro Leu Leu Ser Pro Ala  
 35 40 45

cgc ccg gag cgt cag atc atg ggc gtg gcc aat gcc aat cat gga cag 192  
 Arg Pro Glu Arg Gln Ile Met Gly Val Ala Asn Ala Asn His Gly Gln  
 50 55 60

ctc atc gcc gag gtc ttc cgc gag ttg ggc cgt aca cgc gcg ctt gtt 240  
 Leu Ile Ala Glu Val Phe Arg Glu Leu Gly Arg Thr Arg Ala Leu Val  
 65 70 75 80

gtg cat ggc gca ggc acc gat gag atc gca gtc cac ggc acc acc ttg 288  
 Val His Gly Ala Gly Thr Asp Glu Ile Ala Val His Gly Thr Thr Leu  
 85 90 95

gtg tgg gag ctt aaa gaa gac ggc acc atc gag cat tac acc atc gag 336  
 Val Trp Glu Leu Lys Glu Asp Gly Thr Ile Glu His Tyr Thr Ile Glu  
 100 105 110

cct gag gac ctt ggc ctt ggc cgc tac acc ctt gag gat ctc gta ggt 384  
 Pro Glu Asp Leu Gly Leu Gly Arg Tyr Thr Leu Glu Asp Leu Val Gly  
 115 120 125

ggc ctc ggc act gag aac gcc gaa gct atg cgc gct act ttc gcg ggc 432  
 Gly Leu Gly Thr Glu Asn Ala Glu Ala Met Arg Ala Thr Phe Ala Gly  
 130 135 140

acc ggc cct gat gca cac cgt gat gcg ttg gct gcg tcc gca ggt gcg 480  
 Thr Gly Pro Asp Ala His Arg Asp Ala Leu Ala Ala Ser Ala Gly Ala  
 145 150 155 160





Arg Leu Glu Gly Leu Ile Met Pro Gly Gln Tyr Val Val Asp Pro Ser  
 200 205 210  
 aac gac gcc cag gga atc ctc acc gat ctg atc acg cga tca gca aac 787  
 Asn Asp Ala Gln Gly Ile Leu Thr Asp Leu Ile Thr Arg Ser Ala Asn  
 215 220 225  
 cat ttc caa gaa acc gac atc acg ggc cgt gca gat gcc atc gga ctt 835  
 His Phe Gln Glu Thr Asp Ile Thr Gly Arg Ala Asp Ala Ile Gly Leu  
 230 235 240 245  
 act cca tat gag ctg gtc acc gca gca tct tta atc gag cgc gaa gca 883  
 Thr Pro Tyr Glu Leu Val Thr Ala Ala Ser Leu Ile Glu Arg Glu Ala  
 250 255 260  
 cca gca gga gat ttt gat aag gtc gcc cgc gtc atc ttg aac cgt ctc 931  
 Pro Ala Gly Asp Phe Asp Lys Val Ala Arg Val Ile Leu Asn Arg Leu  
 265 270 275  
 gcc gag cca atg cag ctg caa ttc gac tcc acc gtc aac tac ggt ctg 979  
 Ala Glu Pro Met Gln Leu Gln Phe Asp Ser Thr Val Asn Tyr Gly Leu  
 280 285 290  
 tct gaa caa gaa gta gca acc acc gac gaa gac cgt cag acc gtc acc  
 1027  
 Ser Glu Gln Glu Val Ala Thr Thr Asp Glu Asp Arg Gln Thr Val Thr  
 295 300 305  
 cca tgg aac act tac gcc atg gac ggc ctg cca caa acc ccc atc gcc  
 1075  
 Pro Trp Asn Thr Tyr Ala Met Asp Gly Leu Pro Gln Thr Pro Ile Ala  
 310 315 320 325  
 gca gta tcc acc gaa gca ctc caa gcc atg gaa aac cct gca gaa gga  
 1123  
 Ala Val Ser Thr Glu Ala Leu Gln Ala Met Glu Asn Pro Ala Glu Gly  
 330 335 340  
 aac tgg ctg tac ttt gtc acc atc gac acc gat gga acc acc gtg ttc  
 1171  
 Asn Trp Leu Tyr Phe Val Thr Ile Asp Thr Asp Gly Thr Thr Val Phe  
 345 350 355  
 aac gac acc ttc gaa gag cac gaa gcc gac att gag caa gct ttg aac  
 1219  
 Asn Asp Thr Phe Glu Glu His Glu Ala Asp Ile Glu Gln Ala Leu Asn  
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&lt;221&gt; CDS

&lt;222&gt; (101)..(1243)

&lt;223&gt; RXA02790

&lt;400&gt; 413

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                                         Met Glu Pro Val Tyr
                                         1           5

gta aag cgc cgc caa cgg ttt att gcc gtg acg atc gct tca ctc atc 163
Val Lys Arg Arg Gln Arg Phe Ile Ala Val Thr Ile Ala Ser Leu Ile
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Leu Ile Ile Gly Ala Ile Ile Tyr Ile Gly Val Ala Thr Ser Asn Arg
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Thr Pro His Asp Tyr Glu Gly Ser Gly Asn Gly Val Val Gln Leu Val
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Glu Ile Pro Glu Gly Ser Ser Ile Ser Glu Leu Gly Pro Glu Leu Glu
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Glu Arg Asp Ile Val Ala Thr Asn Ser Ala Phe Gln Thr Ala Ala Ser
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gaa caa atg aac gca gca gct gca gtg tcg gct ctg ctt gat cca gac 451
Glu Gln Met Asn Ala Ala Ala Val Ser Ala Leu Leu Asp Pro Asp
              105              110              115

aac cag gtt gat ctc ctc gac att cac ggc ggc gcc acc ttg atg gac 499
Asn Gln Val Asp Leu Leu Asp Ile His Gly Gly Ala Thr Leu Met Asp
              120              125              130

gtc act gtt gtc ggc gga aac acc cgc gcg gga atc tac tcc cag atc 547
Val Thr Val Val Gly Gly Asn Thr Arg Ala Gly Ile Tyr Ser Gln Ile
              135              140              145

gca gcc gtg acc tgc acc gaa ggc tcc gcc aac tgc atc acc gct gag 595
Ala Ala Val Thr Cys Thr Glu Gly Ser Ala Asn Cys Ile Thr Ala Glu
              150              155              160              165

gat ttg cag cag gtt gcc tcc acc gtg tcg cct gca gaa ttg ggt gtc 643
Asp Leu Gln Gln Val Ala Ser Thr Val Ser Pro Ala Glu Leu Gly Val
              170              175              180

cca gat tgg gca atc gct gct gtg gaa gct cgc gga act gat cca aag 691
Pro Asp Trp Ala Ile Ala Ala Val Glu Ala Arg Gly Thr Asp Pro Lys
              185              190              195

cgc ctc gaa ggc ctg atc atg cct ggc caa tac gtg gtg gat cca tcc 739

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Val Asp Asn Asn Asn Leu Pro Phe Thr Val Asn Ala Gly Glu Val Pro  
 145 150 155 160  
 Glu Gly Gly Val Val Glu Ile Asp Ala Ser Gly Ser Ser Gln Phe Val  
 165 170 175  
 Ser Gly Leu Leu Leu Ser Ala Pro Arg Phe Lys Asn Gly Val Thr Val  
 180 185 190  
 Lys His Val Gly Gly Arg Leu Pro Ser Met Pro His Ile Glu Met Thr  
 195 200 205  
 Val Asp Met Leu Arg Ser Ala Gly Ile Glu Ile Glu Glu Ser Glu Asn  
 210 215 220  
 Gln Trp Val Val His Pro Gly Glu Ile Leu Gly Arg Thr Trp Arg Ile  
 225 230 235 240  
 Glu Pro Asp Leu Ser Asn Ala Thr Pro Phe Leu Ala Ala Ala Ala Val  
 245 250 255  
 Thr Gly Gly Thr Ile Lys Ile Asn His Trp Pro Ile Lys Thr Thr Gln  
 260 265 270  
 Pro Gly Asp Ala Ile Arg Ser Ile Leu Glu Arg Met Gly Cys Glu Val  
 275 280 285  
 Glu Leu Val Ala Gln Gly Glu Gly Tyr Asp Leu Ser Val Thr Gly Pro  
 290 295 300  
 Val Ala Leu Lys Gly Ile Glu Ile Asp Met Ser Asp Ile Gly Glu Leu  
 305 310 315 320  
 Thr Pro Thr Val Ala Ala Leu Ala Ala Leu Ala Ser Thr Glu Ser Arg  
 325 330 335  
 Leu Thr Gly Ile Ala His Leu Arg Gly His Glu Thr Asp Arg Leu Ala  
 340 345 350  
 Ala Leu Thr Ala Glu Ile Asn Lys Leu Gly Gly Lys Cys Thr Glu Leu  
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 Lys Asp Gly Leu Leu Ile Glu Pro Ala Ser Leu His Gly Gly Val Trp  
 370 375 380  
 His Ser Tyr Ala Asp His Arg Met Ala Thr Ala Gly Ala Ile Ile Gly  
 385 390 395 400  
 Leu Ala Val Asp Gly Val Gln Val Glu Asp Ile Lys Thr Thr Ser Lys  
 405 410 415  
 Thr Phe Pro Gly Phe Glu Asn Val Trp Glu Glu Met Val Gly  
 420 425 430

&lt;210&gt; 413

&lt;211&gt; 1266

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

atc aac aaa ctt ggt gga aag tgc act gag ctt aag gat ggt ctg ttg  
1219  
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360 365 370

att gag cct gcg tcg ctg cac ggt ggt gtg tgg cat tca tat gct gat  
1267  
Ile Glu Pro Ala Ser Leu His Gly Gly Val Trp His Ser Tyr Ala Asp  
375 380 385

cac cgt atg gct act gct ggt gcg atc att ggc ctc gcg gtt gat ggc  
1315  
His Arg Met Ala Thr Ala Gly Ala Ile Ile Gly Leu Ala Val Asp Gly  
390 395 400 405

gtt cag gtt gaa gac att aag acc act tcc aaa act ttc cct ggt ttt  
1363  
Val Gln Val Glu Asp Ile Lys Thr Thr Ser Lys Thr Phe Pro Gly Phe  
410 415 420

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Glu Asn Val Trp Glu Glu Met Val Gly  
425 430

ccg  
1413

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Lys Ser Ile Thr Asn Arg Ala Leu Ile Leu Ala Ala Leu Ala Ser Thr  
35 40 45  
Pro Ser Thr Ile Ile Asp Val Leu Arg Ser Arg Asp Thr Asp Leu Met  
50 55 60  
Thr Asp Gly Leu Arg Ser Leu Gly Ile Thr Ile Thr Glu Glu Ala Val  
65 70 75 80  
Asp Arg Tyr Arg Val Glu Pro Gly Gln Leu Ser Ala Gly Ser Val Glu  
85 90 95  
Cys Gly Leu Ala Gly Thr Val Met Arg Phe Leu Pro Pro Val Ala Ala  
100 105 110  
Phe Ala Asp Gly Pro Val His Phe Asp Gly Asp Pro Gln Ala Arg Val  
115 120 125  
Arg Pro Met Thr Ser Ile Leu Asp Ala Leu Arg Ser Leu Gly Val Glu  
130 135 140

att ttg gat gcg ctg cgt tcg ctt ggt gtg gag gta gac aac aac aat	547
Ile Leu Asp Ala Leu Arg Ser Leu Gly Val Glu Val Asp Asn Asn Asn	
135 140 145	
ctg cct ttc act gtt aat gct ggt gag gtc cct gag ggt ggc gtg gtt	595
Leu Pro Phe Thr Val Asn Ala Gly Glu Val Pro Glu Gly Gly Val Val	
150 155 160 165	
gag att gat gct tcc ggc tca tct cag ttt gtt tct ggt ctt ttg ctt	643
Glu Ile Asp Ala Ser Gly Ser Ser Gln Phe Val Ser Gly Leu Leu Leu	
170 175 180	
tca gcg cct cgt ttt aaa aat ggc gtc acc gtt aag cac gtc ggt ggt	691
Ser Ala Pro Arg Phe Lys Asn Gly Val Thr Val Lys His Val Gly Gly	
185 190 195	
cgt ctg ccg agc atg ccg cat att gag atg acc gtc gat atg ctt cgt	739
Arg Leu Pro Ser Met Pro His Ile Glu Met Thr Val Asp Met Leu Arg	
200 205 210	
tcc gca ggc att gag atc gaa gag tca gaa aat cag tgg gtt gtt cat	787
Ser Ala Gly Ile Glu Ile Glu Glu Ser Glu Asn Gln Trp Val Val His	
215 220 225	
cct ggt gag atc ttg ggt cgg acc tgg cgc att gag ccg gat ctt tct	835
Pro Gly Glu Ile Leu Gly Arg Thr Trp Arg Ile Glu Pro Asp Leu Ser	
230 235 240 245	
aat gcg act ccg ttc cta gct gcc gct gcg gtc act ggt gga acc atc	883
Asn Ala Thr Pro Phe Leu Ala Ala Ala Val Thr Gly Gly Thr Ile	
250 255 260	
aag att aac cac tgg cca atc aaa act act cag cct ggc gat gct att	931
Lys Ile Asn His Trp Pro Ile Lys Thr Thr Gln Pro Gly Asp Ala Ile	
265 270 275	
cgt tcg att ctt gag cgc atg ggc tgc gaa gtt gag ctg gtt gct cag	979
Arg Ser Ile Leu Glu Arg Met Gly Cys Glu Val Glu Leu Val Ala Gln	
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1027	
Gly Glu Gly Tyr Asp Leu Ser Val Thr Gly Pro Val Ala Leu Lys Gly	
295 300 305	
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1075	
Ile Glu Ile Asp Met Ser Asp Ile Gly Glu Leu Thr Pro Thr Val Ala	
310 315 320 325	
gcg ttg gct gcg ttg gcg tcg aca gag tct cgt ttg acc ggt att gct	
1123	
Ala Leu Ala Ala Leu Ala Ser Thr Glu Ser Arg Leu Thr Gly Ile Ala	
330 335 340	
cat ctt cgt ggc cat gag acg gat cgt ttg gct gcg ttg act gcg gag	
1171	
His Leu Arg Gly His Glu Thr Asp Arg Leu Ala Ala Leu Thr Ala Glu	
345 350 355	

	260		265		270
Gly Gly Glu Asp Ala Pro Ser Pro Val Glu Thr Pro Glu Ala Val Glu					
275		280		285	
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Pro Gly Arg Ala Asp Phe Gly Asp Val Leu					
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		Met Val Phe Val Ser			
		1 5			
gat tcg tct atc tct ttg ccc att tgg gat gct ccg cgc gct cgc ggc	163				
Asp Ser Ser Ile Ser Leu Pro Ile Trp Asp Ala Pro Arg Ala Arg Gly					
10 15 20					
ccc ata gtc tcg gac ctg gct atc cct ggt tcc aag tcg atc acc aac	211				
Pro Ile Val Ser Asp Leu Ala Ile Pro Gly Ser Lys Ser Ile Thr Asn					
25 30 35					
cgc gcc ctc atc ttg gct gcg ctc gca tca act cca tcc acc atc att	259				
Arg Ala Leu Ile Leu Ala Ala Leu Ala Ser Thr Pro Ser Thr Ile Ile					
40 45 50					
gat gtc ctt cgt agt cgt gat acc gat ctc atg act gat ggt cta cgc	307				
Asp Val Leu Arg Ser Arg Asp Thr Asp Leu Met Thr Asp Gly Leu Arg					
55 60 65					
agc ctc gga atc acc att act gaa gag gca gtc gat cgc tac cgc gtt	355				
Ser Leu Gly Ile Thr Ile Thr Glu Glu Ala Val Asp Arg Tyr Arg Val					
70 75 80 85					
gag ccc gga cag ttg tct gct ggc tcc gtt gag tgt ggt ctt gct ggt	403				
Glu Pro Gly Gln Leu Ser Ala Gly Ser Val Glu Cys Gly Leu Ala Gly					
90 95 100					
acg gtc atg cgc ttt ttg cct cct gtt gct gct ttc gct gat ggt cct	451				
Thr Val Met Arg Phe Leu Pro Pro Val Ala Ala Phe Ala Asp Gly Pro					
105 110 115					
ggt cat ttt gat ggc gat cct caa gct cgt gtt cgt ccg atg acc agc	499				
Val His Phe Asp Gly Asp Pro Gln Ala Arg Val Arg Pro Met Thr Ser					
120 125 130					

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 Phe Gly Asp Val Leu  
 310

<210> 410  
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 <212> PRT  
 <213> Corynebacterium glutamicum

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 Asp Phe Ser Phe Trp Gln Ile Pro Thr Leu Gly Glu Leu Leu Arg Asp  
           35                  40                  45  
 Pro Tyr Cys Ser Leu Pro Ala Glu Ser Arg Trp Ala Met Ser Asp Ser  
       50                  55                  60  
 Glu Glu Cys Arg Leu Leu Ala Thr Gly Pro Phe Asp Pro Phe Met Leu  
   65                  70                  75                  80  
 Arg Leu Lys Val Ala Ala Leu Val Gly Met Val Leu Gly Ser Pro Val  
                   85                  90                  95  
 Trp Leu Ser Gln Leu Trp Gly Phe Ile Thr Pro Gly Leu Met Lys Asn  
           100                  105                  110  
 Glu Arg Arg Tyr Thr Ala Ile Phe Val Thr Ile Ala Val Val Leu Phe  
       115                  120                  125  
 Val Gly Gly Ala Val Leu Ala Tyr Phe Val Val Ala Tyr Gly Leu Glu  
   130                  135                  140  
 Phe Leu Leu Thr Ile Gly Gly Asp Thr Gln Ala Ala Ala Leu Thr Gly  
  145                  150                  155                  160  
 Asp Lys Tyr Phe Gly Phe Leu Leu Ala Leu Leu Ala Ile Phe Gly Val  
           165                  170                  175  
 Ser Phe Glu Val Pro Leu Val Ile Gly Met Leu Asn Ile Val Gly Ile  
       180                  185                  190  
 Leu Pro Tyr Asp Ala Ile Lys Asp Lys Arg Arg Met Ile Ile Met Ile  
       195                  200                  205  
 Leu Phe Val Phe Ala Ala Phe Met Thr Pro Gly Gln Asp Pro Phe Thr  
       210                  215                  220  
 Met Leu Val Leu Ala Leu Ser Leu Thr Val Leu Val Glu Leu Ala Leu  
  225                  230                  235                  240  
 Gln Phe Cys Arg Phe Asn Asp Lys Arg Arg Asp Lys Lys Arg Pro Glu  
           245                  250                  255  
 Trp Leu Asp Gly Asp Asp Leu Ser Ala Ser Pro Leu Asp Thr Ser Ala

ctc gca acc ggc ccg ttt gat cca ttc atg ctt cgc ctt aaa gta gcg	355
Leu Ala Thr Gly Pro Phe Asp Pro Phe Met Leu Arg Leu Lys Val Ala	
70 75 80 85	
gcg ttg gtg ggt atg gtt ctt ggc tca ccc gtg tgg ctg agc cag ctg	403
Ala Leu Val Gly Met Val Leu Gly Ser Pro Val Trp Leu Ser Gln Leu	
90 95 100	
tgg ggc ttt atc acc cca ggt ttg atg aag aat gag cgc cgt tac acc	451
Trp Gly Phe Ile Thr Pro Gly Leu Met Lys Asn Glu Arg Arg Tyr Thr	
105 110 115	
gca atc ttc gtc acg att gct gtt gtg ctg ttt gtc ggc ggt gct gtt	499
Ala Ile Phe Val Thr Ile Ala Val Val Leu Phe Val Gly Gly Ala Val	
120 125 130	
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Leu Ala Tyr Phe Val Val Ala Tyr Gly Leu Glu Phe Leu Leu Thr Ile	
135 140 145	
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Gly Gly Asp Thr Gln Ala Ala Ala Leu Thr Gly Asp Lys Tyr Phe Gly	
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Phe Leu Leu Ala Leu Leu Ala Ile Phe Gly Val Ser Phe Glu Val Pro	
170 175 180	
ctg gtg atc ggc atg ctc aac att gtg ggt atc ttg cct tac gat gcc	691
Leu Val Ile Gly Met Leu Asn Ile Val Gly Ile Leu Pro Tyr Asp Ala	
185 190 195	
att aaa gat aag cga cgc atg atc atc atg att ttg ttc gtg ttc gct	739
Ile Lys Asp Lys Arg Arg Met Ile Ile Met Ile Leu Phe Val Phe Ala	
200 205 210	
gct ttc atg aca ccc ggc cag gat cct ttc acc atg ttg gtg ttg gcg	787
Ala Phe Met Thr Pro Gly Gln Asp Pro Phe Thr Met Leu Val Leu Ala	
215 220 225	
ctt tca ctc acc gtt ctg gta gag ctt gcc ctg cag ttc tgt cgc ttc	835
Leu Ser Leu Thr Val Leu Val Glu Leu Ala Leu Gln Phe Cys Arg Phe	
230 235 240 245	
aac gac aaa cgc cgg gac aag aag cgc cca gaa tgg ctt gat ggc gat	883
Asn Asp Lys Arg Arg Asp Lys Lys Arg Pro Glu Trp Leu Asp Gly Asp	
250 255 260	
gac ctc tct gca tca cca ctg gat act tct gct ggt gga gaa gat gct	931
Asp Leu Ser Ala Ser Pro Leu Asp Thr Ser Ala Gly Gly Glu Asp Ala	
265 270 275	
cca agc cca gtc gaa acc cca gag gcg gtg gag cct tcg cgg atg ctg	979
Pro Ser Pro Val Glu Thr Pro Glu Ala Val Glu Pro Ser Arg Met Leu	
280 285 290	
aac cca agt ggg gag gcg tcg ata agc tat aaa ccc ggg cgc gcc gac	1027
Asn Pro Ser Gly Glu Ala Ser Ile Ser Tyr Lys Pro Gly Arg Ala Asp	
295 300 305	



Asp Val Ser Glu Ala Val Arg His Leu Arg Thr Ile Arg Gly Asp Ile  
 165 170 175  
 Asn Arg Leu Arg Ser Leu Asp Glu Asp Glu Leu Phe Val Ala Ala Lys  
 180 185 190  
 Glu Phe Gln Ala Pro Tyr Asp Leu Val Arg Glu Val Ala Ser Thr Gly  
 195 200 205  
 Lys Leu Pro Val Val Thr Phe Val Ala Gly Gly Val Ala Thr Pro Ala  
 210 215 220  
 Asp Ala Ala Leu Val Arg Gln Met Gly Ala Glu Gly Val Phe Val Gly  
 225 230 235 240  
 Ser Gly Ile Phe Lys Ser Gly Asn Pro Ala Ala Arg Ala Ala Ala Ile  
 245 250 255  
 Val Lys Ala Ala Thr Leu Phe Asp Asp Pro Ser Val Ile Ala Asp Val  
 260 265 270  
 Ser Arg Gly Leu Gly Glu Ala Met Val Gly Ile Asn Val Ser Asp Val  
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 Pro Ala Pro His Arg Leu Ala Glu Arg Gly Trp  
 290 295

<210> 409  
 <211> 1065  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1042)  
 <223> RXC01158

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 Met Ser Ile Val Glu  
 1 5  
 cac atc aaa gag ttt cga cgc cga ctt ctt atc gct ctg gcg ggc atc 163  
 His Ile Lys Glu Phe Arg Arg Arg Leu Leu Ile Ala Leu Ala Gly Ile  
 10 15 20  
 ctc gtg ggc acc att atc ggc ttt att tgg tac gat ttc tca ttt tgg 211  
 Leu Val Gly Thr Ile Ile Gly Phe Ile Trp Tyr Asp Phe Ser Phe Trp  
 25 30 35  
 cag atc ccc act ttg ggc gag ctg ctg agg gat ccg tac tgt tct ctg 259  
 Gln Ile Pro Thr Leu Gly Glu Leu Leu Arg Asp Pro Tyr Cys Ser Leu  
 40 45 50  
 cct gct gaa tcc cgc tgg gcc atg agc gac tca gag gaa tgt cga ctg 307  
 Pro Ala Glu Ser Arg Trp Ala Met Ser Asp Ser Glu Glu Cys Arg Leu  
 55 60 65

Thr Phe Val Ala Gly Gly Val Ala Thr Pro Ala Asp Ala Ala Leu Val  
 215 220 225  
 cgc caa atg ggc gcc gaa ggc gtc ttt gtc ggc tcc ggc atc ttc aaa 835  
 Arg Gln Met Gly Ala Glu Gly Val Phe Val Gly Ser Gly Ile Phe Lys  
 230 235 240 245  
 tcc ggc aat cca gcc gcc cgc gcc gca gcg atc gtc aag gct gca acg 883  
 Ser Gly Asn Pro Ala Ala Arg Ala Ala Ile Val Lys Ala Ala Thr  
 250 255 260  
 ctt ttc gac gac ccc tcc gtc att gcc gac gta tcc cgc ggc ctg ggt 931  
 Leu Phe Asp Asp Pro Ser Val Ile Ala Asp Val Ser Arg Gly Leu Gly  
 265 270 275  
 gaa gcc atg gtg ggc atc aac gta tcc gac gtt cca gca cca cac cga 979  
 Glu Ala Met Val Gly Ile Asn Val Ser Asp Val Pro Ala Pro His Arg  
 280 285 290  
 ctc gcc gag cgc ggc tgg tgatcggttg agtttttagct ctc  
 1020  
 Leu Ala Glu Arg Gly Trp  
 295

&lt;210&gt; 408

&lt;211&gt; 299

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 408

Met Thr Glu Thr Gln Glu Thr Tyr Gln Ala Thr Thr Arg Val Lys Arg  
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 Gly Leu Ala Asp Met Leu Lys Gly Gly Val Ile Met Asp Val Val Thr  
 20 25 30  
 Pro Glu Gln Ala Arg Ile Ala Glu Asp Ala Gly Ala Ser Ala Val Met  
 35 40 45  
 Ala Leu Glu Arg Val Pro Ala Asp Ile Arg Ser Gln Gly Gly Val Ala  
 50 55 60  
 Arg Met Ser Asp Pro Asp Leu Ile Glu Gly Ile Val Asn Ala Val Ser  
 65 70 75 80  
 Ile Pro Val Met Ala Lys Ala Arg Ile Gly His Phe Val Glu Ala Gln  
 85 90 95  
 Val Leu Glu Ala Leu Gly Val Asp Phe Ile Asp Glu Ser Glu Val Leu  
 100 105 110  
 Ser Pro Ala Asp Tyr Thr His His Ile Asn Lys Trp Lys Phe Asp Val  
 115 120 125  
 Pro Phe Val Cys Gly Ala Thr Asn Leu Gly Glu Ala Leu Arg Arg Ile  
 130 135 140  
 Thr Glu Gly Ala Ala Met Ile Arg Ser Lys Gly Glu Ala Gly Thr Gly  
 145 150 155 160

&lt;400&gt; 407

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tcggcaagca tggcttcacg gtcctcaaaa aagtgggtcta atgcaagtga ctgaaagtgg 60

atctaccgct agtccacttt gtggcggttg atcatctgtc atg acc gaa act caa 115
                                         Met Thr Glu Thr Gln
                                         1                               5

gaa act tac caa gca acc act cgt gtg aag cgc ggc ctt gcc gac atg 163
Glu Thr Tyr Gln Ala Thr Thr Arg Val Lys Arg Gly Leu Ala Asp Met
                               10                               15                               20

ctc aag ggt ggt gtg atc atg gat gtg gtc acc cct gaa caa gcg cgc 211
Leu Lys Gly Gly Val Ile Met Asp Val Val Thr Pro Glu Gln Ala Arg
                               25                               30                               35

atc gcc gaa gat gca ggt gcc agc gca gtt atg gca ctc gag cgc gtt 259
Ile Ala Glu Asp Ala Gly Ala Ser Ala Val Met Ala Leu Glu Arg Val
                               40                               45                               50

ccc gcc gat atc cgt tct cag ggc ggc gtt gct cgc atg agt gat cct 307
Pro Ala Asp Ile Arg Ser Gln Gly Gly Val Ala Arg Met Ser Asp Pro
                               55                               60                               65

gac ctg atc gaa gga atc gtc aat gcg gtc tcc atc ccg gtc atg gcg 355
Asp Leu Ile Glu Gly Ile Val Asn Ala Val Ser Ile Pro Val Met Ala
                               70                               75                               80                               85

aaa gct cgc atc ggt cac ttc gtg gaa gct cag gtt ctg gaa gct ctc 403
Lys Ala Arg Ile Gly His Phe Val Glu Ala Gln Val Leu Glu Ala Leu
                               90                               95                               100

ggt gtt gat ttc atc gac gag tcc gaa gtt ctc agc cct gcc gac tac 451
Gly Val Asp Phe Ile Asp Glu Ser Glu Val Leu Ser Pro Ala Asp Tyr
                               105                               110                               115

acg cac cac atc aac aag tgg aag ttc gac gtt cct ttc gtc tgt ggc 499
Thr His His Ile Asn Lys Trp Lys Phe Asp Val Pro Phe Val Cys Gly
                               120                               125                               130

gcg acc aac ctc ggc gaa gct ttg cga cgc atc acc gaa ggc gct gca 547
Ala Thr Asn Leu Gly Glu Ala Leu Arg Arg Ile Thr Glu Gly Ala Ala
                               135                               140                               145

atg atc cgt tcc aag ggc gaa gcc ggc acc ggc gat gtc tct gaa gct 595
Met Ile Arg Ser Lys Gly Glu Ala Gly Thr Gly Asp Val Ser Glu Ala
                               150                               155                               160                               165

gtc cgt cac ctg cgc acc atc cgc ggc gac atc aat cgc ctg cgc tcc 643
Val Arg His Leu Arg Thr Ile Arg Gly Asp Ile Asn Arg Leu Arg Ser
                               170                               175                               180

ctg gat gag gat gaa ctc ttc gtc gcc gcc aag gaa ttc cag gca cca 691
Leu Asp Glu Asp Glu Leu Phe Val Ala Ala Lys Glu Phe Gln Ala Pro
                               185                               190                               195

tac gac ctg gtc cgc gaa gtc gcc tcc acc ggc aag ctc cct gtg gtc 739
Tyr Asp Leu Val Arg Glu Val Ala Ser Thr Gly Lys Leu Pro Val Val
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acc ttc gtt gca ggt ggc gtc gca acc cca gcc gac gct gca ctc gtg 787

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	90	95	100	
gca gaa cgg gcc cga acc ctg ctg acc tcc ggt gtg gcc tca cag aag				451
Ala Glu Arg Ala Arg Thr Leu Leu Thr Ser Gly Val Ala Ser Gln Lys				
	105	110	115	
gct aat tcc gga acc ctg ctg tct gat tgg gcg gag atc atc aat acc				499
Ala Asn Ser Gly Thr Leu Leu Ser Asp Trp Ala Glu Ile Ile Asn Thr				
	120	125	130	
acc acc cat cca ctg gcg gca gtg gta gcc atg att ggc tgc gcg cta				547
Thr Thr His Pro Leu Ala Ala Val Val Ala Met Ile Gly Cys Ala Leu				
	135	140	145	

&lt;210&gt; 406

&lt;211&gt; 149

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 406

Met Lys Pro Arg Val Leu Ser Ala Leu Gly Ile Gly Ala Gly Ala Leu	
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Val Val Trp Ile Ser Ser Arg Met Asn Trp Val Thr Ile Glu Ala Phe	
20 25 30	

Asp Asp Lys Ser Gly Ser Val Thr Gln Ser Ile Val Gly Ala Thr Trp	
35 40 45	

Ser Thr Glu Ile Met Ala Leu Ala Leu Ala Leu Ala Ala Phe Ala	
50 55 60	

Ala Ala Leu Val Leu Lys Arg Met Gly Arg Arg Ile Ile Gly Gly Ile	
65 70 75 80	

Ser Ala Leu Ile Ala Val Gly Ala Ser Leu Ser Pro Leu Ala Leu Leu	
85 90 95	

Thr Gln Asp Pro Asp Ala Glu Arg Ala Arg Thr Leu Leu Thr Ser Gly	
100 105 110	

Val Ala Ser Gln Lys Ala Asn Ser Gly Thr Leu Leu Ser Asp Trp Ala	
115 120 125	

Glu Ile Ile Asn Thr Thr Thr His Pro Leu Ala Ala Val Val Ala Met	
130 135 140	

Ile Gly Cys Ala Leu
145

&lt;210&gt; 407

&lt;211&gt; 1020

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(997)

&lt;223&gt; RXC01656

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 225 230 235 240  
 Val Gly Ser Gln Leu Thr Ser Gln Glu Asn Val Asp Leu Ala Ala Arg  
 245 250 255  
 Glu Leu Val Tyr Gly Pro Asn Lys Val Cys Gly Leu Thr Ser Pro Ser  
 260 265 270  
 Ala Ala Gln Thr Ala Arg Ala Ala Gly Ala Val Tyr Gly Gly Leu Ile  
 275 280 285  
 Phe Glu Glu Ala Ser Pro Arg Asn Val Ser Arg Glu Thr Leu Gln Lys  
 290 295 300  
 Ile Ile Ala Ala Glu Pro Asn Leu Arg Tyr Val Ala Val Ser Arg Arg  
 305 310 315 320  
 Thr Ser Gly Tyr Lys Asp Leu Leu Val Asp Gly Ile Phe Ala Val Gln  
 325 330 335  
 Ile His Ala Pro Leu Gln Asp Ser Val Glu Ala Glu Lys Ala Leu Ile  
 340 345 350  
 Ala Ala Val Arg Glu Glu Val Gly Pro Gln Val Gln Val Trp Arg Ala  
 355 360 365  
 Ile Ser Met Ser Ser Pro Leu Gly Ala Glu Val Ala Ala Ala Val Glu  
 370 375 380  
 Gly Asp Val Asp Lys Leu Ile Leu Asp Ala His Glu Gly Gly Ser Gly  
 385 390 395 400  
 Glu Val Phe Asp Trp Ala Thr Val Pro Ala Ala Val Lys Ala Lys Ser  
 405 410 415  
 Leu Leu Ala Gly Gly Ile Ser Pro Asp Asn Ala Ala Gln Ala Leu Ala  
 420 425 430  
 Val Gly Cys Ala Gly Leu Asp Ile Asn Ser Gly Val Glu Tyr Pro Ala  
 435 440 445  
 Gly Ala Gly Thr Trp Ala Gly Ala Lys Asp Ala Gly Ala Leu Leu Lys  
 450 455 460  
 Ile Leu Ala Thr Ile Ser Thr Phe His Tyr  
 465 470

&lt;210&gt; 433

&lt;211&gt; 494

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(471)

&lt;223&gt; RXA02814

&lt;400&gt; 433

Leu Asp Ile Asn Ser Gly Val Glu Tyr Pro Ala Gly Ala Gly Thr Trp  
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gct ggg gcg aaa gac gcc ggc gcg ctg ctg aaa att tta gcg acc atc  
 1507

Ala Gly Ala Lys Asp Ala Gly Ala Leu Leu Lys Ile Leu Ala Thr Ile  
 455 460 465

tcc aca ttc cat tac taaaggttta aataggatca tga  
 1545

Ser Thr Phe His Tyr  
 470

<210> 432

<211> 474

<212> PRT

<213> Corynebacterium glutamicum

<400> 432

Met Thr Ser Asn Asn Leu Pro Thr Val Leu Glu Ser Ile Val Glu Gly  
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Arg Arg Gly His Leu Glu Glu Ile Arg Ala Arg Ile Ala His Val Asp  
 20 25 30

Val Asp Ala Leu Pro Lys Ser Thr Arg Ser Leu Phe Asp Ser Leu Asn  
 35 40 45

Gln Gly Arg Gly Gly Ala Arg Phe Ile Met Glu Cys Lys Ser Ala Ser  
 50 55 60

Pro Ser Leu Gly Met Ile Arg Glu His Tyr Gln Pro Gly Glu Ile Ala  
 65 70 75 80

Arg Val Tyr Ser Arg Tyr Ala Ser Gly Ile Ser Val Leu Cys Glu Pro  
 85 90 95

Asp Arg Phe Gly Gly Asp Tyr Asp His Leu Ala Thr Val Ala Ala Thr  
 100 105 110

Ser His Leu Pro Val Leu Cys Lys Asp Phe Ile Ile Asp Pro Val Gln  
 115 120 125

Val His Ala Ala Arg Tyr Phe Gly Ala Asp Ala Ile Leu Leu Met Leu  
 130 135 140

Ser Val Leu Asp Asp Glu Glu Tyr Ala Ala Leu Ala Ala Glu Ala Ala  
 145 150 155 160

Arg Phe Asp Leu Asp Ile Leu Thr Glu Val Ile Asp Glu Glu Glu Val  
 165 170 175

Ala Arg Ala Ile Lys Leu Gly Ala Lys Ile Phe Gly Val Asn His Arg  
 180 185 190

Asn Leu His Asp Leu Ser Ile Asp Leu Asp Arg Ser Arg Arg Leu Ser  
 195 200 205

Lys Leu Ile Pro Ala Asp Ala Val Leu Val Ser Glu Ser Gly Val Arg  
 210 215 220

230	235	240	245	
acc agc cag gaa aac gtc gat ctg gca gcc cgc gaa tta gtc tac ggc				883
Thr Ser Gln Glu Asn Val Asp Leu Ala Ala Arg Glu Leu Val Tyr Gly	250	255	260	
ccc aac aaa gtc tgc gga ctc acc tca cca agt gca gca caa acc gct				931
Pro Asn Lys Val Cys Gly Leu Thr Ser Pro Ser Ala Ala Gln Thr Ala	265	270	275	
cgc gca gcg ggt gcg gtc tac ggc ggg ctc atc ttc gaa gag gca tcg				979
Arg Ala Ala Gly Ala Val Tyr Gly Gly Leu Ile Phe Glu Glu Ala Ser	280	285	290	
cca cgc aat gtt tca cgt gaa aca ttg caa aaa atc atc gcc gca gag				
1027				
Pro Arg Asn Val Ser Arg Glu Thr Leu Gln Lys Ile Ile Ala Ala Glu	295	300	305	
ccc aac ctg cgc tac gtc gcg gtc agc cgt cgc acc tcc ggg tac aag				
1075				
Pro Asn Leu Arg Tyr Val Ala Val Ser Arg Arg Thr Ser Gly Tyr Lys	310	315	320	325
gat ttg ctt gtc gac ggc atc ttc gcc gta caa atc cac gcc cca ctg				
1123				
Asp Leu Leu Val Asp Gly Ile Phe Ala Val Gln Ile His Ala Pro Leu	330	335	340	
cag gac agc gtc gaa gca gaa aag gca ttg atc gcc gcc gtt cgt gaa				
1171				
Gln Asp Ser Val Glu Ala Glu Lys Ala Leu Ile Ala Ala Val Arg Glu	345	350	355	
gag gtt gga ccg cag gtc cag gtc tgg cgc gcg atc tcg atg tcc agc				
1219				
Glu Val Gly Pro Gln Val Gln Val Trp Arg Ala Ile Ser Met Ser Ser	360	365	370	
ccc ttg ggg gct gaa gtg gca gct gcg gtg gag ggt gac gtc gat aag				
1267				
Pro Leu Gly Ala Glu Val Ala Ala Ala Val Glu Gly Asp Val Asp Lys	375	380	385	
cta att ctt gat gcc cat gaa ggt ggc agc ggg gaa gta ttc gac tgg				
1315				
Leu Ile Leu Asp Ala His Glu Gly Gly Ser Gly Glu Val Phe Asp Trp	390	395	400	405
gct acg gtg ccg gcc gct gtg aag gca aag tct ttg ctc gcg gga ggc				
1363				
Ala Thr Val Pro Ala Ala Val Lys Ala Lys Ser Leu Leu Ala Gly Gly	410	415	420	
atc tct ccg gac aac gct gcg cag gca ctc gct gtg ggc tgc gca ggt				
1411				
Ile Ser Pro Asp Asn Ala Ala Gln Ala Leu Ala Val Gly Cys Ala Gly	425	430	435	
ttg gac atc aac tct ggc gtg gaa tac ccc gcc ggt gca ggc acg tgg				
1459				

															Met Thr Ser Asn Asn
															1 5
ctg ccc aca gtg ttg gaa agc atc gtc gag ggt cgt cgc gga cac ctg															163
Leu Pro Thr Val Leu Glu Ser Ile Val Glu Gly Arg Arg Gly His Leu															
			10					15						20	
gag gaa att cgc gct cgc atc gct cac gtg gat gtg gat gcg ctt cca															211
Glu Glu Ile Arg Ala Arg Ile Ala His Val Asp Val Asp Ala Leu Pro															
			25					30						35	
aaa tcc acc cgt tct ctg ttt gat tcc ctc aac cag ggt agg gga ggg															259
Lys Ser Thr Arg Ser Leu Phe Asp Ser Leu Asn Gln Gly Arg Gly Gly															
			40					45						50	
gcg cgt ttc atc atg gag tgc aag tcc gca tcg cct tct ttg gga atg															307
Ala Arg Phe Ile Met Glu Cys Lys Ser Ala Ser Pro Ser Leu Gly Met															
			55					60						65	
att cgt gag cac tac cag ccg ggt gaa atc gct cgc gtg tac tct cgc															355
Ile Arg Glu His Tyr Gln Pro Gly Glu Ile Ala Arg Val Tyr Ser Arg															
			70					75						80 85	
tac gcc agc ggc att tcc gtg ctg tgc gag ccg gat cgt ttt ggt ggc															403
Tyr Ala Ser Gly Ile Ser Val Leu Cys Glu Pro Asp Arg Phe Gly Gly															
								90						100	
gat tac gat cac ctc gct acc gtt gcc gct acc tct cat ctt ccg gtg															451
Asp Tyr Asp His Leu Ala Thr Val Ala Ala Thr Ser His Leu Pro Val															
								105						115	
ctg tgc aaa gac ttc atc att gat cct gtc cag gta cac gcg gcg cgt															499
Leu Cys Lys Asp Phe Ile Ile Asp Pro Val Gln Val His Ala Ala Arg															
								120						130	
tac ttt ggt gct gat gcc atc ctg ctc atg ctc tct gtg ctt gat gat															547
Tyr Phe Gly Ala Asp Ala Ile Leu Leu Met Leu Ser Val Leu Asp Asp															
								135						145	
gaa gag tac gca gca ctc gct gcc gag gct gcg cgt ttt gat ctg gat															595
Glu Glu Tyr Ala Ala Leu Ala Ala Glu Ala Ala Arg Phe Asp Leu Asp															
								150						165	
atc ctc acc gag gtt att gat gag gag gaa gtc gcc cgc gcc atc aag															643
Ile Leu Thr Glu Val Ile Asp Glu Glu Glu Val Ala Arg Ala Ile Lys															
								170						180	
ctg ggt gcg aag atc ttt ggc gtc aac cac cgc aac ctg cat gat ctg															691
Leu Gly Ala Lys Ile Phe Gly Val Asn His Arg Asn Leu His Asp Leu															
								185						195	
tcc att gat ttg gat cgt tca cgt cgc ctg tcc aag ctc att cca gca															739
Ser Ile Asp Leu Asp Arg Ser Arg Arg Leu Ser Lys Leu Ile Pro Ala															
								200						210	
gat gcc gtg ctc gtg tct gag tct ggc gtg cgc gat acc gaa acc gtc															787
Asp Ala Val Leu Val Ser Glu Ser Gly Val Arg Asp Thr Glu Thr Val															
								215						225	
gcg cag cta ggt ggg cac tcc aat gca ttc ctc gtt ggc tcc cag ctg															835
Arg Gln Leu Gly Gly His Ser Asn Ala Phe Leu Val Gly Ser Gln Leu															



Arg Ser Ala Gly Leu Thr Ala Ala Phe Asp Ile Ala Ser Val Phe Phe  
                   35                                  40                                  45  
 Ser Ser Gly Cys Asn Val Val Val Ala Phe Asp Arg Phe Ala Ser Asn  
                   50                                  55                                  60  
 Trp Ser Asp His Ser Asp His Val Asp Tyr Ala Ala Gln Val Ala Gly  
                   65                                  70                                  75                                  80  
 Phe Gly Ala Ser Met Leu Ala Tyr Thr Val Arg Arg Gly Gln Phe Asp  
                                   85                                  90                                  95  
 Thr Ala Val Arg Asp Ile Arg Asp Ile Lys Ser Glu Val Asp Ile Pro  
                                   100                                  105                                  110  
 Ile Leu Leu His Asp Pro Ile Ile Asp Pro Tyr Gln Ile His Glu Ala  
                   115                                  120                                  125  
 Arg Val Met Gly Ile Asp Ala Leu Gln Phe Pro Val Trp Ala Met Glu  
                   130                                  135                                  140  
 Gln Ala Arg Leu Glu Ser Leu Val Asp Arg Thr Glu Ser Leu Gly Met  
                   145                                  150                                  155                                  160  
 Thr Ala Ile Val Ser Val Arg Asn His Glu Glu Ala His Arg Ala Val  
                                   165                                  170                                  175  
 Asp Ala Gly Ala Thr Val Val Ala Ile Asp Ile Thr Gly Tyr Thr Gly  
                   180                                  185                                  190  
 Ser Leu Thr Leu Pro Glu Ala Phe Ser Gly Ile Thr Gln Phe Met Pro  
                   195                                  200                                  205  
 Lys Glu Val Ala Arg Ile Val Leu Gly Gly Cys Ser Ser Pro Lys Glu  
                   210                                  215                                  220  
 Leu Met Arg Phe Ala Arg His Ser Ala Asp Ala Ile Phe Val Pro His  
                   225                                  230                                  235                                  240  
 Ala Asp Leu Ala Thr Thr Lys Ser Leu Val Thr Ala Gly Met His Pro  
                                   245                                  250                                  255  
 Ala Cys Pro Ser Arg  
                                   260

&lt;210&gt; 431

&lt;211&gt; 1545

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1522)

&lt;223&gt; RXA00955

&lt;400&gt; 431

gatggtgcac aaaaggcgct ttccttgctt gccgacggca ccacccaggc atggttggcc 60

aagcacgaag agatcgatta ctcagaaaag gagtcttcca atg act agt aat aat 115

Asp His Val Asp Tyr Ala Ala Gln Val Ala Gly Phe Gly Ala Ser Met  
 70 75 80 85  
 ctt gca tat acg gtg cgc agg gga cag ttt gat acc gca gta cgc gat 403  
 Leu Ala Tyr Thr Val Arg Arg Gly Gln Phe Asp Thr Ala Val Arg Asp  
 90 95 100  
 atc agg gac atc aaa tct gaa gta gac att ccc att ctg ctt cat gat 451  
 Ile Arg Asp Ile Lys Ser Glu Val Asp Ile Pro Ile Leu Leu His Asp  
 105 110 115  
 ccc atc atc gat ccg tat caa atc cac gaa gcc cgc gtc atg ggc atc 499  
 Pro Ile Ile Asp Pro Tyr Gln Ile His Glu Ala Arg Val Met Gly Ile  
 120 125 130  
 gac gct ctt caa ttc ccc gta tgg gcg atg gaa caa gct cga ctg gaa 547  
 Asp Ala Leu Gln Phe Pro Val Trp Ala Met Glu Gln Ala Arg Leu Glu  
 135 140 145  
 tct ttg gtg gac cgc acc gaa tca ttg ggc atg aca gcc atc gtg tct 595  
 Ser Leu Val Asp Arg Thr Glu Ser Leu Gly Met Thr Ala Ile Val Ser  
 150 155 160 165  
 gtg cga aac cac gaa gaa gcg cat cgt gca gtg gac gca gga gcg aca 643  
 Val Arg Asn His Glu Glu Ala His Arg Ala Val Asp Ala Gly Ala Thr  
 170 175 180  
 gtg gta gca att gat att act ggt tat acc ggc tca ctc act ttg cct 691  
 Val Val Ala Ile Asp Ile Thr Gly Tyr Thr Gly Ser Leu Thr Leu Pro  
 185 190 195  
 gaa gcg ttt tcg ggt atc acc caa ttc atg ccc aaa gag gta gcc cgc 739  
 Glu Ala Phe Ser Gly Ile Thr Gln Phe Met Pro Lys Glu Val Ala Arg  
 200 205 210  
 att gtg ctc gga ggt tgc agc agc cct aaa gaa ctc atg cgg ttt gca 787  
 Ile Val Leu Gly Gly Cys Ser Ser Pro Lys Glu Leu Met Arg Phe Ala  
 215 220 225  
 cga cat tct gca gac gcc atc ttt gtt cca cat gca gac ctc gcc acc 835  
 Arg His Ser Ala Asp Ala Ile Phe Val Pro His Ala Asp Leu Ala Thr  
 230 235 240 245  
 aca aaa tct ctt gtg aca gca ggt atg cat cca gcg tgc cca tcg cgt 883  
 Thr Lys Ser Leu Val Thr Ala Gly Met His Pro Ala Cys Pro Ser Arg  
 250 255 260  
 tgaagaggtg ctctgtggtc agc 906

&lt;210&gt; 430

&lt;211&gt; 261

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 430

Met Val Ala Thr Glu Asn Arg Met Leu Met Glu Ile Ala Ala Glu Ile  
 1 5 10 15  
 Ser Ala Arg Glu Ala Thr Leu Gly Phe Gln Glu Val Lys Thr Lys Ser  
 20 25 30

195					200					205					
Val	Phe	Leu	Asp	Asp	Asn	Gly	Val	Tyr	Arg	Asn	Thr	Asn	Arg	Ala	Gly
210						215					220				
Gly	Leu	Glu	Gly	Gly	Met	Thr	Asn	Gly	Glu	Thr	Leu	Arg	Val	Arg	Ala
225					230					235					240
Gly	Met	Lys	Pro	Ile	Ser	Thr	Val	Pro	Arg	Ala	Leu	Lys	Thr	Ile	Asp
				245					250					255	
Met	Glu	Asn	Gly	Lys	Ala	Ala	Thr	Gly	Ile	His	Gln	Arg	Ser	Asp	Val
			260					265					270		
Cys	Ala	Val	Pro	Ala	Ala	Gly	Val	Val	Ala	Glu	Ala	Met	Val	Thr	Leu
		275					280					285			
Val	Leu	Ala	Arg	Ala	Val	Leu	Gln	Lys	Phe	Gly	Gly	Asp	Ser	Leu	Ser
	290					295					300				
Glu	Thr	Lys	Ser	Asn	Ile	Asp	Thr	Tyr	Leu	Lys	Asn	Ile	Glu	Glu	Arg
305				310						315					320
Met	Lys	Phe	Glu	Gly	Leu	Glu	Asp	Gly	Ala						
				325					330						

&lt;210&gt; 429

&lt;211&gt; 906

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(883)

&lt;223&gt; RXA01095

&lt;400&gt; 429

gaaacccag gtcaaagcta ggggtgtggca ccctgatttc tttcgccatg tgtgttcggg 60

ataaccttaa	acacagcatt	ggttggaagg	agggttggggc	atg	gtt	gca	aca	gag	115
				Met	Val	Ala	Thr	Glu	
				1				5	

aac	cgc	atg	ttg	atg	gaa	atc	gct	gcg	gaa	ata	tcg	gct	cgg	gaa	gca	163
Asn	Arg	Met	Leu	Met	Glu	Ile	Ala	Ala	Glu	Ile	Ser	Ala	Arg	Glu	Ala	
			10					15						20		

acg	ctt	ggc	ttt	caa	gaa	gtc	aaa	act	aaa	tct	cga	tca	gca	ggc	ctc	211
Thr	Leu	Gly	Phe	Gln	Glu	Val	Lys	Thr	Lys	Ser	Arg	Ser	Ala	Gly	Leu	
			25					30					35			

acg	gcg	gct	ttc	gat	att	gct	tca	gtc	ttt	ttt	tcg	tct	gga	tgt	aat	259
Thr	Ala	Ala	Phe	Asp	Ile	Ala	Ser	Val	Phe	Phe	Ser	Ser	Gly	Cys	Asn	
		40					45					50				

gtc	gta	gtc	gcc	ttt	gat	cgt	ttt	gca	tcc	aat	tgg	tct	gat	cat	tcg	307
Val	Val	Val	Ala	Phe	Asp	Arg	Phe	Ala	Ser	Asn	Trp	Ser	Asp	His	Ser	
		55				60					65					

gat	cat	gtg	gac	tac	gct	gca	cag	gtt	gcg	ggc	ttt	ggc	gca	tca	atg	355
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

gtt ctc gcc cgc gca gtc ctg cag aaa ttc ggc ggt gac tcc ctg agc 912  
 Val Leu Ala Arg Ala Val Leu Gln Lys Phe Gly Gly Asp Ser Leu Ser  
 290 295 300

gaa acc aag agc aac att gac acc tac ctc aaa aac att gag gaa cga 960  
 Glu Thr Lys Ser Asn Ile Asp Thr Tyr Leu Lys Asn Ile Glu Glu Arg  
 305 310 315 320

atg aaa ttc gaa ggt tta gag gat gga gcg taatgaagtg aatgatcaaa  
 1010  
 Met Lys Phe Glu Gly Leu Glu Asp Gly Ala  
 325 330

ttc  
 1013

<210> 428

<211> 330

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 428

Gly Asn Thr Glu Trp Asp Lys Trp Thr Thr Ile Met Ser Ser Asp Ala  
 1 5 10 15

Leu Asp Met Glu Asp Pro Asp Asn Val Ala Ala Met Ser Ser Gly Arg  
 20 25 30

Gly Ala Lys Leu Thr Arg Pro Arg Pro Gly His Ala Asp Tyr Ala Gly  
 35 40 45

Met Leu Lys Tyr Gly Phe Asp Asp Ala Arg Asn Val Leu Glu Arg Ser  
 50 55 60

Ser Ala Arg Glu Thr Ala Ala Arg Val Ala Ala Thr Val Ala Arg  
 65 70 75 80

Ser Phe Leu Arg Glu Thr Leu Gly Val Glu Val Leu Ser His Val Ile  
 85 90 95

Ser Ile Gly Ala Ser Glu Pro Tyr Thr Gly Ala Glu Pro Thr Phe Ala  
 100 105 110

Asp Ile Gln Ala Ile Asp Asp Ser Pro Val Arg Ala Phe Gly Lys Asp  
 115 120 125

Ala Glu Glu Ser Met Ile Ala Glu Ile Glu Ala Ala Lys Lys Ala Gly  
 130 135 140

Asp Thr Leu Gly Gly Ile Val Glu Val Ile Val Glu Gly Leu Pro Ile  
 145 150 155 160

Gly Leu Gly Ser His Ile Ser Gly Glu Asp Arg Leu Asp Ala Gln Ile  
 165 170 175

Ala Ala Ala Leu Met Gly Ile Gln Ala Ile Lys Gly Val Glu Ile Gly  
 180 185 190

Asp Gly Phe Glu Glu Ala Arg Arg Arg Gly Ser Glu Ala His Asp Glu

35					40					45										
atg	ctc	aag	tac	gga	ttc	gat	gat	gcc	cgc	aac	gtg	ctg	gag	cgt	tct	192				
Met	Leu	Lys	Tyr	Gly	Phe	Asp	Asp	Ala	Arg	Asn	Val	Leu	Glu	Arg	Ser					
50					55					60										
tca	gcc	cgt	gag	acg	gca	gca	cgc	gtg	gca	gca	gca	acc	gtt	gcg	cgt	240				
Ser	Ala	Arg	Glu	Thr	Ala	Ala	Arg	Val	Ala	Ala	Ala	Thr	Val	Ala	Arg					
65					70					75					80					
tcc	ttc	ctg	cgt	gaa	acc	ttg	ggc	gtg	gaa	gtg	ctt	tcc	cac	gta	att	288				
Ser	Phe	Leu	Arg	Glu	Thr	Leu	Gly	Val	Glu	Val	Leu	Ser	His	Val	Ile					
					85					90					95					
tcc	att	ggt	gcg	tcc	gag	cct	tac	act	ggc	gcg	gag	cca	acc	ttt	gca	336				
Ser	Ile	Gly	Ala	Ser	Glu	Pro	Tyr	Thr	Gly	Ala	Glu	Pro	Thr	Phe	Ala					
					100					105					110					
gat	att	caa	gca	atc	gat	gat	tcc	cca	gtt	cgt	gca	ttc	ggt	aaa	gac	384				
Asp	Ile	Gln	Ala	Ile	Asp	Asp	Ser	Pro	Val	Arg	Ala	Phe	Gly	Lys	Asp					
					115					120					125					
gct	gaa	gaa	tcc	atg	atc	gcg	gaa	atc	gag	gcc	gca	aag	aaa	gcc	ggc	432				
Ala	Glu	Glu	Ser	Met	Ile	Ala	Glu	Ile	Glu	Ala	Ala	Lys	Lys	Ala	Gly					
130					135					140										
gat	acc	ctc	ggt	ggc	atc	gtg	gaa	gtg	att	gtt	gaa	ggc	ctg	ccc	atc	480				
Asp	Thr	Leu	Gly	Gly	Ile	Val	Glu	Val	Ile	Val	Glu	Gly	Leu	Pro	Ile					
145					150					155					160					
ggt	ttg	ggc	tca	cac	att	tct	ggc	gaa	gat	cgc	ctc	gat	gcg	cag	atc	528				
Gly	Leu	Gly	Ser	His	Ile	Ser	Gly	Glu	Asp	Arg	Leu	Asp	Ala	Gln	Ile					
					165					170					175					
gca	gct	gca	ctc	atg	ggc	att	cag	gcc	atc	aag	ggc	gtg	gaa	atc	ggt	576				
Ala	Ala	Ala	Leu	Met	Gly	Ile	Gln	Ala	Ile	Lys	Gly	Val	Glu	Ile	Gly					
					180					185					190					
gac	ggt	ttc	gaa	gaa	gct	cgt	cga	cgt	ggc	tcc	gaa	gcc	cac	gat	gaa	624				
Asp	Gly	Phe	Glu	Glu	Ala	Arg	Arg	Arg	Gly	Ser	Glu	Ala	His	Asp	Glu					
					195					200					205					
gtg	ttc	ctg	gat	gac	aac	ggc	gta	tac	cgc	aac	acc	aac	cgt	gca	ggt	672				
Val	Phe	Leu	Asp	Asp	Asn	Gly	Val	Tyr	Arg	Asn	Thr	Asn	Arg	Ala	Gly					
210					215					220										
ggc	ctc	gaa	ggc	ggc	atg	acc	aac	ggt	gaa	acc	ctg	cgc	gtt	cgt	gct	720				
Gly	Leu	Glu	Gly	Gly	Met	Thr	Asn	Gly	Glu	Thr	Leu	Arg	Val	Arg	Ala					
225					230					235					240					
ggc	atg	aag	cca	att	tct	act	gtg	cct	cgc	gcc	ctg	aaa	acc	att	gat	768				
Gly	Met	Lys	Pro	Ile	Ser	Thr	Val	Pro	Arg	Ala	Leu	Lys	Thr	Ile	Asp					
					245					250					255					
atg	gaa	aac	ggc	aag	gca	gca	acc	gga	atc	cac	cag	cgt	tcc	gac	gtg	816				
Met	Glu	Asn	Gly	Lys	Ala	Ala	Thr	Gly	Ile	His	Gln	Arg	Ser	Asp	Val					
					260					265					270					
tgc	gct	gtt	cca	gcc	gcc	ggt	gtc	gtt	gca	gaa	gca	atg	gtc	acc	ctg	864				
Cys	Ala	Val	Pro	Ala	Ala	Gly	Val	Val	Ala	Glu	Ala	Met	Val	Thr	Leu					
275					280					285										

Ala Glu Glu Ser Met Ile Ala Glu Ile Glu Ala Ala Lys Lys Ala Gly  
 210 215 220  
 Asp Thr Leu Gly Gly Ile Val Glu Val Ile Val Glu Gly Leu Pro Ile  
 225 230 235 240  
 Gly Leu Gly Ser His Ile Ser Gly Glu Asp Arg Leu Asp Ala Gln Ile  
 245 250 255  
 Ala Ala Ala Leu Met Gly Ile Gln Ala Ile Lys Gly Val Glu Ile Gly  
 260 265 270  
 Asp Gly Phe Glu Glu Ala Arg Arg Arg Gly Ser Glu Ala His Asp Glu  
 275 280 285  
 Val Phe Leu Asp Asp Asn Gly Val Tyr Arg Asn Thr Asn Arg Ala Gly  
 290 295 300  
 Gly Leu Glu Gly Gly Met Thr Asn Gly Glu Thr Leu Arg Val Arg Ala  
 305 310 315 320  
 Gly Met Lys Pro Ile Ser Thr Val Pro Arg Ala Leu Lys Thr Ile Asp  
 325 330 335  
 Met Glu Asn Gly Lys Ala Ala Thr Gly Ile His Gln Arg Ser Asp Val  
 340 345 350  
 Cys Ala Val Pro Ala Ala Gly Val Val Ala Glu Ala Met Val Thr Leu  
 355 360 365  
 Val Leu Ala Arg Ala Val Leu Gln Lys Phe Gly Gly Asp Ser Leu Ser  
 370 375 380  
 Glu Thr Lys Ser Asn Ile Asp Thr Tyr Leu Lys Asn Ile Glu Glu Arg  
 385 390 395 400  
 Met Lys Phe Glu Gly Leu Glu Asp Gly Ala  
 405 410

<210> 427  
 <211> 1013  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(990)  
 <223> FRXA01698

<400> 427  
 ggc aac act gag tgg gat aag tgg acc acc atc atg tcc tct gac gct 48  
 Gly Asn Thr Glu Trp Asp Lys Trp Thr Thr Ile Met Ser Ser Asp Ala  
 1 5 10 15  
 ttg gac atg gaa gac cca gat aac gtt gcg gcg atg tct tcg ggt cgg 96  
 Leu Asp Met Glu Asp Pro Asp Asn Val Ala Ala Met Ser Ser Gly Arg  
 20 25 30  
 ggc gca aaa ctg act cgt ccg cgt cca ggc cac gct gat tac gca ggc 144  
 Gly Ala Lys Leu Thr Arg Pro Arg Pro Gly His Ala Asp Tyr Ala Gly

gtc ctg cag aaa ttc ggc ggt gac tcc ctg agc gaa acc aag agc aac  
 1267  
 Val Leu Gln Lys Phe Gly Gly Asp Ser Leu Ser Glu Thr Lys Ser Asn  
           375                          380                          385

att gac acc tac ctc aaa aac att gag gaa cga atg aaa ttc gaa ggt  
 1315  
 Ile Asp Thr Tyr Leu Lys Asn Ile Glu Glu Arg Met Lys Phe Glu Gly  
           390                          395                          400                          405

tta gag gat gga gcg taatgaagtg aatgatcaaa ttc  
 1353  
 Leu Glu Asp Gly Ala  
                           410

<210> 426

<211> 410

<212> PRT

<213> Corynebacterium glutamicum

<400> 426

Met Leu Gly Met Leu Arg Trp Thr Thr Ala Gly Glu Ser His Gly Gln  
       1                          5                          10                          15

Ala Leu Ile Ala Thr Val Glu His Met Pro Ala Gly Val Pro Val Thr  
                           20                          25                          30

Lys Asp Glu Val Ser Tyr Gln Leu Ala Arg Arg Arg Leu Gly Tyr Gly  
           35                          40                          45

Arg Gly Ala Arg Met Lys Phe Glu Gln Asp Ala Leu Thr Phe Leu Thr  
           50                          55                          60

Gly Ile Arg His Gly Leu Thr Leu Gly Ser Pro Ile Ser Ile Met Ile  
       65                          70                          75                          80

Gly Asn Thr Glu Trp Asp Lys Trp Thr Thr Ile Met Ser Ser Asp Ala  
                           85                          90                          95

Leu Asp Met Glu Asp Pro Asp Asn Val Ala Ala Met Ser Ser Gly Arg  
           100                          105                          110

Gly Ala Lys Leu Thr Arg Pro Arg Pro Gly His Ala Asp Tyr Ala Gly  
           115                          120                          125

Met Leu Lys Tyr Gly Phe Asp Asp Ala Arg Asn Val Leu Glu Arg Ser  
           130                          135                          140

Ser Ala Arg Glu Thr Ala Ala Arg Val Ala Ala Ala Thr Val Ala Arg  
       145                          150                          155                          160

Ser Phe Leu Arg Glu Thr Leu Gly Val Glu Val Leu Ser His Val Ile  
                           165                          170                          175

Ser Ile Gly Ala Ser Glu Pro Tyr Thr Gly Ala Glu Pro Thr Phe Ala  
           180                          185                          190

Asp Ile Gln Ala Ile Asp Asp Ser Pro Val Arg Ala Phe Gly Lys Asp  
           195                          200                          205

gca gca cgc gtg gca gca gca acc gtt gcg cgt tcc ttc ctg cgt gaa 595  
 Ala Ala Arg Val Ala Ala Ala Thr Val Ala Arg Ser Phe Leu Arg Glu  
 150 155 160 165

acc ttg ggc gtg gaa gtg ctt tcc cac gta att tcc att ggt gcg tcc 643  
 Thr Leu Gly Val Glu Val Leu Ser His Val Ile Ser Ile Gly Ala Ser  
 170 175 180

gag cct tac act ggc gcg gag cca acc ttt gca gat att caa gca atc 691  
 Glu Pro Tyr Thr Gly Ala Glu Pro Thr Phe Ala Asp Ile Gln Ala Ile  
 185 190 195

gat gat tcc cca gtt cgt gca ttc ggt aaa gac gct gaa gaa tcc atg 739  
 Asp Asp Ser Pro Val Arg Ala Phe Gly Lys Asp Ala Glu Glu Ser Met  
 200 205 210

atc gcg gaa atc gag gcc gca aag aaa gcc ggc gat acc ctc ggt ggc 787  
 Ile Ala Glu Ile Glu Ala Ala Lys Lys Ala Gly Asp Thr Leu Gly Gly  
 215 220 225

atc gtg gaa gtg att gtt gaa ggc ctg ccc atc ggt ttg ggc tca cac 835  
 Ile Val Glu Val Ile Val Glu Gly Leu Pro Ile Gly Leu Gly Ser His  
 230 235 240 245

att tct ggc gaa gat cgc ctc gat gcg cag atc gca gct gca ctc atg 883  
 Ile Ser Gly Glu Asp Arg Leu Asp Ala Gln Ile Ala Ala Ala Leu Met  
 250 255 260

ggc att cag gcc atc aag ggc gtg gaa atc ggt gac ggt ttc gaa gaa 931  
 Gly Ile Gln Ala Ile Lys Gly Val Glu Ile Gly Asp Gly Phe Glu Glu  
 265 270 275

gct cgt cga cgt ggc tcc gaa gcc cac gat gaa gtg ttc ctg gat gac 979  
 Ala Arg Arg Arg Gly Ser Glu Ala His Asp Glu Val Phe Leu Asp Asp  
 280 285 290

aac ggc gta tac cgc aac acc aac cgt gca ggt ggc ctc gaa ggc ggc 1027  
 Asn Gly Val Tyr Arg Asn Thr Asn Arg Ala Gly Gly Leu Glu Gly Gly  
 295 300 305

atg acc aac ggt gaa acc ctg cgc gtt cgt gct ggc atg aag cca att 1075  
 Met Thr Asn Gly Glu Thr Leu Arg Val Arg Ala Gly Met Lys Pro Ile  
 310 315 320 325

tct act gtg cct cgc gcc ctg aaa acc att gat atg gaa aac ggc aag 1123  
 Ser Thr Val Pro Arg Ala Leu Lys Thr Ile Asp Met Glu Asn Gly Lys  
 330 335 340

gca gca acc gga atc cac cag cgt tcc gac gtg tgc gct gtt cca gcc 1171  
 Ala Ala Thr Gly Ile His Gln Arg Ser Asp Val Cys Ala Val Pro Ala  
 345 350 355

gcc ggt gtc gtt gca gaa gca atg gtc acc ctg gtt ctc gcc cgc gca 1219  
 Ala Gly Val Val Ala Glu Ala Met Val Thr Leu Val Leu Ala Arg Ala  
 360 365 370



Thr Pro Gln Thr Asp Gln Leu Ala Lys Leu His Lys Ala Asp Glu Trp  
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Val Arg Ala Ala Ser Glu Gly Arg Lys Leu Asn  
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<210> 425

<211> 1353

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101) .. (1330)

<223> RXN01698

<400> 425

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 Met Leu Gly Met Leu  
 1 5

cga tgg act aca gca ggt gaa tcc cac ggc cag gcg ctt atc gcc acg 163  
 Arg Trp Thr Thr Ala Gly Glu Ser His Gly Gln Ala Leu Ile Ala Thr  
 10 15 20

gtt gaa cac atg cca gca ggc gtg ccc gtg act aaa gat gag gtc tcg 211  
 Val Glu His Met Pro Ala Gly Val Pro Val Thr Lys Asp Glu Val Ser  
 25 30 35

tat caa ttg gcg cgc cga cgc ctt gga tat ggt cgc ggc gct cgc atg 259  
 Tyr Gln Leu Ala Arg Arg Arg Leu Gly Tyr Gly Arg Gly Ala Arg Met  
 40 45 50

aag ttt gag caa gac gcg ttg acc ttc ctc acc ggc atc cgc cac ggc 307  
 Lys Phe Glu Gln Asp Ala Leu Thr Phe Leu Thr Gly Ile Arg His Gly  
 55 60 65

ctc act ttg ggt agc ccc atc tca atc atg atc ggc aac act gag tgg 355  
 Leu Thr Leu Gly Ser Pro Ile Ser Ile Met Ile Gly Asn Thr Glu Trp  
 70 75 80 85

gat aag tgg acc acc atc atg tcc tct gac gct ttg gac atg gaa gac 403  
 Asp Lys Trp Thr Thr Ile Met Ser Ser Asp Ala Leu Asp Met Glu Asp  
 90 95 100

cca gat aac gtt gcg gcg atg tct tcg ggt cgg ggc gca aaa ctg act 451  
 Pro Asp Asn Val Ala Ala Met Ser Ser Gly Arg Gly Ala Lys Leu Thr  
 105 110 115

cgt ccg cgt cca ggc cac gct gat tac gca ggc atg ctc aag tac gga 499  
 Arg Pro Arg Pro Gly His Ala Asp Tyr Ala Gly Met Leu Lys Tyr Gly  
 120 125 130

ttc gat gat gcc cgc aac gtg ctg gag cgt tct tca gcc cgt gag acg 547  
 Phe Asp Asp Ala Arg Asn Val Leu Glu Arg Ser Ser Ala Arg Glu Thr  
 135 140 145

&lt;210&gt; 424

&lt;211&gt; 315

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 424

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Phe Thr Glu Glu Ala Leu Tyr Lys Phe Ala Asp Ala Gly Val Phe Gly
          20           25           30
Asp Gly Glu Ile Glu Gln Leu Pro Ala Lys Ser Pro Gln Glu Ala Val
          35           40           45
Asp Ala Val Arg His Gly Thr Ala Gln Phe Ala Val Val Ala Ile Glu
          50           55           60
Asn Phe Val Asp Gly Pro Val Thr Pro Thr Phe Asp Ala Leu Asp Gln
          65           70           75           80
Gly Ser Asn Val Gln Ile Ile Ala Glu Glu Glu Leu Asp Ile Ala Phe
          85           90           95
Ser Ile Met Val Arg Pro Gly Thr Ser Leu Ala Asp Val Lys Thr Leu
          100          105          110
Ala Thr His Pro Val Gly Tyr Gln Gln Val Lys Asn Trp Met Ala Thr
          115          120          125
Thr Ile Pro Asp Ala Met Tyr Leu Ser Ala Ser Ser Asn Gly Ala Gly
          130          135          140
Ala Gln Met Val Ala Glu Gly Thr Ala Asp Ala Ala Ala Ala Pro Ser
          145          150          155          160
Arg Ala Ala Glu Leu Phe Gly Leu Glu Arg Leu Val Asp Asp Val Ala
          165          170          175
Asp Val Arg Gly Ala Arg Thr Arg Phe Val Ala Val Gln Ala Gln Ala
          180          185          190
Ala Val Ser Glu Pro Thr Gly His Asp Arg Thr Ser Val Ile Phe Ser
          195          200          205
Leu Pro Asn Val Pro Gly Ser Leu Val Arg Ala Leu Asn Glu Phe Ala
          210          215          220
Ile Arg Gly Val Asp Leu Thr Arg Ile Glu Ser Arg Pro Thr Arg Lys
          225          230          235          240
Val Phe Gly Thr Tyr Arg Phe His Leu Asp Ile Ser Gly His Ile Arg
          245          250          255
Asp Ile Pro Val Ala Glu Ala Leu Arg Ala Leu His Leu Gln Ala Glu
          260          265          270
Glu Leu Val Phe Val Gly Ser Trp Pro Ser Asn Arg Ala Glu Asp Ser
          275          280          285

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atc atc gcc gaa gaa gaa ctc gac atc gcc ttt tcc atc atg gtc cgg 403  
 Ile Ile Ala Glu Glu Glu Leu Asp Ile Ala Phe Ser Ile Met Val Arg  
                     90                    95                    100

cca ggg act tcg ctt gcc gac gtc aaa acc ctc gcc acc cac ccg gtt 451  
 Pro Gly Thr Ser Leu Ala Asp Val Lys Thr Leu Ala Thr His Pro Val  
                     105                    110                    115

ggg tac caa caa gtg aaa aac tgg atg gca acc acc att ccg gac gcc 499  
 Gly Tyr Gln Gln Val Lys Asn Trp Met Ala Thr Thr Ile Pro Asp Ala  
                     120                    125                    130

atg tat ctt tca gca agc tcc aac ggc gcc ggc gca caa atg gtt gcc 547  
 Met Tyr Leu Ser Ala Ser Ser Asn Gly Ala Gly Ala Gln Met Val Ala  
                     135                    140                    145

gaa gga acc gcc gac gca gcc gca gcg ccc tcc cgc gca gcc gaa ctc 595  
 Glu Gly Thr Ala Asp Ala Ala Ala Pro Ser Arg Ala Ala Glu Leu  
                     150                    155                    160                    165

ttc gga ctg gaa cgc ctt gtt gat gat gtc gcc gac gtc cgt ggc gcc 643  
 Phe Gly Leu Glu Arg Leu Val Asp Asp Val Ala Asp Val Arg Gly Ala  
                     170                    175                    180

cgc acc cgc ttc gtt gct gtc caa gcc caa gca gcc gtt tcc gaa ccg 691  
 Arg Thr Arg Phe Val Ala Val Gln Ala Gln Ala Ala Val Ser Glu Pro  
                     185                    190                    195

acc ggc cac gac cgc acc tcc gtc att ttc tcc cta ccg aat gtg cca 739  
 Thr Gly His Asp Arg Thr Ser Val Ile Phe Ser Leu Pro Asn Val Pro  
                     200                    205                    210

ggc agc ctc gtg cgc gcc ctc aac gaa ttc gcc atc cgc ggc gtt gac 787  
 Gly Ser Leu Val Arg Ala Leu Asn Glu Phe Ala Ile Arg Gly Val Asp  
                     215                    220                    225

ctc acc cgc atc gaa tcc cgc ccc acc cgc aaa gtc ttc gga acc tac 835  
 Leu Thr Arg Ile Glu Ser Arg Pro Thr Arg Lys Val Phe Gly Thr Tyr  
                     230                    235                    240                    245

cgc ttc cac ctg gac ata tcc gga cat atc cgc gat atc ccc gtc gcc 883  
 Arg Phe His Leu Asp Ile Ser Gly His Ile Arg Asp Ile Pro Val Ala  
                     250                    255                    260

gaa gcc ctc cgc gca ctc cac ctc caa gcc gaa gaa ctc gtc ttc gtc 931  
 Glu Ala Leu Arg Ala Leu His Leu Gln Ala Glu Glu Leu Val Phe Val  
                     265                    270                    275

ggc tcc tgg ccc tcc aac cgt gcg gaa gac agc acg ccc caa acc gac 979  
 Gly Ser Trp Pro Ser Asn Arg Ala Glu Asp Ser Thr Pro Gln Thr Asp  
                     280                    285                    290

caa cta gct aag cta cac aag gcg gac gaa tgg gtt cgc gca gca agc  
 1027  
 Gln Leu Ala Lys Leu His Lys Ala Asp Glu Trp Val Arg Ala Ala Ser  
                     295                    300                    305

gaa gga agg aaa ctt aac tagccatggc cggccggatt att  
 1068  
 Glu Gly Arg Lys Leu Asn  
                     310                    315

260 265 270  
 Ala Cys Met Asn Met Gly Thr Leu Thr Gly Ala Pro Lys Leu Arg Ala  
 275 280 285  
 Met Glu Leu Leu Arg Gly Val Glu Lys Arg Arg Arg Gly Ser Tyr Gly  
 290 295 300  
 Gly Ala Val Gly Tyr Leu Arg Gly Asn Gly Asp Met Asp Asn Cys Ile  
 305 310 315 320  
 Val Ile Arg Ser Ala Phe Val Gln Asp Gly Val Ala Ala Val Gln Ala  
 325 330 335  
 Gly Ala Gly Val Val Arg Asp Ser Asn Pro Gln Ser Glu Ala Asp Glu  
 340 345 350  
 Thr Leu His Lys Ala Tyr Ala Val Leu Asn Ala Ile Ala Leu Ala Ala  
 355 360 365  
 Gly Ser Thr Leu Glu Val Ile Arg  
 370 375  
  
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 <223> RXA02687  
  
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 Met Ser Asp Ala Pro  
 1 5  
 act gtt gtg gcc tat ttg ggg cct gcc gga acc ttc acc gaa gaa gcc 163  
 Thr Val Val Ala Tyr Leu Gly Pro Ala Gly Thr Phe Thr Glu Glu Ala  
 10 15 20  
 ctc tac aaa ttt gcc gac gcc ggc gta ttc ggc gac ggt gag atc gag 211  
 Leu Tyr Lys Phe Ala Asp Ala Gly Val Phe Gly Asp Gly Glu Ile Glu  
 25 30 35  
 cag cta cca gcc aaa tcg cca caa gaa gct gtc gac gcc gtc cgc cac 259  
 Gln Leu Pro Ala Lys Ser Pro Gln Glu Ala Val Asp Ala Val Arg His  
 40 45 50  
 ggc acc gcc cag ttc gcg gtg gtc gcc atc gaa aac ttc gtc gac ggc 307  
 Gly Thr Ala Gln Phe Ala Val Val Ala Ile Glu Asn Phe Val Asp Gly  
 55 60 65  
 ccc gtc acc ccc acc ttc gac gcc ctt gac cag ggc tcc aac gtg caa 355  
 Pro Val Thr Pro Thr Phe Asp Ala Leu Asp Gln Gly Ser Asn Val Gln  
 70 75 80 85

ggt tcc act ttg gag gtc atc cga tgacacacgt tggtctcatt gat

1151

Gly Ser Thr Leu Glu Val Ile Arg

370

375

<210> 422

<211> 376

<212> PRT

<213> Corynebacterium glutamicum

<400> 422

Asp Phe Leu Glu Thr Phe Glu Thr Leu Pro Ala Val Glu Glu Ser Val  
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Asn Thr Tyr Pro Asp Tyr Gln Phe Val Leu Ala Glu Ile Val Leu Asp  
20 25 30

Ile Asn His Gln Asp Gln Thr Ala Lys Leu Ala Gly Val Ser Asn Ala  
35 40 45

Pro Gly Glu Leu Glu Ala Glu Leu Asn Lys Leu Ser Leu Leu Ile Asp  
50 55 60

Ala Ala Leu Pro Ala Thr Glu His Ala Tyr Gln Thr Thr Pro His Asp  
65 70 75 80

Gly Asp Thr Leu Arg Val Val Ala Asp Ile Pro Asp Ala Gln Phe Arg  
85 90 95

Thr Gln Ile Asn Glu Leu Lys Glu Asn Ile Tyr Asn Gly Asp Ile Tyr  
100 105 110

Gln Val Val Pro Ala Arg Thr Phe Thr Ala Pro Cys Pro Asp Ala Phe  
115 120 125

Ala Ala Tyr Leu Gln Leu Arg Ala Thr Asn Pro Ser Pro Tyr Met Phe  
130 135 140

Tyr Ile Arg Gly Leu Asn Glu Gly Arg Ser Tyr Glu Leu Phe Gly Ala  
145 150 155 160

Ser Pro Glu Ser Asn Leu Lys Phe Thr Ala Ala Asn Arg Glu Leu Gln  
165 170 175

Leu Tyr Pro Ile Ala Gly Thr Arg Pro Arg Gly Leu Asn Pro Asp Gly  
180 185 190

Ser Ile Asn Asp Glu Leu Asp Ile Arg Asn Glu Leu Asp Met Arg Thr  
195 200 205

Asp Ala Lys Glu Ile Ala Glu His Thr Met Leu Val Asp Leu Ala Arg  
210 215 220

Asn Asp Leu Ala Arg Val Ser Val Pro Ala Ser Arg Arg Val Ala Asp  
225 230 235 240

Leu Leu Gln Val Asp Arg Tyr Ser Arg Val Met His Leu Val Ser Arg  
245 250 255

Val Thr Ala Thr Leu Asp Pro Glu Leu Asp Ala Leu Asp Ala Tyr Arg

130	135	140	
tat atc cgt ggc ctc aac gaa ggc cgc tcc	tat gaa ctt ttt ggc gca	480	
Tyr Ile Arg Gly Leu Asn Glu Gly Arg Ser	Tyr Glu Leu Phe Gly Ala		
145	150 155 160		
tcc cct gag tcc aac ctc aag ttc acc gct	gct aac cgt gag ctg cag	528	
Ser Pro Glu Ser Asn Leu Lys Phe Thr	Ala Ala Asn Arg Glu Leu Gln		
165	170 175		
ctg tac cca atc gca ggt acc cgc ccc cgt	gga ctc aac cca gat ggc	576	
Leu Tyr Pro Ile Ala Gly Thr Arg Pro	Arg Gly Leu Asn Pro Asp Gly		
180	185 190		
tcc atc aac gat gag cta gat atc cgc aat	gag ttg gat atg cgc act	624	
Ser Ile Asn Asp Glu Leu Asp Ile Arg	Asn Glu Leu Asp Met Arg Thr		
195	200 205		
gat gcc aaa gag atc gcg gag cac acc atg	ctt gtc gat ctc gcc cgc	672	
Asp Ala Lys Glu Ile Ala Glu His Thr	Met Leu Val Asp Leu Ala Arg		
210	215 220		
aac gac ctg gcc cgc gtc tcg gtc cca gcg	tcg cgc cgg gtt gcg gat	720	
Asn Asp Leu Ala Arg Val Ser Val Pro	Ala Ser Arg Arg Val Ala Asp		
225	230 235 240		
ctt ttg cag gtg gat cgc tat tcc cgc gtg	atg cac ttg gtg tcc cgt	768	
Leu Leu Gln Val Asp Arg Tyr Ser Arg	Val Met His Leu Val Ser Arg		
245	250 255		
gtg acg gcg acg ttg gac cca gag ctt gat	gct ttg gac gcc tat cgg	816	
Val Thr Ala Thr Leu Asp Pro Glu Leu	Asp Ala Tyr Arg		
260	265 270		
gcg tgc atg aat atg ggc acg ttg acc ggc	gct ccg aag ttg cgc gct	864	
Ala Cys Met Asn Met Gly Thr Leu Thr	Gly Ala Pro Lys Leu Arg Ala		
275	280 285		
atg gag ctg ttg cgc ggc gtc gaa aag cgc	agg cgt ggt tct tat ggt	912	
Met Glu Leu Leu Arg Gly Val Glu Lys	Arg Arg Gly Ser Tyr Gly		
290	295 300		
ggg gca gtg ggg tac ctg cgc ggc aat ggc	gat atg gat aat tgc att	960	
Gly Ala Val Gly Tyr Leu Arg Gly Asn	Gly Asp Met Asp Asn Cys Ile		
305	310 315 320		
gtt att cgt tcg gcg ttt gtc cag gat ggt	gtg gct gct gtg cag gct	1008	
Val Ile Arg Ser Ala Phe Val Gln Asp	Gly Val Ala Ala Val Gln Ala		
325	330 335		
ggt gct ggt gtg gtc cgc gat tct aat cct	caa tct gaa gcc gat gag	1056	
Gly Ala Gly Val Val Arg Asp Ser Asn	Pro Gln Ser Glu Ala Asp Glu		
340	345 350		
acg ttg cac aag gcg tat gcc gtg ttg aat	gcc att gcg ctt gct gct	1104	
Thr Leu His Lys Ala Tyr Ala Val Leu	Asn Ala Ile Ala Leu Ala Ala		
355	360 365		

gaa ggc gca ccg ttt tct gca gca gct gca gca gcc gga att gat ccc 546  
 Glu Gly Ala Pro Phe Ser Ala Ala Ala Ala Ala Gly Ile Asp Pro  
 135 140 145 150  
  
 att tac atc gct ccg gcc aac gcc agc gag aaa acc ctc gag ggt gtc 594  
 Ile Tyr Ile Ala Pro Ala Asn Ala Ser Glu Lys Thr Leu Glu Gly Val  
 155 160 165  
  
 tcc gcc gca tca aag ggc tac atc tac gcc atc tcc cgc gac ggc gtc 642  
 Ser Ala Ala Ser Lys Gly Tyr Ile Tyr Ala Ile Ser Arg Asp Gly Val  
 170 175 180  
  
 acc ggc acc gaa cgt gaa tca tcc acc gac ggc ctg tcc gca gtg gtg 690  
 Thr Gly Thr Glu Arg Glu Ser Ser Thr Asp Gly Leu Ser Ala Val Val  
 185 190 195  
  
 gac aac atc aag aaa ttt gat ggc gca ccc atc ctc ttg ggc ttc ggc 738  
 Asp Asn Ile Lys Lys Phe Asp Gly Ala Pro Ile Leu Leu Gly Phe Gly  
 200 205 210  
  
 atc tca tcc cct cag cac gtg gca gac gcg att gca gcg ggt gct tcc 786  
 Ile Ser Ser Pro Gln His Val Ala Asp Ala Ile Ala Ala Gly Ala Ser  
 215 220 225 230  
  
 ggt gcg atc acg ggt tcc gcg atc acc aag atc att gct tcc cac tgc 834  
 Gly Ala Ile Thr Gly Ser Ala Ile Thr Lys Ile Ile Ala Ser His Cys  
 235 240 245  
  
 gaa ggt gag cac ccg aac ccg tcc acc att cga gat atg gac ggt ttg 882  
 Glu Gly Glu His Pro Asn Pro Ser Thr Ile Arg Asp Met Asp Gly Leu  
 250 255 260  
  
 aag aag gat ctc act gag ttc atc tct gcg atg aag gca gcg acc aag 930  
 Lys Lys Asp Leu Thr Glu Phe Ile Ser Ala Met Lys Ala Ala Thr Lys  
 265 270 275  
  
 aag gtt taggccttta aatgtggcaa tgt 959  
 Lys Val  
 280

&lt;210&gt; 444

&lt;211&gt; 280

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 444

Met Ser Arg Tyr Asp Asp Leu Phe Ala Arg Leu Asp Thr Ala Gly Glu  
 1 5 10 15  
  
 Gly Ala Phe Val Pro Phe Ile Met Leu Ser Asp Pro Ser Pro Glu Glu  
 20 25 30  
  
 Ala Phe Gln Ile Ile Ser Thr Ala Ile Glu Ala Gly Ala Asp Ala Leu  
 35 40 45  
  
 Glu Leu Gly Val Pro Phe Ser Asp Pro Val Ala Asp Gly Pro Thr Val  
 50 55 60  
  
 Ala Glu Ser His Leu Arg Ala Leu Asp Gly Gly Ala Thr Val Asp Ser  
 65 70 75 80

130 135 140

Asp Pro Ala Glu His Tyr Arg Asn Leu Val Lys Val Arg Thr Pro Leu  
 145 150 155 160

Tyr Glu Glu Val Ala Thr Tyr Arg Leu Arg Thr Asn Asn Arg Ser Pro  
 165 170 175

Gln Gln Val Val Ala Ala Val Leu His His Leu Glu Ile Asp  
 180 185 190

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 <223> RXA00952

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 Met Ser Arg Tyr Asp Asp  
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ctt ttt gca cgc ctc gac acg gca ggg gag ggc gcc ttt gtt ccc ttc 162  
 Leu Phe Ala Arg Leu Asp Thr Ala Gly Glu Gly Ala Phe Val Pro Phe  
 10 15 20

atc atg ctg agc gac cct tca cca gag gag gct ttc cag atc atc tcc 210  
 Ile Met Leu Ser Asp Pro Ser Pro Glu Glu Ala Phe Gln Ile Ile Ser  
 25 30 35

aca gca atc gaa gct ggc gca gat gca ctg gaa ctt ggc gta cct ttc 258  
 Thr Ala Ile Glu Ala Gly Ala Asp Ala Leu Glu Leu Gly Val Pro Phe  
 40 45 50

tcc gac cca gtt gcc gat ggc ccc acc gtc gcg gaa tcc cac ctc cgc 306  
 Ser Asp Pro Val Ala Asp Gly Pro Thr Val Ala Glu Ser His Leu Arg  
 55 60 65 70

gca ctc gac ggc ggc gcc acc gta gac agc gca ctc gag cag atc aag 354  
 Ala Leu Asp Gly Gly Ala Thr Val Asp Ser Ala Leu Glu Gln Ile Lys  
 75 80 85

cgc gtg cgc gca gcc tac cca gag gtt ccc atc gga atg ctc atc tac 402  
 Arg Val Arg Ala Ala Tyr Pro Glu Val Pro Ile Gly Met Leu Ile Tyr  
 90 95 100

ggc aac gtt cct ttc acc cgt ggc ttg gat cgc ttc tac caa gag ttc 450  
 Gly Asn Val Pro Phe Thr Arg Gly Leu Asp Arg Phe Tyr Gln Glu Phe  
 105 110 115

gct gaa gct ggc gca gac tcc atc ctc ctg cca gac gtc cca gtc cga 498  
 Ala Glu Ala Gly Ala Asp Ser Ile Leu Leu Pro Asp Val Pro Val Arg  
 120 125 130



His Val Ala Glu Ala Leu Lys Ser Ser Gly Val Val Ser Leu Gly Gly  
 90 95 100  
 gga tct gtg ctg aca gaa tcc acc cgt gaa ctg ctc aaa ggc cag gac 451  
 Gly Ser Val Leu Thr Glu Ser Thr Arg Glu Leu Leu Lys Gly Gln Asp  
 105 110 115  
 gtg gtc tgg atc gac gtg cca gta gaa gaa ggc atc agg cgc acc gca 499  
 Val Val Trp Ile Asp Val Pro Val Glu Glu Gly Ile Arg Arg Thr Ala  
 120 125 130  
 aac gag cgt tcc cgc ccc gtg ctg caa gcc gcc gac ccc gcc gag cac 547  
 Asn Glu Arg Ser Arg Pro Val Leu Gln Ala Ala Asp Pro Ala Glu His  
 135 140 145  
 tac cgc aac ctg gtg aaa gtg cgc acc ccg ttg tac gaa gag gtg gca 595  
 Tyr Arg Asn Leu Val Lys Val Arg Thr Pro Leu Tyr Glu Glu Val Ala  
 150 155 160 165  
 acc tac cga ctt cgc acc aac aac cgc agc ccc cag caa gtg gtg gca 643  
 Thr Tyr Arg Leu Arg Thr Asn Asn Arg Ser Pro Gln Gln Val Val Ala  
 170 175 180  
 gca gtg ttg cat cat cta gaa atc gat taattaaacc gggcacctga 690  
 Ala Val Leu His His Leu Glu Ile Asp  
 185 190  
 tta 693  
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 <213> *Corynebacterium glutamicum*  
 <400> 442  
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 Asp Asp Thr Ser Glu Cys Ser Cys Pro Ile Val Val Leu Val Gly Leu  
 20 25 30  
 Pro Gly Ala Gly Lys Ser Thr Ile Gly Arg Arg Leu Ala Arg Ala Leu  
 35 40 45  
 Asn Thr Glu Leu Val Asp Ser Asp Glu Leu Ile Glu Arg Ala Thr Gly  
 50 55 60  
 Lys Ala Cys Gly Ala Val Phe Ser Glu Leu Gly Glu Pro Ala Phe Arg  
 65 70 75 80  
 Glu Leu Glu Ala Ile His Val Ala Glu Ala Leu Lys Ser Ser Gly Val  
 85 90 95  
 Val Ser Leu Gly Gly Gly Ser Val Leu Thr Glu Ser Thr Arg Glu Leu  
 100 105 110  
 Leu Lys Gly Gln Asp Val Val Trp Ile Asp Val Pro Val Glu Glu Gly  
 115 120 125  
 Ile Arg Arg Thr Ala Asn Glu Arg Ser Arg Pro Val Leu Gln Ala Ala

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<222> (101)..(670)  
<223> RXA01699
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				Met	Glu	Arg	Asn	Glu								
				1				5								
gtg	aat	gat	caa	att	cac	tta	gat	cat	caa	tca	gat	gac	acc	tct	gaa	163
Val	Asn	Asp	Gln	Ile	His	Leu	Asp	His	Gln	Ser	Asp	Asp	Thr	Ser	Glu	
				10					15					20		
tgc	tcc	tgc	ccg	atc	gtg	gtt	ctt	gtg	ggg	ttg	cca	gga	gct	gga	aaa	211
Cys	Ser	Cys	Pro	Ile	Val	Val	Leu	Val	Gly	Leu	Pro	Gly	Ala	Gly	Lys	
			25					30					35			
tcc	acc	att	gga	cgt	cga	tta	gcg	cgc	gcc	tta	aac	act	gaa	ctc	gtc	259
Ser	Thr	Ile	Gly	Arg	Arg	Leu	Ala	Arg	Ala	Leu	Asn	Thr	Glu	Leu	Val	
		40					45					50				
gac	tcc	gac	gaa	ctg	att	gag	cgc	gcc	acc	gga	aaa	gcc	tgt	ggc	gcc	307
Asp	Ser	Asp	Glu	Leu	Ile	Glu	Arg	Ala	Thr	Gly	Lys	Ala	Cys	Gly	Ala	
	55					60					65					
gtg	ttc	agc	gag	ctc	ggc	gag	cca	gcc	ttc	cgc	gag	ctc	gag	gcc	atc	355
Val	Phe	Ser	Glu	Leu	Gly	Glu	Pro	Ala	Phe	Arg	Glu	Leu	Glu	Ala	Ile	
70					75					80					85	
cac	gtg	gcc	gaa	gca	ctg	aaa	tcc	tcc	gga	gtg	gtg	agc	ttg	gga	ggc	403

gca atc gca ggc ctc gaa gac acc ctt gcg atc gcc cca gtc ctc gac 739  
 Ala Ile Ala Gly Leu Glu Asp Thr Leu Ala Ile Ala Pro Val Leu Asp  
 200 205 210  
 gtc atc tac gac ccc tgg cca aca cca ctc gta gaa gtc aca cga gcc 787  
 Val Ile Tyr Asp Pro Trp Pro Thr Pro Leu Val Glu Val Thr Arg Ala  
 215 220 225  
 aaa ggc ctc aaa gct gtc gga ggc cac gtc atg ctg gca cac cag tcc 835  
 Lys Gly Leu Lys Ala Val Gly Gly His Val Met Leu Ala His Gln Ser  
 230 235 240 245  
 tac gga cag ttt gaa caa ttc acc gga atg gat gca ccc cgc gat gcc 883  
 Tyr Gly Gln Phe Glu Gln Phe Thr Gly Met Asp Ala Pro Arg Asp Ala  
 250 255 260  
 atg cgt gag gct ttg gaa gag tct tta ggc atc tca gaa gaa cac 928  
 Met Arg Glu Ala Leu Glu Glu Ser Leu Gly Ile Ser Glu Glu His  
 265 270 275  
 taagtcccg ccacctcctc aac 951

<210> 440  
 <211> 276  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 440  
 Leu Gly Ser His Ile Thr His Arg Ala Ala Val Leu Gly Ser Pro Ile  
 1 5 10 15  
 Glu His Ser Lys Ser Pro Val Leu His Asn Thr Gly Tyr Lys Ala Leu  
 20 25 30  
 Gly Leu Asp Gln Trp Glu Tyr Asp Arg Phe Glu Cys Thr Gly Asp Met  
 35 40 45  
 Leu Pro Gly Ile Val Ser Gly Ala Asp Glu Thr Tyr Cys Gly Phe Ser  
 50 55 60  
 Val Thr Met Pro Ser Lys Phe Ala Ala Leu Glu Phe Ala Asp Glu Val  
 65 70 75 80  
 Thr Glu Arg Ala Cys Ala Ile Gly Ser Ala Asn Thr Leu Leu Arg Thr  
 85 90 95  
 Ala Thr Gly Trp Arg Ala Asp Asn Thr Asp Val Asp Gly Ile Arg Gly  
 100 105 110  
 Ala Leu Gly Glu Leu Leu Gly Gly Ala Ser Leu Ala Gly Lys His Ala  
 115 120 125  
 Ile Val Ile Gly Ser Gly Gly Thr Ala Arg Pro Ala Ile Trp Ala Leu  
 130 135 140  
 Ile Glu Ala Gly Val Ala Arg Ile Thr Val Leu Asn Arg Ser Asp Arg  
 145 150 155 160  
 Thr Ala Glu Leu Gln Thr Leu Phe Asp Glu Thr Pro Thr Thr Leu Ala  
 165 170 175

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(928)

&lt;223&gt; RXA02791

&lt;400&gt; 439

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accgtgttca acgacacctt cgaagagcac gaagccgaca ttgagcaagc tttgaacagt 60
ggcgttcttag acagcaaccg ataaggatca gcgaataaaa ttg ggt tct cac atc 115
                                   Leu Gly Ser His Ile
                                   1 5
act cac cgg gcg gcc gta ctc ggc tca ccc atc gag cat tcc aaa tcc 163
Thr His Arg Ala Ala Val Leu Gly Ser Pro Ile Glu His Ser Lys Ser
                                   10 15 20
cca gtc ctc cac aac acc ggc tat aaa gcc ctc gga ctg gac caa tgg 211
Pro Val Leu His Asn Thr Gly Tyr Lys Ala Leu Gly Leu Asp Gln Trp
                                   25 30 35
gaa tac gac cgc ttt gag tgc acc ggc gac atg ctc ccc ggc atc gtc 259
Glu Tyr Asp Arg Phe Glu Cys Thr Gly Asp Met Leu Pro Gly Ile Val
                                   40 45 50
tcc ggc gct gat gaa acc tac tgc gga ttc tcc gtc acc atg ccg tct 307
Ser Gly Ala Asp Glu Thr Tyr Cys Gly Phe Ser Val Thr Met Pro Ser
                                   55 60 65
aaa ttc gca gct ctt gaa ttc gcc gac gaa gta acc gaa cgc gcc tgc 355
Lys Phe Ala Ala Leu Glu Phe Ala Asp Glu Val Thr Glu Arg Ala Cys
                                   70 75 80 85
gcc atc ggc tcc gca aac acc ttg ctg cgc acg gcc acc gga tgg cgc 403
Ala Ile Gly Ser Ala Asn Thr Leu Leu Arg Thr Ala Thr Gly Trp Arg
                                   90 95 100
gcc gac aac acc gac gtc gac ggc atc agg gga gct ctc ggt gaa ctc 451
Ala Asp Asn Thr Asp Val Asp Gly Ile Arg Gly Ala Leu Gly Glu Leu
                                   105 110 115
ctc ggc ggc gca tca ctg gcc ggc aaa cac gcc atc gtc atc ggc tcc 499
Leu Gly Gly Ala Ser Leu Ala Gly Lys His Ala Ile Val Ile Gly Ser
                                   120 125 130
ggc ggc acc gca cgc ccc gcc atc tgg gca ctc atc gaa gcc ggg gtc 547
Gly Gly Thr Ala Arg Pro Ala Ile Trp Ala Leu Ile Glu Ala Gly Val
                                   135 140 145
gcc cgg atc acg gtg ctc aac cgc tcc gat cgc acc gcc gaa ctg caa 595
Ala Arg Ile Thr Val Leu Asn Arg Ser Asp Arg Thr Ala Glu Leu Gln
                                   150 155 160 165
acg ctt ttc gac gaa acc ccc acc acc ttg gcc tac gcc ccg ctc gag 643
Thr Leu Phe Asp Glu Thr Pro Thr Thr Leu Ala Tyr Ala Pro Leu Glu
                                   170 175 180
cat ctc cac atc gaa gcc gac gtc gta gtc tct aca gtg ccc tcc gca 691
His Leu His Ile Glu Ala Asp Val Val Val Ser Thr Val Pro Ser Ala
                                   185 190 195

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&lt;211&gt; 268

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 438

```

Met Val Asn Tyr Val Asp Arg Glu Thr Thr Leu Cys Ile Ser Leu Ala
 1           5           10           15

Ala Arg Pro Ser Asn His Gly Val Arg Phe His Asn Trp Leu Tyr Ala
          20           25           30

Glu Leu Gly Leu Asn Tyr Leu Tyr Lys Ala Val Ala Pro Ala Asp Ile
      35           40           45

Thr Ala Ala Val Ala Gly Ile Arg Gly Leu Asn Ile Arg Gly Ala Gly
      50           55           60

Val Ser Met Pro Tyr Lys Ser Asp Val Ile Pro Leu Ile Asp Glu Leu
      65           70           75           80

His Pro Ser Ala Glu Arg Ile Arg Ser Val Asn Thr Ile Val Asn Asn
          85           90           95

Asp Gly His Leu Val Gly Tyr Asn Thr Asp Tyr Thr Ala Val Tyr His
          100          105          110

Leu Leu Glu Glu His Arg Val Asn Pro Asn Ala Arg Val Ala Ile Lys
      115          120          125

Gly Ser Gly Gly Met Ala Asn Ala Val Val Ala Ala Leu Ala Glu Tyr
      130          135          140

Gly Leu Ser Gly Thr Val Val Ala Arg Asn His Thr Thr Gly Ser Ala
      145          150          155          160

Leu Ala Ser Arg Tyr Gly Trp Glu Tyr Ser Ala Thr Val Pro Glu Asp
          165          170          175

Ala Lys Ile Leu Val Asn Val Thr Pro Met Gly Met Asn Gly Pro Asp
          180          185          190

Gln Asp Val Val Ser Phe Gly Glu Asp Glu Val Asp Arg Ala Asp Val
          195          200          205

Ile Phe Asp Cys Val Ala Phe Pro Val Glu Thr Pro Leu Ile Lys Leu
      210          215          220

Ala Lys Glu Lys Gly Lys Gln Thr Ile Asp Gly Gly Glu Val Ala Ala
      225          230          235          240

Leu Gln Ala Ala Glu Gln Phe His Leu Tyr Thr Gly Val Leu Pro Thr
          245          250          255

Asn Asp Gln Ile Ile Ala Ala Glu Glu Phe Ser Lys
          260          265

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&lt;210&gt; 439

&lt;211&gt; 951

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

Tyr Leu Tyr Lys Ala Val Ala Pro Ala Asp Ile Thr Ala Ala Val Ala  
           40                                  45                                  50  
 ggt atc cgt ggt ctg aac att cgc ggc gca ggt gtc tcc atg cca tac 307  
 Gly Ile Arg Gly Leu Asn Ile Arg Gly Ala Gly Val Ser Met Pro Tyr  
           55                                  60                                  65  
 aag agc gat gtc atc cca ctc atc gat gag ttg cat cct tcc gca gag 355  
 Lys Ser Asp Val Ile Pro Leu Ile Asp Glu Leu His Pro Ser Ala Glu  
           70                                  75                                  80                                  85  
 cgc ata cgt tct gtt aac acc atc gtc aac aat gac gga cac ctt gtc 403  
 Arg Ile Arg Ser Val Asn Thr Ile Val Asn Asn Asp Gly His Leu Val  
                                   90                                  95                                  100  
 gga tac aac acc gac tac act gcg gtg tac cac ctc ctt gaa gaa cac 451  
 Gly Tyr Asn Thr Asp Tyr Thr Ala Val Tyr His Leu Leu Glu Glu His  
                                   105                                  110                                  115  
 cgc gtg aac ccc aat gca cga gta gct atc aag gga tcc ggc ggc atg 499  
 Arg Val Asn Pro Asn Ala Arg Val Ala Ile Lys Gly Ser Gly Gly Met  
                                   120                                  125                                  130  
 gcc aat gct gtt gtt gca gct ctt gct gag tat ggt ctg agt ggc acc 547  
 Ala Asn Ala Val Val Ala Ala Leu Ala Glu Tyr Gly Leu Ser Gly Thr  
                                   135                                  140                                  145  
 gtc gtt gcc cgc aac cac acc acc ggt tct gcg cta gct tcc cgt tac 595  
 Val Val Ala Arg Asn His Thr Thr Gly Ser Ala Leu Ala Ser Arg Tyr  
                                   150                                  155                                  160                                  165  
 ggt tgg gaa tac tcc gca act gtt ccg gaa gac gca aaa att ttg gtt 643  
 Gly Trp Glu Tyr Ser Ala Thr Val Pro Glu Asp Ala Lys Ile Leu Val  
                                   170                                  175                                  180  
 aat gta acc cca atg gga atg aat gga cct gac caa gac gtt gta tct 691  
 Asn Val Thr Pro Met Gly Met Asn Gly Pro Asp Gln Asp Val Val Ser  
                                   185                                  190                                  195  
 ttt ggt gag gat gaa gta gac cga gcc gac gta atc ttt gac tgc gta 739  
 Phe Gly Glu Asp Glu Val Asp Arg Ala Asp Val Ile Phe Asp Cys Val  
                                   200                                  205                                  210  
 gca ttc ccc gtc gag acc cca ctg att aag ttg gcc aag gaa aag ggt 787  
 Ala Phe Pro Val Glu Thr Pro Leu Ile Lys Leu Ala Lys Glu Lys Gly  
                                   215                                  220                                  225  
 aag caa acc atc gac ggc gga gaa gtt gcc gct ctt cag gca gca gag 835  
 Lys Gln Thr Ile Asp Gly Gly Glu Val Ala Ala Leu Gln Ala Ala Glu  
                                   230                                  235                                  240                                  245  
 cag ttc cac ctc tac acc gga gtt ctt cca acc aac gac cag atc att 883  
 Gln Phe His Leu Tyr Thr Gly Val Leu Pro Thr Asn Asp Gln Ile Ile  
                                   250                                  255                                  260  
 gct gcg gag gag ttc tcc aag taaattttctc tcccctattt tta 927  
 Ala Ala Glu Glu Phe Ser Lys  
                                   265

&lt;210&gt; 438

Glu Gly Leu Pro Asn Ala Lys Leu Asp Ser Val Val Gln Val Gly Ala  
 100 105 110  
 Gly Gly Val Glu Asn Ala Val Ala Tyr Ala Leu Val Thr His Gly Val  
 115 120 125  
 Gln Lys Leu Gln Val Ala Asp Leu Asp Thr Ser Arg Ala Gln Ala Leu  
 130 135 140  
 Ala Asp Val Ile Asn Asn Ala Val Gly Arg Glu Ala Val Val Gly Val  
 145 150 155 160  
 Asp Ala Arg Gly Ile Glu Asp Val Ile Ala Ala Ala Asp Gly Val Val  
 165 170 175  
 Asn Ala Thr Pro Met Gly Met Pro Ala His Pro Gly Thr Ala Phe Asp  
 180 185 190  
 Val Ser Cys Leu Thr Lys Asp His Trp Val Gly Asp Val Val Tyr Met  
 195 200 205  
 Pro Ile Glu Thr Glu Leu Leu Lys Ala Ala Arg Ala Leu Gly Cys Glu  
 210 215 220  
 Thr Leu Asp Gly Thr Arg Met Ala Ile His Gln Ala Val Asp Ala Phe  
 225 230 235 240  
 Arg Leu Phe Thr Gly Leu Glu Pro Asp Val Ser Arg Met Arg Glu Thr  
 245 250 255  
 Phe Leu Ser Leu  
 260

&lt;210&gt; 437

&lt;211&gt; 927

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(904)

&lt;223&gt; RXA02093

&lt;400&gt; 437

ggcaggaatt tcccgaaaac ttccaccaat aatcaagcca tatcccacac aatcaggcat 60

ttgctcttcc tttgctccgc atgagtataa aatcactgtc atg gtc aac tac gtc 115  
 Met Val Asn Tyr Val  
 1 5

gac agg gaa aca acc ctg tgc atc tct ctc gct gct cgt cca tcc aac 163  
 Asp Arg Glu Thr Thr Leu Cys Ile Ser Leu Ala Ala Arg Pro Ser Asn  
 10 15 20

cat ggt gtt cgt ttc cac aac tgg ctt tac gct gaa ctt gga ttg aac 211  
 His Gly Val Arg Phe His Asn Trp Leu Tyr Ala Glu Leu Gly Leu Asn  
 25 30 35

tac ctg tac aag gct gtt gcc cca gca gat atc acc gct gca gtc gca 259

cag aaa ctt cag gtc gct gac ctc gac act tcc cgc gcg cag gca ctg 432  
 Gln Lys Leu Gln Val Ala Asp Leu Asp Thr Ser Arg Ala Gln Ala Leu  
 130 135 140

gca gat gtc atc aac aac gca gtc ggc cgt gaa gcc gtc gtg gga gta 480  
 Ala Asp Val Ile Asn Asn Ala Val Gly Arg Glu Ala Val Val Gly Val  
 145 150 155 160

gac gcc cgc ggc atc gaa gac gtc atc gcc gcc gcc gac gga gta gtc 528  
 Asp Ala Arg Gly Ile Glu Asp Val Ile Ala Ala Ala Asp Gly Val Val  
 165 170 175

aac gca acc ccc atg gga atg cca gca cac ccc ggc acc gcc ttt gat 576  
 Asn Ala Thr Pro Met Gly Met Pro Ala His Pro Gly Thr Ala Phe Asp  
 180 185 190

gtc agc tgc ctc acc aag gat cac tgg gtt ggc gac gtc gtg tac atg 624  
 Val Ser Cys Leu Thr Lys Asp His Trp Val Gly Asp Val Val Tyr Met  
 195 200 205

ccc atc gaa act gaa ctt ctc aaa gcc gcc cgt gcc ctc ggc tgc gaa 672  
 Pro Ile Glu Thr Glu Leu Leu Lys Ala Ala Arg Ala Leu Gly Cys Glu  
 210 215 220

acc ctc gac gga acc cgc atg gca atc cac caa gcc gtc gat gcc ttc 720  
 Thr Leu Asp Gly Thr Arg Met Ala Ile His Gln Ala Val Asp Ala Phe  
 225 230 235 240

cga ctg ttc acc ggc ctc gaa ccc gac gtc tcc cgc atg cgg gaa act 768  
 Arg Leu Phe Thr Gly Leu Glu Pro Asp Val Ser Arg Met Arg Glu Thr  
 245 250 255

ttc ctg tcc ctc taaaagagtc agtaaaacct cga 803  
 Phe Leu Ser Leu  
 260

<210> 436  
 <211> 260  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 436  
 Glu Ala Lys Gly Leu Ala Gln Gly Arg Ala Thr Val Tyr Arg Arg Ile  
 1 5 10 15  
 Asp Thr Leu Gly Ser Arg Ala Ser Gly Gln Asp Leu Asn Thr Leu Leu  
 20 25 30  
 Asp Ala Ala Leu Tyr Leu Gly Phe Ser Gly Leu Asn Ile Thr His Pro  
 35 40 45  
 Tyr Lys Gln Ala Val Leu Pro Leu Leu Gly Glu Val Ser Glu Gln Ala  
 50 55 60  
 Thr Gln Leu Gly Ala Val Asn Thr Val Val Met Asp Ala Thr Gly His  
 65 70 75 80  
 Thr Thr Gly His Asn Thr Asp Val Ser Gly Phe Gly Arg Gly Met Glu  
 85 90 95



His Pro Thr Pro Ala Ile Cys Gly Thr Pro Thr Asp Ala Ala Glu Ala  
 65 70 75 80  
 Leu Ile Ile Glu Ala Glu Ser Pro Arg Asn Phe Tyr Ala Gly Ala Ala  
 85 90 95  
 Gly Trp Cys Asp Ser Thr Gly Asp Gly Glu Tyr Met Val Ala Ile Arg  
 100 105 110  
 Cys Ala Glu Val Ser Glu Asp Gly Thr Trp Ala Arg Ala Trp Ala Gly  
 115 120 125  
 Gly Gly Ile Val Ala Glu Ser Asp Ala Gln Glu Glu Phe Asp Glu Thr  
 130 135 140  
 Thr Ala Lys Leu Gln Thr Ile Met Arg Ser Leu Gly Leu  
 145 150 155

<210> 435  
 <211> 803  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (1)..(780)  
 <223> RXA00229

<400> 435  
 gag gcg aaa ggc ctc gcg cag gga cgt gcg acg gtg tac agg cgc atc 48  
 Glu Ala Lys Gly Leu Ala Gln Gly Arg Ala Thr Val Tyr Arg Arg Ile  
 1 5 10 15  
 gac acg ctt ggg tgc cgt gct tcc ggg caa gat tta aat acg ctt ctc 96  
 Asp Thr Leu Gly Ser Arg Ala Ser Gly Gln Asp Leu Asn Thr Leu Leu  
 20 25 30  
 gac gcc gcc ctc tac ctt ggc ttc agc ggc ctg aac atc act cac ccg 144  
 Asp Ala Ala Leu Tyr Leu Gly Phe Ser Gly Leu Asn Ile Thr His Pro  
 35 40 45  
 tac aag caa gca gta tta ccc ctg ctt ggc gaa gtc tcc gaa caa gcc 192  
 Tyr Lys Gln Ala Val Leu Pro Leu Leu Gly Glu Val Ser Glu Gln Ala  
 50 55 60  
 acc caa ctc ggc gca gtg aat act gtc gtt atg gac gcc acc ggc cac 240  
 Thr Gln Leu Gly Ala Val Asn Thr Val Val Met Asp Ala Thr Gly His  
 65 70 75 80  
 acc acc ggc cac aac acc gac gtc tcc gga ttt ggc cgc gga atg gaa 288  
 Thr Thr Gly His Asn Thr Asp Val Ser Gly Phe Gly Arg Gly Met Glu  
 85 90 95  
 gaa ggc ctc ccc aac gcc aag ctc gat tcc gtc gtg cag gtc ggc gcc 336  
 Glu Gly Leu Pro Asn Ala Lys Leu Asp Ser Val Val Gln Val Gly Ala  
 100 105 110  
 ggc ggc gta gaa aac gca gtg gca tac gcc ctg gtc acc cac ggt gtg 384  
 Gly Gly Val Glu Asn Ala Val Ala Tyr Ala Leu Val Thr His Gly Val  
 115 120 125

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gcc aaa aac cta gaa gaa cac tcc tac gtg gtc aac cac ctg cgc acc 48
Ala Lys Asn Leu Glu Glu His Ser Tyr Val Val Asn His Leu Arg Thr
1 5 10 15

atc ctg gaa cca ctg tgc tca caa ttc gac gcc cca aca gtt cct gaa 96
Ile Leu Glu Pro Leu Cys Ser Gln Phe Asp Ala Pro Thr Val Pro Glu
20 25 30

ctg acc aaa acc aac gaa atg tgg cac ctc gca aca ccc atc gtt ggc 144
Leu Thr Lys Thr Asn Glu Met Trp His Leu Ala Thr Pro Ile Val Gly
35 40 45

acc ctc aag tac cca cac atc acc gca cta gaa cta gcc ata cga aca 192
Thr Leu Lys Tyr Pro His Ile Thr Ala Leu Glu Leu Ala Ile Arg Thr
50 55 60

cac ccc acc ccc gcg atc tgt ggc acc ccc acc gac gcc gcc gaa gcc 240
His Pro Thr Pro Ala Ile Cys Gly Thr Pro Thr Asp Ala Ala Glu Ala
65 70 75 80

ctc atc atc gaa gcg gaa tcc ccc cga aac ttc tac gcc gga gca gcc 288
Leu Ile Ile Glu Ala Glu Ser Pro Arg Asn Phe Tyr Ala Gly Ala Ala
85 90 95

ggc tgg tgt gac tcc acc gga gac ggc gaa tac atg gta gcc atc cgc 336
Gly Trp Cys Asp Ser Thr Gly Asp Gly Glu Tyr Met Val Ala Ile Arg
100 105 110

tgc gcc gaa gta tcc gaa gac gga acc tgg gcc aga gca tgg gca ggc 384
Cys Ala Glu Val Ser Glu Asp Gly Thr Trp Ala Arg Ala Trp Ala Gly
115 120 125

gga ggc atc gtc gcc gaa tca gac gcc caa gaa gag ttt gat gaa acc 432
Gly Gly Ile Val Ala Glu Ser Asp Ala Gln Glu Glu Phe Asp Glu Thr
130 135 140

acc gcg aag ctc caa acc atc atg cgc tcg ctt ggt ttg tgagatgtgg 481
Thr Ala Lys Leu Gln Thr Ile Met Arg Ser Leu Gly Leu
145 150 155

tcttaaaaca ccg 494

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&lt;210&gt; 434

&lt;211&gt; 157

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 434

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Ala Lys Asn Leu Glu Glu His Ser Tyr Val Val Asn His Leu Arg Thr
1 5 10 15

Ile Leu Glu Pro Leu Cys Ser Gln Phe Asp Ala Pro Thr Val Pro Glu
20 25 30

Leu Thr Lys Thr Asn Glu Met Trp His Leu Ala Thr Pro Ile Val Gly
35 40 45

Thr Leu Lys Tyr Pro His Ile Thr Ala Leu Glu Leu Ala Ile Arg Thr
50 55 60

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&lt;223&gt; RXN00448

&lt;400&gt; 451

ccatttacct tcaactaagg tagccgtaac tgcaaagctc aggccatcct cttcagtggt 60

catagagata accgtagtag gtatgtgccca cacttgtcag gtg act acc aaa gac 115  
 Val Thr Thr Lys Asp  
 1 5

att tcc cgc cca gta tgc atc ctg ggc ctc ggc ctc atc ggc gga tcc 163  
 Ile Ser Arg Pro Val Cys Ile Leu Gly Leu Gly Leu Ile Gly Gly Ser  
 10 15 20

ctc ctc cgc gac ctc cat gca gcc aac cac tcc gtc ttc ggc tac aac 211  
 Leu Leu Arg Asp Leu His Ala Ala Asn His Ser Val Phe Gly Tyr Asn  
 25 30 35

cgc tca cgc tcc ggc gct aaa tca gcc gtc gac gaa ggc ttc gac gtt 259  
 Arg Ser Arg Ser Gly Ala Lys Ser Ala Val Asp Glu Gly Phe Asp Val  
 40 45 50

tcc gcc gat ctt gaa gca acc ctc cag cgt gca gcc gcc gaa gat gcg 307  
 Ser Ala Asp Leu Glu Ala Thr Leu Gln Arg Ala Ala Ala Glu Asp Ala  
 55 60 65

ctc atc gtc ctc gcg gtc ccc atg acc gca atc gat tcg ctt ctc gac 355  
 Leu Ile Val Leu Ala Val Pro Met Thr Ala Ile Asp Ser Leu Leu Asp  
 70 75 80 85

gcc gtc cac acc cac gca cca aac aac ggc ttc acc gac gtc gta tcc 403  
 Ala Val His Thr His Ala Pro Asn Asn Gly Phe Thr Asp Val Val Ser  
 90 95 100

gta aaa acc gcc gtc tac gac gca gta aaa gcc cgc aac atg caa cac 451  
 Val Lys Thr Ala Val Tyr Asp Ala Val Lys Ala Arg Asn Met Gln His  
 105 110 115

cgt tat gtg gga tcc cac ccc atg gca ggc acc gcc aac tcc ggc tgg 499  
 Arg Tyr Val Gly Ser His Pro Met Ala Gly Thr Ala Asn Ser Gly Trp  
 120 125 130

agc gca tcc atg gac gga ctg ttc aaa cga gca gta tgg gtg gtc acc 547  
 Ser Ala Ser Met Asp Gly Leu Phe Lys Arg Ala Val Trp Val Val Thr  
 135 140 145

ttc gac cag ctt ttc gac ggc acc gac atc aac tcc acc tgg atc agc 595  
 Phe Asp Gln Leu Phe Asp Gly Thr Asp Ile Asn Ser Thr Trp Ile Ser  
 150 155 160 165

atc tgg aaa gac gtc gtc caa atg gca ctc gcc gtg ggc gct gaa gtt 643  
 Ile Trp Lys Asp Val Val Gln Met Ala Leu Ala Val Gly Ala Glu Val  
 170 175 180

gtc cca tcc cga gtt ggc cca cac gat gca gca gca gca cga gtg tct 691  
 Val Pro Ser Arg Val Gly Pro His Asp Ala Ala Ala Ala Arg Val Ser  
 185 190 195

cat tta aca cac atc ctg gct gaa acc ctc gcc atc gtc ggt gac aac 739  
 His Leu Thr His Ile Leu Ala Glu Thr Leu Ala Ile Val Gly Asp Asn  
 200 205 210

Met Asn Glu Asp Gly Pro Asp Met Asp Ala Val Glu Glu Leu Val Lys  
 165 170 175  
 Asn Pro Gln Val Lys Gly Met Trp Val Val Pro Val Phe Ser Asn Pro  
 180 185 190  
 Thr Gly Phe Thr Val Thr Glu Asp Val Ala Lys Arg Leu Ser Ala Met  
 195 200 205  
 Glu Thr Ala Ala Pro Asp Phe Arg Val Val Trp Asp Asn Ala Tyr Ala  
 210 215 220  
 Val His Thr Leu Thr Asp Glu Phe Pro Glu Val Ile Asp Ile Val Gly  
 225 230 235 240  
 Leu Gly Glu Ala Ala Gly Asn Pro Asn Arg Phe Trp Ala Phe Thr Ser  
 245 250 255  
 Thr Ser Lys Ile Thr Leu Ala Gly Ala Gly Val Ser Phe Phe Leu Thr  
 260 265 270  
 Ser Ala Glu Asn Arg Lys Trp Tyr Thr Gly His Ala Gly Ile Arg Gly  
 275 280 285  
 Ile Gly Pro Asn Lys Val Asn Gln Leu Ala His Ala Arg Tyr Phe Gly  
 290 295 300  
 Asp Ala Glu Gly Val Arg Ala Val Met Arg Lys His Ala Ala Ser Leu  
 305 310 315 320  
 Ala Pro Lys Phe Asn Lys Val Leu Glu Ile Leu Asp Ser Arg Leu Ala  
 325 330 335  
 Glu Tyr Gly Val Ala Gln Trp Thr Val Pro Ala Gly Gly Tyr Phe Ile  
 340 345 350  
 Ser Leu Asp Val Val Pro Gly Thr Ala Ser Arg Val Ala Glu Leu Ala  
 355 360 365  
 Lys Glu Ala Gly Ile Ala Leu Thr Gly Ala Gly Ser Ser Tyr Pro Leu  
 370 375 380  
 Arg Gln Asp Pro Glu Asn Lys Asn Leu Arg Leu Ala Pro Ser Leu Pro  
 385 390 395 400  
 Pro Val Glu Glu Leu Glu Val Ala Met Asp Gly Val Ala Thr Cys Val  
 405 410 415  
 Leu Leu Ala Ala Ala Glu His Tyr Ala Asn  
 420 425

&lt;210&gt; 451

&lt;211&gt; 1143

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1120)

cct ggt acg gcg tct cgc gtg gct gag ttg gct aag gaa gcc ggc atc  
 1219  
 Pro Gly Thr Ala Ser Arg Val Ala Glu Leu Ala Lys Glu Ala Gly Ile  
           360                                  365                                  370

gcg ttg acg ggt gcg ggt tct tct tac ccg ctg cgt cag gat ccg gag  
 1267  
 Ala Leu Thr Gly Ala Gly Ser Ser Tyr Pro Leu Arg Gln Asp Pro Glu  
           375                                  380                                  385

aac aaa aat ctc cgt ttg gca ccg tcg ctg cct cca gtt gag gaa ctt  
 1315  
 Asn Lys Asn Leu Arg Leu Ala Pro Ser Leu Pro Pro Val Glu Glu Leu  
           390                                  395                                  400                                  405

gag gtt gcc atg gat ggc gtg gct acc tgt gtg ctg ttg gca gca gcg  
 1363  
 Glu Val Ala Met Asp Gly Val Ala Thr Cys Val Leu Leu Ala Ala Ala  
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 Glu His Tyr Ala Asn  
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<212> PRT

<213> Corynebacterium glutamicum

<400> 450

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Phe His Glu Asp Ile Lys Arg Lys Phe Asp Glu Leu Lys Ser Lys Asn  
                                   20                                  25                                  30

Leu Lys Leu Asp Leu Thr Arg Gly Lys Pro Ser Ser Glu Gln Leu Asp  
                                   35                                  40                                  45

Phe Ala Asp Glu Leu Leu Ala Leu Pro Gly Lys Gly Asp Phe Lys Ala  
                                   50                                  55                                  60

Ala Asp Gly Thr Asp Val Arg Asn Tyr Gly Gly Leu Asp Gly Ile Val  
                                   65                                  70                                  75                                  80

Asp Ile Arg Gln Ile Trp Ala Asp Leu Leu Gly Val Pro Val Glu Gln  
                                   85                                  90                                  95

Val Leu Ala Gly Asp Ala Ser Ser Leu Asn Ile Met Phe Asp Val Ile  
                                   100                                  105                                  110

Ser Trp Ser Tyr Ile Phe Gly Asn Asn Asp Ser Val Gln Pro Trp Ser  
                                   115                                  120                                  125

Lys Glu Glu Thr Val Lys Trp Ile Cys Pro Val Pro Gly Tyr Asp Arg  
                                   130                                  135                                  140

His Phe Ser Ile Thr Glu Arg Phe Gly Phe Glu Met Ile Ser Val Pro  
                                   145                                  150                                  155                                  160

aag tgg att tgc cct gtt ccg ggc tat gat cgc cat ttc tcc atc acg 547  
 Lys Trp Ile Cys Pro Val Pro Gly Tyr Asp Arg His Phe Ser Ile Thr  
 135 140 145

gag cgt ttc ggc ttt gag atg att tct gtg cca atg aat gaa gac ggc 595  
 Glu Arg Phe Gly Phe Glu Met Ile Ser Val Pro Met Asn Glu Asp Gly  
 150 155 160 165

cct gat atg gat gct gtt gag gaa ttg gtg aag aat ccg cag gtt aag 643  
 Pro Asp Met Asp Ala Val Glu Glu Leu Val Lys Asn Pro Gln Val Lys  
 170 175 180

ggc atg tgg gtt gtt ccg gtg ttt tct aac ccg act ggt ttc acg gtg 691  
 Gly Met Trp Val Val Pro Val Phe Ser Asn Pro Thr Gly Phe Thr Val  
 185 190 195

aca gaa gac gtc gca aag cgt cta agc gca atg gaa acc gca gct ccg 739  
 Thr Glu Asp Val Ala Lys Arg Leu Ser Ala Met Glu Thr Ala Ala Pro  
 200 205 210

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 215 220 225

gat gaa ttc cct gag gtt atc gat atc gtc ggg ctt ggt gag gcc gct 835  
 Asp Glu Phe Pro Glu Val Ile Asp Ile Val Gly Leu Gly Glu Ala Ala  
 230 235 240 245

ggc aac ccg aac cgt ttc tgg gcg ttc act tct act tcg aag atc act 883  
 Gly Asn Pro Asn Arg Phe Trp Ala Phe Thr Ser Thr Ser Lys Ile Thr  
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ctc gcg ggt gcg ggc gtg tcg ttc ttc ctc acc tct gcg gag aac cgc 931  
 Leu Ala Gly Ala Gly Val Ser Phe Phe Leu Thr Ser Ala Glu Asn Arg  
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aag tgg tac acc ggc cat gcg ggt atc cgt ggc att ggc cct aac aag 979  
 Lys Trp Tyr Thr Gly His Ala Gly Ile Arg Gly Ile Gly Pro Asn Lys  
 280 285 290

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 1027  
 Val Asn Gln Leu Ala His Ala Arg Tyr Phe Gly Asp Ala Glu Gly Val  
 295 300 305

cgc gcg gtg atg cgt aag cat gct gcg tcg ttg gct ccg aag ttc aac  
 1075  
 Arg Ala Val Met Arg Lys His Ala Ala Ser Leu Ala Pro Lys Phe Asn  
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aag gtt ctg gag att ctg gat tct cgc ctt gct gag tac ggt gtc gcg  
 1123  
 Lys Val Leu Glu Ile Leu Asp Ser Arg Leu Ala Glu Tyr Gly Val Ala  
 330 335 340

cag tgg act gtc cct gcg ggc ggt tac ttc att tcc ctt gat gtg gtt  
 1171  
 Gln Trp Thr Val Pro Ala Gly Gly Tyr Phe Ile Ser Leu Asp Val Val  
 345 350 355

325 330 335  
 Val Gly Ile Thr Asp Ala Glu Ala Leu Gln Ala Phe Gln Tyr Leu Ala  
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 <213> Corynebacterium glutamicum

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 <223> RXA00064

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 Met Ser Ser Val Ser  
 1 5  
 ctg cag gat ttt gat gca gag cga att ggt ttg ttc cac gag gac att 163  
 Leu Gln Asp Phe Asp Ala Glu Arg Ile Gly Leu Phe His Glu Asp Ile  
 10 15 20  
 aag cgc aag ttt gat gag ctc aag tca aaa aat ctg aag ctg gat ctt 211  
 Lys Arg Lys Phe Asp Glu Leu Lys Ser Lys Asn Leu Lys Leu Asp Leu  
 25 30 35  
 act cgc ggt aag cct tcg tcg gag cag ttg gat ttc gct gat gag ttg 259  
 Thr Arg Gly Lys Pro Ser Ser Glu Gln Leu Asp Phe Ala Asp Glu Leu  
 40 45 50  
 ttg gcg ttg cct ggt aag ggt gat ttc aag gct gcg gat ggt act gat 307  
 Leu Ala Leu Pro Gly Lys Gly Asp Phe Lys Ala Ala Asp Gly Thr Asp  
 55 60 65  
 gtc cgt aac tat ggc ggg ctg gat ggc atc gtt gat att cgc cag att 355  
 Val Arg Asn Tyr Gly Gly Leu Asp Gly Ile Val Asp Ile Arg Gln Ile  
 70 75 80 85  
 tgg gcg gat ttg ctg ggt gtt cct gtg gag cag gtc ttg gcg ggg gat 403  
 Trp Ala Asp Leu Leu Gly Val Pro Val Glu Gln Val Leu Ala Gly Asp  
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 gct tcg agc ttg aac atc atg ttt gat gtg atc agc tgg tcg tac att 451  
 Ala Ser Ser Leu Asn Ile Met Phe Asp Val Ile Ser Trp Ser Tyr Ile  
 105 110 115  
 ttc ggt aac aat gat tcg gtt cag cct tgg tcg aag gaa gaa acc gtt 499  
 Phe Gly Asn Asn Asp Ser Val Gln Pro Trp Ser Lys Glu Glu Thr Val  
 120 125 130

Met Thr Glu Lys Glu Asn Leu Gly Gly Ser Thr Leu Leu Pro Ala Tyr  
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 Phe Gly Glu Phe Gly Gly Gln Phe Val Ala Glu Ser Leu Leu Pro Ala  
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 Leu Asp Gln Leu Glu Lys Ala Phe Val Asp Ala Thr Asn Ser Pro Glu  
 35 40 45  
 Phe Arg Glu Glu Leu Gly Gly Tyr Leu Arg Asp Tyr Leu Gly Arg Pro  
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 Thr Pro Leu Thr Glu Cys Ser Asn Leu Pro Leu Ala Gly Glu Gly Lys  
 65 70 75 80  
 Gly Phe Ala Arg Ile Phe Leu Lys Arg Glu Asp Leu Val His Gly Gly  
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 Ala His Lys Thr Asn Gln Val Ile Gly Gln Val Leu Leu Ala Lys Arg  
 100 105 110  
 Met Gly Lys Thr Arg Ile Ile Ala Glu Thr Gly Ala Gly Gln His Gly  
 115 120 125  
 Thr Ala Thr Ala Leu Ala Cys Ala Leu Met Gly Leu Glu Cys Val Val  
 130 135 140  
 Tyr Met Gly Ala Lys Asp Val Ala Arg Gln Gln Pro Asn Val Tyr Arg  
 145 150 155 160  
 Met Gln Leu His Gly Ala Lys Val Ile Pro Val Glu Ser Gly Ser Gly  
 165 170 175  
 Thr Leu Lys Asp Ala Val Asn Glu Ala Leu Arg Asp Trp Thr Ala Thr  
 180 185 190  
 Phe His Glu Ser His Tyr Leu Leu Gly Thr Pro Ala Gly Pro His Pro  
 195 200 205  
 Phe Pro Thr Ile Val Arg Glu Phe His Lys Val Ile Ser Glu Glu Ala  
 210 215 220  
 Lys Ala Gln Met Leu Glu Arg Thr Gly Lys Leu Pro Asp Val Val Val  
 225 230 235 240  
 Ala Cys Val Gly Gly Gly Ser Asn Ala Ile Gly Met Phe Ala Asp Phe  
 245 250 255  
 Ile Asp Asp Glu Gly Val Glu Leu Val Gly Ala Glu Pro Ala Gly Glu  
 260 265 270  
 Gly Leu Asp Ser Gly Lys His Gly Ala Thr Ile Thr Asn Gly Gln Ile  
 275 280 285  
 Gly Ile Leu His Gly Thr Arg Ser Tyr Leu Met Arg Asn Ser Asp Gly  
 290 295 300  
 Gln Val Glu Glu Ser Tyr Ser Ile Ser Ala Gly Leu Asp Tyr Pro Gly  
 305 310 315 320  
 Val Gly Pro Gln His Ala His Leu His Ala Thr Gly Arg Ala Thr Tyr



tac ctt ctc ggc acc ccc gcc ggc ccg cac cca ttc cca acc atc gtg 739  
 Tyr Leu Leu Gly Thr Pro Ala Gly Pro His Pro Phe Pro Thr Ile Val  
 200 205 210

cgt gaa ttc cac aag gtg atc tct gag gaa gcc aag gca cag atg cta 787  
 Arg Glu Phe His Lys Val Ile Ser Glu Glu Ala Lys Ala Gln Met Leu  
 215 220 225

gag cgc acc ggc aag ctt ccc gac gtt gtg gtc gcc tgt gtc ggt ggt 835  
 Glu Arg Thr Gly Lys Leu Pro Asp Val Val Val Ala Cys Val Gly Gly  
 230 235 240 245

ggc tcc aac gcc atc ggc atg ttc gca gac ttc att gac gat gaa ggt 883  
 Gly Ser Asn Ala Ile Gly Met Phe Ala Asp Phe Ile Asp Asp Glu Gly  
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gta gag ctc gtc ggc gct gag cca gcc ggt gaa ggc ctc gac tcc ggc 931  
 Val Glu Leu Val Gly Ala Glu Pro Ala Gly Glu Gly Leu Asp Ser Gly  
 265 270 275

aag cac ggc gca acc atc acc aac ggt cag atc ggc atc ctg cac ggc 979  
 Lys His Gly Ala Thr Ile Thr Asn Gly Gln Ile Gly Ile Leu His Gly  
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acc cgt tcc tac ctg atg cgc aac tcc gac ggc caa gtg gaa gag tcc  
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 Thr Arg Ser Tyr Leu Met Arg Asn Ser Asp Gly Gln Val Glu Glu Ser  
 295 300 305

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 Tyr Ser Ile Ser Ala Gly Leu Asp Tyr Pro Gly Val Gly Pro Gln His  
 310 315 320 325

gca cac ctg cac gcc acc ggc cgc gcc acc tac gtt ggt atc acc gac  
 1123  
 Ala His Leu His Ala Thr Gly Arg Ala Thr Tyr Val Gly Ile Thr Asp  
 330 335 340

gcc gaa gcc ctc caa gca ttc cag tac ctc gcc cgc tac gaa ggc atc  
 1171  
 Ala Glu Ala Leu Gln Ala Phe Gln Tyr Leu Ala Arg Tyr Glu Gly Ile  
 345 350 355

atc ccc gca ctg gaa tcc tca cac gcg ttc gcc tac gca ctc aag cgc  
 1219  
 Ile Pro Ala Leu Glu Ser Ser His Ala Phe Ala Tyr Ala Leu Lys Arg  
 360 365 370

gcc aag acc gcc  
 1231  
 Ala Lys Thr Ala  
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&lt;210&gt; 448

&lt;211&gt; 377

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 448

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1231)

&lt;223&gt; FRXA00956

&lt;400&gt; 447

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accatctcca cattccatta ctaaagggtt aaataggatc atg act gaa aaa gaa 115
                                         Met Thr Glu Lys Glu
                                         1           5
aac ttg ggc ggc tcc acg ctg ctg cct gca tac ttc ggt gaa ttc ggc 163
Asn Leu Gly Gly Ser Thr Leu Leu Pro Ala Tyr Phe Gly Glu Phe Gly
          10                      15                      20
ggc cag ttc gtc gcg gaa tcc ctc ctg cct gct ctc gac cag ctg gag 211
Gly Gln Phe Val Ala Glu Ser Leu Leu Pro Ala Leu Asp Gln Leu Glu
          25                      30                      35
aag gcc ttc gtt gac gcg acc aac agc cca gag ttc cgc gaa gaa ctc 259
Lys Ala Phe Val Asp Ala Thr Asn Ser Pro Glu Phe Arg Glu Glu Leu
          40                      45                      50
ggc ggc tac ctc cgc gat tac ctc ggc cgc cca acc ccg ctg acc gaa 307
Gly Gly Tyr Leu Arg Asp Tyr Leu Gly Arg Pro Thr Pro Leu Thr Glu
          55                      60                      65
tgc tcc aac ctg cca ctc gca ggc gaa ggc aaa ggc ttt gcg cgg atc 355
Cys Ser Asn Leu Pro Leu Ala Gly Glu Gly Lys Gly Phe Ala Arg Ile
          70                      75                      80                      85
ttc ctc aag cgc gaa gac ctc gtc cac ggc ggt gca cac aaa act aac 403
Phe Leu Lys Arg Glu Asp Leu Val His Gly Gly Ala His Lys Thr Asn
          90                      95                      100
cag gtg atc ggc cag gtg ctg ctt gcc aag cgc atg ggc aaa acc cgc 451
Gln Val Ile Gly Gln Val Leu Leu Ala Lys Arg Met Gly Lys Thr Arg
          105                      110                      115
atc atc gca gag acc ggc gca ggc cag cac ggc acc gcc acc gct ctc 499
Ile Ile Ala Glu Thr Gly Ala Gly Gln His Gly Thr Ala Thr Ala Leu
          120                      125                      130
gca tgt gcg ctc atg ggc ctc gag tgc gtt gtc tac atg ggc gcc aag 547
Ala Cys Ala Leu Met Gly Leu Glu Cys Val Val Tyr Met Gly Ala Lys
          135                      140                      145
gac gtt gcc cgc cag cag ccc aac gtc tac cgc atg cag ctg cac ggc 595
Asp Val Ala Arg Gln Gln Pro Asn Val Tyr Arg Met Gln Leu His Gly
          150                      155                      160                      165
gcg aag gtc atc ccc gtg gaa tct ggt tcc ggc acc ctg aag gac gcc 643
Ala Lys Val Ile Pro Val Glu Ser Gly Ser Gly Thr Leu Lys Asp Ala
          170                      175                      180
gtg aat gaa gcg ctg cgc gat tgg acc gca acc ttc cac gag tcc cac 691
Val Asn Glu Ala Leu Arg Asp Trp Thr Ala Thr Phe His Glu Ser His
          185                      190                      195

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Met	Gly	Lys	Thr	Arg	Ile	Ile	Ala	Glu	Thr	Gly	Ala	Gly	Gln	His	Gly				
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Thr	Ala	Thr	Ala	Leu	Ala	Cys	Ala	Leu	Met	Gly	Leu	Glu	Cys	Val	Val				
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Tyr	Met	Gly	Ala	Lys	Asp	Val	Ala	Arg	Gln	Gln	Pro	Asn	Val	Tyr	Arg				
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Thr	Leu	Lys	Asp	Ala	Val	Asn	Glu	Ala	Leu	Arg	Asp	Trp	Thr	Ala	Thr				
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Phe	His	Glu	Ser	His	Tyr	Leu	Leu	Gly	Thr	Pro	Ala	Gly	Pro	His	Pro				
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Phe	Pro	Thr	Ile	Val	Arg	Glu	Phe	His	Lys	Val	Ile	Ser	Glu	Glu	Ala				
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Lys	Ala	Gln	Met	Leu	Glu	Arg	Thr	Gly	Lys	Leu	Pro	Asp	Val	Val	Val				
225					230					235					240				
Ala	Cys	Val	Gly	Gly	Gly	Ser	Asn	Ala	Ile	Gly	Met	Phe	Ala	Asp	Phe				
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Ile	Asp	Asp	Glu	Gly	Val	Glu	Leu	Val	Gly	Ala	Glu	Pro	Ala	Gly	Glu				
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Gly	Leu	Asp	Ser	Gly	Lys	His	Gly	Ala	Thr	Ile	Thr	Asn	Gly	Gln	Ile				
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Gly	Ile	Leu	His	Gly	Thr	Arg	Ser	Tyr	Leu	Met	Arg	Asn	Ser	Asp	Gly				
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Gln	Val	Glu	Glu	Ser	Tyr	Ser	Ile	Ser	Ala	Gly	Leu	Asp	Tyr	Pro	Gly				
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Val	Gly	Pro	Gln	His	Ala	His	Leu	His	Ala	Thr	Gly	Arg	Ala	Thr	Tyr				
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Val	Gly	Ile	Thr	Asp	Ala	Glu	Ala	Leu	Gln	Ala	Phe	Gln	Tyr	Leu	Ala				
			340				345					350							
Arg	Tyr	Glu	Gly	Ile	Ile	Pro	Ala	Leu	Glu	Ser	Ser	His	Ala	Phe	Ala				
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<213> *Corynebacterium glutamicum*

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 265 270 275

aag cac ggc gca acc atc acc aac ggt cag atc ggc atc ctg cac ggc 979  
 Lys His Gly Ala Thr Ile Thr Asn Gly Gln Ile Gly Ile Leu His Gly  
 280 285 290

acc cgt tcc tac ctg atg cgc aac tcc gac ggc caa gtg gaa gag tcc  
 1027  
 Thr Arg Ser Tyr Leu Met Arg Asn Ser Asp Gly Gln Val Glu Glu Ser  
 295 300 305

tac tcc atc tcc gcc gga ctt gat tac cca ggc gtc ggc cca cag cac  
 1075  
 Tyr Ser Ile Ser Ala Gly Leu Asp Tyr Pro Gly Val Gly Pro Gln His  
 310 315 320 325

gca cac ctg cac gcc acc ggc cgc gcc acc tac gtt ggt atc acc gac  
 1123  
 Ala His Leu His Ala Thr Gly Arg Ala Thr Tyr Val Gly Ile Thr Asp  
 330 335 340

gcc gaa gcc ctc caa gca ttc cag tac ctc gcc cgc tac gaa ggc atc  
 1171  
 Ala Glu Ala Leu Gln Ala Phe Gln Tyr Leu Ala Arg Tyr Glu Gly Ile  
 345 350 355

atc ccc gca ctg gaa tcc tca cac gcg ttc gcc tac gca ctc aag cgc  
 1219  
 Ile Pro Ala Leu Glu Ser Ser His Ala Phe Ala Tyr Ala Leu Lys Arg  
 360 365 370

gcc aag acc gcc gaa gta  
 1237  
 Ala Lys Thr Ala Glu Val  
 375

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 <211> 379  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

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 Leu Asp Gln Leu Glu Lys Ala Phe Val Asp Ala Thr Asn Ser Pro Glu  
 35 40 45  
 Phe Arg Glu Glu Leu Gly Gly Tyr Leu Arg Asp Tyr Leu Gly Arg Pro  
 50 55 60  
 Thr Pro Leu Thr Glu Cys Ser Asn Leu Pro Leu Ala Gly Glu Gly Lys  
 65 70 75 80  
 Gly Phe Ala Arg Ile Phe Leu Lys Arg Glu Asp Leu Val His Gly Gly

ggc cag ttc gtc gcg gaa tcc ctc ctg cct gct ctc gac cag ctg gag	211
Gly Gln Phe Val Ala Glu Ser Leu Leu Pro Ala Leu Asp Gln Leu Glu	
25 30 35	
aag gcc ttc gtt gac gcg acc aac agc cca gag ttc cgc gaa gaa ctc	259
Lys Ala Phe Val Asp Ala Thr Asn Ser Pro Glu Phe Arg Glu Glu Leu	
40 45 50	
ggc ggc tac ctc cgc gat tac ctc ggc cgc cca acc ccg ctg acc gaa	307
Gly Gly Tyr Leu Arg Asp Tyr Leu Gly Arg Pro Thr Pro Leu Thr Glu	
55 60 65	
tgc tcc aac ctg cca ctc gca ggc gaa ggc aaa ggc ttt gcg cgg atc	355
Cys Ser Asn Leu Pro Leu Ala Gly Glu Gly Lys Gly Phe Ala Arg Ile	
70 75 80 85	
ttc ctc aag cgc gaa gac ctc gtc cac ggc ggt gca cac aaa act aac	403
Phe Leu Lys Arg Glu Asp Leu Val His Gly Gly Ala His Lys Thr Asn	
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cag gtg atc ggc cag gtg ctg ctt gcc aag cgc atg ggc aaa acc cgc	451
Gln Val Ile Gly Gln Val Leu Leu Ala Lys Arg Met Gly Lys Thr Arg	
105 110 115	
atc atc gca gag acc ggc gca ggc cag cac ggc acc gcc acc gct ctc	499
Ile Ile Ala Glu Thr Gly Ala Gly Gln His Gly Thr Ala Thr Ala Leu	
120 125 130	
gca tgt gcg ctc atg ggc ctc gag tgc gtt gtc tac atg ggc gcc aag	547
Ala Cys Ala Leu Met Gly Leu Glu Cys Val Val Tyr Met Gly Ala Lys	
135 140 145	
gac gtt gcc cgc cag cag ccc aac gtc tac cgc atg cag ctg cac ggc	595
Asp Val Ala Arg Gln Gln Pro Asn Val Tyr Arg Met Gln Leu His Gly	
150 155 160 165	
gcg aag gtc atc ccc gtg gaa tct ggt tcc ggc acc ctg aag gac gcc	643
Ala Lys Val Ile Pro Val Glu Ser Gly Ser Gly Thr Leu Lys Asp Ala	
170 175 180	
gtg aat gaa gcg ctg cgc gat tgg acc gca acc ttc cac gag tcc cac	691
Val Asn Glu Ala Leu Arg Asp Trp Thr Ala Thr Phe His Glu Ser His	
185 190 195	
tac ctt ctc ggc acc ccc gcc ggc ccg cac cca ttc cca acc atc gtg	739
Tyr Leu Leu Gly Thr Pro Ala Gly Pro His Pro Phe Pro Thr Ile Val	
200 205 210	
cgt gaa ttc cac aag gtg atc tct gag gaa gcc aag gca cag atg cta	787
Arg Glu Phe His Lys Val Ile Ser Glu Glu Ala Lys Ala Gln Met Leu	
215 220 225	
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Glu Arg Thr Gly Lys Leu Pro Asp Val Val Val Ala Cys Val Gly Gly	
230 235 240 245	
ggc tcc aac gcc atc ggc atg ttc gca gac ttc att gac gat gaa ggt	883
Gly Ser Asn Ala Ile Gly Met Phe Ala Asp Phe Ile Asp Asp Glu Gly	
250 255 260	

Ala Leu Glu Gln Ile Lys Arg Val Arg Ala Ala Tyr Pro Glu Val Pro  
85 90 95  
Ile Gly Met Leu Ile Tyr Gly Asn Val Pro Phe Thr Arg Gly Leu Asp  
100 105 110  
Arg Phe Tyr Gln Glu Phe Ala Glu Ala Gly Ala Asp Ser Ile Leu Leu  
115 120 125  
Pro Asp Val Pro Val Arg Glu Gly Ala Pro Phe Ser Ala Ala Ala Ala  
130 135 140  
Ala Ala Gly Ile Asp Pro Ile Tyr Ile Ala Pro Ala Asn Ala Ser Glu  
145 150 155 160  
Lys Thr Leu Glu Gly Val Ser Ala Ala Ser Lys Gly Tyr Ile Tyr Ala  
165 170 175  
Ile Ser Arg Asp Gly Val Thr Gly Thr Glu Arg Glu Ser Ser Thr Asp  
180 185 190  
Gly Leu Ser Ala Val Val Asp Asn Ile Lys Lys Phe Asp Gly Ala Pro  
195 200 205  
Ile Leu Leu Gly Phe Gly Ile Ser Ser Pro Gln His Val Ala Asp Ala  
210 215 220  
Ile Ala Ala Gly Ala Ser Gly Ala Ile Thr Gly Ser Ala Ile Thr Lys  
225 230 235 240  
Ile Ile Ala Ser His Cys Glu Gly Glu His Pro Asn Pro Ser Thr Ile  
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Arg Asp Met Asp Gly Leu Lys Lys Asp Leu Thr Glu Phe Ile Ser Ala  
260 265 270  
Met Lys Ala Ala Thr Lys Lys Val  
275 280

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<212> DNA  
<213> Corynebacterium glutamicum

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<222> (101)..(1237)  
<223> RXN00956

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Met Thr Glu Lys Glu  
1 5  
aac ttg ggc ggc tcc acg ctg ctg cct gca tac ttc ggt gaa ttc ggc 163  
Asn Leu Gly Gly Ser Thr Leu Leu Pro Ala Tyr Phe Gly Glu Phe Gly  
10 15 20

Gly Ser Met Thr Gly Ala Pro Lys Leu Arg Thr Met Glu Ile Ile Asp  
 530 535 540  
 Glu Leu Glu Ala Ala Pro Arg Gly Ile Tyr Ser Gly Gly Leu Gly Tyr  
 545 550 555 560  
 Phe Ser Leu Asp Gly Ala Val Asp Leu Ser Met Val Ile Arg Thr Leu  
 565 570 575  
 Val Ile Gln Asn Asn His Val Glu Tyr Gly Val Gly Gly Ala Leu Leu  
 580 585 590  
 Ala Leu Ser Asp Pro Glu Ala Glu Trp Glu Glu Ile Arg Val Lys Ser  
 595 600 605  
 Arg Pro Leu Leu Asn Leu Phe Gly Val Glu Phe Pro  
 610 615 620

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 <213> Corynebacterium glutamicum

<220>  
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 <223> RXA00958

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 Met Thr His Val Val  
 1 5  
 ctc att gat aat cac gat tct ttt gtc tac aac ctg gtg gat gcg ttc 163  
 Leu Ile Asp Asn His Asp Ser Phe Val Tyr Asn Leu Val Asp Ala Phe  
 10 15 20  
 gcc gtg gcc ggt tat aag tgc acg gtg ttc cgc aat acg gtg cca gtg 211  
 Ala Val Ala Gly Tyr Lys Cys Thr Val Phe Arg Asn Thr Val Pro Val  
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 gaa acc att ttg gca gcc aac ccg gac ctg atc tgc ctt tca cct gga 259  
 Glu Thr Ile Leu Ala Ala Asn Pro Asp Leu Ile Cys Leu Ser Pro Gly  
 40 45 50  
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 Pro Gly Tyr Pro Ala Asp Ala Gly Asn Met Met Ala Leu Ile Glu Arg  
 55 60 65  
 aca ctc ggc cag att cct tta ctg ggt att tgc ctc ggc tac cag gca 355  
 Thr Leu Gly Gln Ile Pro Leu Leu Gly Ile Cys Leu Gly Tyr Gln Ala  
 70 75 80 85  
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 Leu Ile Glu Tyr His Gly Gly Lys Val Glu Pro Cys Gly Pro Val His  
 90 95 100  
 ggc acc acc gac aac atg atc ctt act gat gca ggt gtg cag agc cct 451

Thr Phe Phe Ala His Ser Ser His Ala Phe Trp Leu Asp Asp Ala Gln  
 210 215 220  
 Gly Thr Ser Tyr Leu Gly Asp Ala Ser Gly Pro Leu Ala Arg Thr Lys  
 225 230 235 240  
 Thr His Asn Val Gly Glu Gly Asp Phe Phe Thr Trp Leu Lys Glu Asp  
 245 250 255  
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 Val Gly Tyr Val Gly Tyr Glu Leu Lys Ala Glu Ala Gly Ala Arg Ala  
 275 280 285  
 Ala His Thr Ser Ser Leu Pro Asp Ala His Leu Ile Phe Ala Asp Arg  
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 Ala Ile Ala Val Glu Ser Asp Gln Val Arg Leu Leu Ala Leu Gly Glu  
 305 310 315 320  
 Gln Asp Glu Trp Phe Glu Glu Thr Ile Lys Lys Leu His Asn Leu Val  
 325 330 335  
 Ala Pro Arg Ile Pro Ala Ser Gly His Leu Ala Leu Gln Val Arg Asp  
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 Ser Lys Asp Glu Tyr Leu Asp Lys Ile Arg Arg Ala Gln Glu Leu Ile  
 355 360 365  
 Thr Arg Gly Glu Ser Tyr Glu Ile Cys Leu Thr Thr Lys Leu Gln Gly  
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 385 390 395 400  
 Asn Pro Thr Ala Tyr Gly Ala Tyr Leu Gln Leu Gly Asp Thr Ser Ile  
 405 410 415  
 Leu Ser Ser Ser Pro Glu Arg Phe Ile Thr Ile Asp Ser Ala Gly Tyr  
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 Val Glu Ser Lys Pro Ile Lys Gly Thr Arg Pro Arg Gly Arg Thr Ala  
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 450 455 460  
 Arg Ala Glu Asn Leu Met Ile Val Asp Leu Val Arg Asn Asp Leu Ala  
 465 470 475 480  
 Arg Gly Ala Leu Pro Thr Thr Val Lys Thr Ser Lys Leu Phe Asp Val  
 485 490 495  
 Glu Thr Tyr Ala Thr Val His Gln Leu Val Ser Thr Val Ser Ala Glu  
 500 505 510  
 Leu Gly Pro Arg Ser Pro Ile Glu Cys Val Arg Ala Ala Phe Pro Gly  
 515 520 525



cac gtg gag tac gga gtg ggc ggt gca ctt ctt gct ctg tct gat ccg  
1891

His Val Glu Tyr Gly Val Gly Gly Ala Leu Leu Ala Leu Ser Asp Pro  
585 590 595

gag gct gag tgg gag gaa atc cgc gtt aaa tca cgg cct ctg ctg aat  
1939

Glu Ala Glu Trp Glu Glu Ile Arg Val Lys Ser Arg Pro Leu Leu Asn  
600 605 610

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1983

Leu Phe Gly Val Glu Phe Pro  
615 620

<210> 460

<211> 620

<212> PRT

<213> Corynebacterium glutamicum

<400> 460

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Asn Asp Gln Glu Ile Asp Glu Met Leu Phe Asp Ala Val Ile Leu Ser  
35 40 45

Pro Gly Pro Gly His Ala Gly Val Ala Ala Asp Phe Gly Ile Cys Ala  
50 55 60

Gly Val Ile Glu Arg Ala Arg Val Pro Ile Leu Gly Val Cys Leu Gly  
65 70 75 80

His Gln Gly Ile Ala Leu Ala Tyr Gly Gly Asp Val Asp Leu Ala Pro  
85 90 95

Arg Pro Val His Gly Glu Val Ser Gln Ile Thr His Asp Gly Ser Gly  
100 105 110

Leu Phe Ala Gly Ile Pro Glu Thr Phe Glu Ala Val Arg Tyr His Ser  
115 120 125

Met Val Ala Thr Arg Leu Pro Glu Ser Leu Lys Ala Thr Ala Thr Ser  
130 135 140

Asp Asp Gly Leu Ile Met Ala Leu Ala His Glu Val Leu Pro Gln Trp  
145 150 155 160

Gly Val Gln Phe His Pro Glu Ser Ile Gly Gly Gln Phe Gly His Gln  
165 170 175

Ile Ile Lys Asn Phe Leu Asn Leu Ala Arg Thr Tyr Arg Trp Gln Leu  
180 185 190

Thr Glu Lys Thr Ile Pro Leu Ser Val Asp Ser Ala Ala Val Phe Glu  
195 200 205

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 cct ctg gct gcc tat cta gca ctg cgt ggg gcc aat ccc acc gca tat  
 1315  
 Pro Leu Ala Ala Tyr Leu Ala Leu Arg Gly Ala Asn Pro Thr Ala Tyr  
 390                      395                      400                      405  
 ggt gcg tat ctt cag ctg ggg gat acc tct att ttg agt tcc tcg ccg  
 1363  
 Gly Ala Tyr Leu Gln Leu Gly Asp Thr Ser Ile Leu Ser Ser Ser Pro  
 410                      415                      420  
 gag cgg ttc atc acc att gat tcg gca ggg tat gtg gaa tca aag ccc  
 1411  
 Glu Arg Phe Ile Thr Ile Asp Ser Ala Gly Tyr Val Glu Ser Lys Pro  
 425                      430                      435  
 att aaa ggc acc agg ccg cgt ggg cga aca gcg caa gaa gac caa gaa  
 1459  
 Ile Lys Gly Thr Arg Pro Arg Gly Arg Thr Ala Gln Glu Asp Gln Glu  
 440                      445                      450  
 atc att gct gag ctg cgc agt aat cct aaa gat cgt gca gaa aac ttg  
 1507  
 Ile Ile Ala Glu Leu Arg Ser Asn Pro Lys Asp Arg Ala Glu Asn Leu  
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 Met Ile Val Asp Leu Val Arg Asn Asp Leu Ala Arg Gly Ala Leu Pro  
 470                      475                      480                      485  
 acc aca gtt aaa aca tcc aag ctt ttc gac gtc gaa acc tac gcc aca  
 1603  
 Thr Thr Val Lys Thr Ser Lys Leu Phe Asp Val Glu Thr Tyr Ala Thr  
 490                      495                      500  
 gtc cac caa ctt gtc agc acc gtc tct gca gag ttg ggg cca cgc agt  
 1651  
 Val His Gln Leu Val Ser Thr Val Ser Ala Glu Leu Gly Pro Arg Ser  
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 ccg att gag tgc gtg cgc gca gca ttc ccc ggt ggt tcg atg act ggt  
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 Pro Ile Glu Cys Val Arg Ala Ala Phe Pro Gly Gly Ser Met Thr Gly  
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 Ala Pro Lys Leu Arg Thr Met Glu Ile Ile Asp Glu Leu Glu Ala Ala  
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 1795  
 Pro Arg Gly Ile Tyr Ser Gly Gly Leu Gly Tyr Phe Ser Leu Asp Gly  
 550                      555                      560                      565  
 gca gtt gat ctc tcc atg gtg atc aga act ctc gtc atc cag aac aat  
 1843  
 Ala Val Asp Leu Ser Met Val Ile Arg Thr Leu Val Ile Gln Asn Asn  
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 Pro Glu Ser Ile Gly Gly Gln Phe Gly His Gln Ile Ile Lys Asn Phe  
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ctt aat tta gcg cgc aca tat cgc tgg caa ctc acg gag aaa act att 691  
 Leu Asn Leu Ala Arg Thr Tyr Arg Trp Gln Leu Thr Glu Lys Thr Ile  
 185 190 195

ccg ctc agc gtt gat tca gca gcg gtt ttt gaa aca ttc ttt gcc cat 739  
 Pro Leu Ser Val Asp Ser Ala Ala Val Phe Glu Thr Phe Phe Ala His  
 200 205 210

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 215 220 225

ggt gat gcc agc ggt cct ctc gca gcg aca aaa acc cat aat gtc ggc 835  
 Gly Asp Ala Ser Gly Pro Leu Ala Arg Thr Lys Thr His Asn Val Gly  
 230 235 240 245

gag ggg gat ttc ttc acc tgg cta aag gag gat ctc gcc gcc aac tca 883  
 Glu Gly Asp Phe Phe Thr Trp Leu Lys Glu Asp Leu Ala Ala Asn Ser  
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gtt gcg ccc ggt caa ggt ttt cgt ctt ggc tgg gtt ggt tac gtt ggt 931  
 Val Ala Pro Gly Gln Gly Phe Arg Leu Gly Trp Val Gly Tyr Val Gly  
 265 270 275

tat gag ctt aaa gcg gaa gct ggc gca cgg gct gcg cac act tcg agt 979  
 Tyr Glu Leu Lys Ala Glu Ala Gly Ala Arg Ala Ala His Thr Ser Ser  
 280 285 290

ctt ccg gat gcg cac ctc att ttt gcc gat cgc gcc atc gca gtg gaa  
 1027  
 Leu Pro Asp Ala His Leu Ile Phe Ala Asp Arg Ala Ile Ala Val Glu  
 295 300 305

tcg gat cag gtt cgg ttg ctg gcg ttg ggg gag cag gac gag tgg ttt  
 1075  
 Ser Asp Gln Val Arg Leu Leu Ala Leu Gly Glu Gln Asp Glu Trp Phe  
 310 315 320 325

gaa gaa acc atc aag aag ctg cat aat ctt gtc gcc ccg cgg ata cct  
 1123  
 Glu Glu Thr Ile Lys Lys Leu His Asn Leu Val Ala Pro Arg Ile Pro  
 330 335 340

gcg tcc gga cac ctc gct ttg cag gtt cga gat tcc aaa gat gag tat  
 1171  
 Ala Ser Gly His Leu Ala Leu Gln Val Arg Asp Ser Lys Asp Glu Tyr  
 345 350 355

ctc gac aaa att cgc aga gcc cag gag ctg att act cgc ggc gaa tcg  
 1219  
 Leu Asp Lys Ile Arg Arg Ala Gln Glu Leu Ile Thr Arg Gly Glu Ser  
 360 365 370

tat gaa atc tgc ctg acc aca aaa ctt cag ggc acc act gat gtg gcc  
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Glu Arg Arg Ala Ala Ala Lys  
370 375

<210> 459

<211> 1983

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1960)

<223> RXA00579

<400> 459

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                                         Met Arg Val Leu Ile
                                         1 5
att gat aat tat gat tct ttc acg ttt aat ctc gcc acc tat gtg gaa 163
Ile Asp Asn Tyr Asp Ser Phe Thr Phe Asn Leu Ala Thr Tyr Val Glu
                        10 15 20
gag gtt acg ggt cag gca cct gtg gtg gtg cct aat gat caa gaa ata 211
Glu Val Thr Gly Gln Ala Pro Val Val Val Pro Asn Asp Gln Glu Ile
                        25 30 35
gat gag atg ctt ttc gac gcc gtc atc ctc tca cct ggc ccg ggc cac 259
Asp Glu Met Leu Phe Asp Ala Val Ile Leu Ser Pro Gly Pro Gly His
                        40 45 50
gcc ggc gtt gcg gct gat ttt ggt atc tgt gca ggc gtc att gag cgt 307
Ala Gly Val Ala Ala Asp Phe Gly Ile Cys Ala Gly Val Ile Glu Arg
                        55 60 65
gca cgc gtt ccg att ttg ggt gtg tgt tta ggc cac cag ggc att gcg 355
Ala Arg Val Pro Ile Leu Gly Val Cys Leu Gly His Gln Gly Ile Ala
                        70 75 80 85
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Leu Ala Tyr Gly Gly Asp Val Asp Leu Ala Pro Arg Pro Val His Gly
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gag gtt tcg cag atc acc cat gat ggt tca ggt tta ttt gca ggc atc 451
Glu Val Ser Gln Ile Thr His Asp Gly Ser Gly Leu Phe Ala Gly Ile
                        105 110 115
cct gaa acg ttt gag gcg gtg cgt tat cac tcg atg gtg gca acc cgc 499
Pro Glu Thr Phe Glu Ala Val Arg Tyr His Ser Met Val Ala Thr Arg
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Leu Pro Glu Ser Leu Lys Ala Thr Ala Thr Ser Asp Asp Gly Leu Ile
                        135 140 145
atg gca ttg gca cat gaa gtg ctt ccg cag tgg ggt gtg caa ttt cat 595
Met Ala Leu Ala His Glu Val Leu Pro Gln Trp Gly Val Gln Phe His
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Gln	Ala	Ser	Lys	Val	Glu	Gln	Asp	Arg	Gln	Asp	Ile	Ala	Asp	Ile	Phe
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Ala	Gly	Asp	Asp	Asp	Arg	Leu	Val	Val	Val	Val	Gly	Pro	Cys	Ser	Val
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His	Asp	Pro	Glu	Ala	Ala	Ile	Asp	Tyr	Ala	Asn	Arg	Leu	Ala	Pro	Leu
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Ala	Lys	Arg	Leu	Asp	Gln	Asp	Leu	Lys	Ile	Val	Met	Arg	Val	Tyr	Phe
			100					105					110		
Glu	Lys	Pro	Arg	Thr	Ile	Val	Gly	Trp	Lys	Gly	Leu	Ile	Asn	Asp	Pro
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His	Leu	Asn	Glu	Thr	Tyr	Asp	Ile	Pro	Glu	Gly	Leu	Arg	Ile	Ala	Arg
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Lys	Val	Leu	Ile	Asp	Val	Val	Asn	Leu	Asp	Leu	Pro	Val	Gly	Cys	Glu
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Phe	Leu	Glu	Pro	Asn	Ser	Pro	Gln	Tyr	Tyr	Ala	Asp	Thr	Val	Ala	Trp
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Gly	Ala	Ile	Gly	Ala	Arg	Thr	Thr	Glu	Ser	Gln	Val	His	Arg	Gln	Leu
			180					185					190		
Ala	Ser	Gly	Met	Ser	Met	Pro	Ile	Gly	Phe	Lys	Asn	Gly	Thr	Asp	Gly
		195					200					205			
Asn	Ile	Gln	Val	Ala	Val	Asp	Ala	Val	Gln	Ala	Ala	Gln	Asn	Pro	His
	210					215					220				
Phe	Phe	Phe	Gly	Thr	Ser	Asp	Asp	Gly	Ala	Leu	Ser	Val	Val	Glu	Thr
225					230					235					240
Ala	Gly	Asn	Ser	Asn	Ser	His	Ile	Ile	Leu	Arg	Gly	Gly	Thr	Ser	Gly
				245					250					255	
Pro	Asn	His	Asp	Ala	Ala	Ser	Val	Glu	Ala	Val	Val	Glu	Lys	Leu	Gly
			260					265					270		
Glu	Asn	Ala	Arg	Leu	Met	Ile	Asp	Ala	Ser	His	Ala	Asn	Ser	Gly	Lys
	275						280					285			
Asp	His	Ile	Arg	Gln	Val	Glu	Val	Val	Arg	Glu	Ile	Ala	Glu	Gln	Ile
	290					295					300				
Ser	Gly	Gly	Ser	Glu	Ala	Val	Ala	Gly	Ile	Met	Ile	Glu	Ser	Phe	Leu
305					310					315					320
Val	Gly	Gly	Ala	Gln	Asn	Leu	Asp	Pro	Ala	Lys	Leu	Arg	Ile	Asn	Gly
				325					330					335	
Gly	Glu	Gly	Leu	Val	Tyr	Gly	Gln	Ser	Val	Thr	Asp	Lys	Cys	Ile	Asp
			340					345					350		
Ile	Asp	Thr	Thr	Ile	Asp	Leu	Leu	Ala	Glu	Leu	Ala	Ala	Ala	Val	Arg
		355					360					365			

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 Ser Asp Asp Gly Ala Leu Ser Val Val Glu Thr Ala Gly Asn Ser Asn  
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tcc cac atc att ttg cgc ggc ggt acc tcc ggc ccg aat cat gat gca 883  
 Ser His Ile Ile Leu Arg Gly Gly Thr Ser Gly Pro Asn His Asp Ala  
 250 255 260

gct tcg gtg gag gcc gtc gtc gag aag ctt ggt gaa aac gct cgt ctc 931  
 Ala Ser Val Glu Ala Val Val Glu Lys Leu Gly Glu Asn Ala Arg Leu  
 265 270 275

atg atc gat gct tcc cat gct aac tcc ggc aag gat cat atc cga cag 979  
 Met Ile Asp Ala Ser His Ala Asn Ser Gly Lys Asp His Ile Arg Gln  
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gtt gag gtt gtt cgt gaa atc gca gag cag att tct ggc ggt tct gaa  
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 Val Glu Val Val Arg Glu Ile Ala Glu Gln Ile Ser Gly Gly Ser Glu  
 295 300 305

gct gtg gct gga atc atg att gag tcc ttc ctc gtt ggt ggc gca cag  
 1075  
 Ala Val Ala Gly Ile Met Ile Glu Ser Phe Leu Val Gly Gly Ala Gln  
 310 315 320 325

aac ctt gat cct gcg aaa ttg cgc atc aat ggc ggt gaa ggc ctg gtg  
 1123  
 Asn Leu Asp Pro Ala Lys Leu Arg Ile Asn Gly Gly Glu Gly Leu Val  
 330 335 340

tac gga cag tct gtg acc gat aag tgc atc gat att gac acc acc atc  
 1171  
 Tyr Gly Gln Ser Val Thr Asp Lys Cys Ile Asp Ile Asp Thr Thr Ile  
 345 350 355

gat ttg ctc gct gag ctg gcc gca gca gta agg gaa cgc cga gca gca  
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 Ala Lys  
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<210> 458

<211> 375

<212> PRT

<213> Corynebacterium glutamicum

<400> 458

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agaggggctg cttttttgtt tcttaaattc accccatccc atg cat agc cct gaa 115  
Met His Ser Pro Glu  
1 5

agg caa gaa aaa atg agt tct cca gtc tca ctc gaa aac gcg gcg tca 163  
Arg Gln Glu Lys Met Ser Ser Pro Val Ser Leu Glu Asn Ala Ala Ser  
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acc agc aac aag cgc gtc gtg gct ttc cac gag ctg cct agc cct aca 211  
Thr Ser Asn Lys Arg Val Val Ala Phe His Glu Leu Pro Ser Pro Thr  
25 30 35

gat ctc atc gcc gca aac cca ctg aca cca aag cag gct tcc aag gtg 259  
Asp Leu Ile Ala Ala Asn Pro Leu Thr Pro Lys Gln Ala Ser Lys Val  
40 45 50

gag cag gat cgc cag gac atc gct gat atc ttc gct ggc gac gat gac 307  
Glu Gln Asp Arg Gln Asp Ile Ala Asp Ile Phe Ala Gly Asp Asp Asp  
55 60 65

cgc ctc gtt gtc gtt gtg gga cct tgc tca gtt cac gat cct gaa gca 355  
Arg Leu Val Val Val Val Gly Pro Cys Ser Val His Asp Pro Glu Ala  
70 75 80 85

gcc atc gat tac gca aac cgc ctg gct ccg ctg gca aag cgc ctt gat 403  
Ala Ile Asp Tyr Ala Asn Arg Leu Ala Pro Leu Ala Lys Arg Leu Asp  
90 95 100

cag gac ctc aag att gtc atg cgc gtg tac ttc gag aag cct cgc acc 451  
Gln Asp Leu Lys Ile Val Met Arg Val Tyr Phe Glu Lys Pro Arg Thr  
105 110 115

atc gtc gga tgg aag gga ttg atc aat gat cct cac ctc aac gaa acc 499  
Ile Val Gly Trp Lys Gly Leu Ile Asn Asp Pro His Leu Asn Glu Thr  
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tac gac atc cca gag ggc ttg cgc att gcg cgc aaa gtg ctt atc gac 547  
Tyr Asp Ile Pro Glu Gly Leu Arg Ile Ala Arg Lys Val Leu Ile Asp  
135 140 145

gtt gtg aac ctt gat ctc cca gtc ggc tgc gaa ttc ctc gaa cca aac 595  
Val Val Asn Leu Asp Leu Pro Val Gly Cys Glu Phe Leu Glu Pro Asn  
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agc cct cag tac tac gcc gac act gtc gca tgg gga gca atc ggc gct 643  
Ser Pro Gln Tyr Tyr Ala Asp Thr Val Ala Trp Gly Ala Ile Gly Ala  
170 175 180

cgt acc acc gaa tct cag gtg cac cgc cag ctg gct tct ggg atg tct 691  
Arg Thr Thr Glu Ser Gln Val His Arg Gln Leu Ala Ser Gly Met Ser  
185 190 195

atg cca att ggt ttc aag aac gga act gac gga aac atc cag gtt gca 739  
Met Pro Ile Gly Phe Lys Asn Gly Thr Asp Gly Asn Ile Gln Val Ala  
200 205 210

gtc gac gcg gta cag gct gcc cag aac cca cac ttc ttc ttc gga acc 787  
Val Asp Ala Val Gln Ala Ala Gln Asn Pro His Phe Phe Phe Gly Thr  
215 220 225

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Ile Ser Arg Pro Val Cys Ile Leu Gly Leu Gly Leu Ile Gly Gly Ser
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ctc ctc cgc gac ctc cat gca gcc aac cac tcc gtc ttc ggc tac aac 211
Leu Leu Arg Asp Leu His Ala Ala Asn His Ser Val Phe Gly Tyr Asn
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cgc tca cgc tcc ggc gct aaa tca gcc gtc gac gaa ggc ttc gac gtt 259
Arg Ser Arg Ser Gly Ala Lys Ser Ala Val Asp Glu Gly Phe Asp Val
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tcc gcc gat ctt gaa gca acc ctc cag cgt gca gcc gcc gaa gat gcg 307
Ser Ala Asp Leu Glu Ala Thr Leu Gln Arg Ala Ala Ala Glu Asp Ala
           55           60           65

ctc atc gtc ctc gcg gtc ccc atg acc gca atc gat tcg 346
Leu Ile Val Leu Ala Val Pro Met Thr Ala Ile Asp Ser
           70           75           80

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&lt;210&gt; 456

&lt;211&gt; 82

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 456

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Leu Ile Gly Gly Ser Leu Leu Arg Asp Leu His Ala Ala Asn His Ser
           20           25           30

Val Phe Gly Tyr Asn Arg Ser Arg Ser Gly Ala Lys Ser Ala Val Asp
           35           40           45

Glu Gly Phe Asp Val Ser Ala Asp Leu Glu Ala Thr Leu Gln Arg Ala
           50           55           60

Ala Ala Glu Asp Ala Leu Ile Val Leu Ala Val Pro Met Thr Ala Ile
           65           70           75           80

Asp Ser

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&lt;210&gt; 457

&lt;211&gt; 1248

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

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&lt;221&gt; CDS

&lt;222&gt; (101)..(1225)

&lt;223&gt; RXA00584

&lt;400&gt; 457



<211> 222  
 <212> PRT  
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<400> 454

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Asp Gln Leu Phe Asp Gly Thr Asp Ile Asn Ser Thr Trp Ile Ser Ile
      35              40              45

Trp Lys Asp Val Val Gln Met Ala Leu Ala Val Gly Ala Glu Val Val
      50              55              60

Pro Ser Arg Val Gly Pro His Asp Ala Ala Ala Arg Val Ser His
      65              70              75              80

Leu Thr His Ile Leu Ala Glu Thr Leu Ala Ile Val Gly Asp Asn Gly
      85              90              95

Gly Ala Leu Ser Leu Ser Leu Ala Ala Gly Ser Tyr Arg Asp Ser Thr
      100              105              110

Arg Val Ala Gly Thr Asp Pro Gly Leu Val Arg Ala Met Cys Glu Ser
      115              120              125

Asn Ala Gly Pro Leu Val Lys Ala Leu Asp Glu Ala Leu Ala Ile Leu
      130              135              140

His Glu Ala Arg Glu Gly Leu Thr Ala Glu Gln Pro Asn Ile Glu Gln
      145              150              155              160

Leu Ala Asp Asn Gly Tyr Arg Ser Arg Ile Arg Tyr Glu Ala Arg Ser
      165              170              175

Gly Gln Arg Arg Ala Lys Glu Ser Val Ser Pro Thr Ile Thr Ser Ser
      180              185              190

Arg Pro Val Leu Arg Leu His Pro Gly Thr Pro Asn Trp Glu Lys Gln
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Leu Ile His Ala Glu Thr Leu Gly Ala Arg Ile Glu Val Phe
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<400> 453

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Tyr Val Gly Ser His Pro Met Ala Gly Thr Ala Asn Ser Gly Trp Ser	
1 5 10 15	
gca tcc atg gac gga ctg ttc aaa cga gca gta tgg gtg gtc acc ttc	96
Ala Ser Met Asp Gly Leu Phe Lys Arg Ala Val Trp Val Val Thr Phe	
20 25 30	
gac cag ctt ttc gac ggc acc gac atc aac tcc acc tgg atc agc atc	144
Asp Gln Leu Phe Asp Gly Thr Asp Ile Asn Ser Thr Trp Ile Ser Ile	
35 40 45	
tgg aaa gac gtc gtc caa atg gca ctc gcc gtg ggc gct gaa gtt gtc	192
Trp Lys Asp Val Val Gln Met Ala Leu Ala Val Gly Ala Glu Val Val	
50 55 60	
cca tcc cga gtt ggc cca cac gat gca gca gca gca cga gtg tct cat	240
Pro Ser Arg Val Gly Pro His Asp Ala Ala Ala Arg Val Ser His	
65 70 75 80	
tta aca cac atc ctg gct gaa acc ctc gcc atc gtc ggt gac aac ggt	288
Leu Thr His Ile Leu Ala Glu Thr Leu Ala Ile Val Gly Asp Asn Gly	
85 90 95	
ggc gca ctg tct ctc tct tta gcc gct ggc agc tac cgc gac tcc acc	336
Gly Ala Leu Ser Leu Ser Leu Ala Ala Gly Ser Tyr Arg Asp Ser Thr	
100 105 110	
cgc gtt gca ggc acc gac cca gga ctc gtc cgc gcc atg tgt gaa agc	384
Arg Val Ala Gly Thr Asp Pro Gly Leu Val Arg Ala Met Cys Glu Ser	
115 120 125	
aac gcc ggc cca ctg gtc aaa gcc ctc gac gaa gca ctg gcg atc ctc	432
Asn Ala Gly Pro Leu Val Lys Ala Leu Asp Glu Ala Leu Ala Ile Leu	
130 135 140	
cac gaa gcc cgc gaa ggc ctc acc gca gaa cag cca aac atc gag caa	480
His Glu Ala Arg Glu Gly Leu Thr Ala Glu Gln Pro Asn Ile Glu Gln	
145 150 155 160	
ctt gcc gac aac ggc tac cga tcc cgc atc cgc tac gaa gcc cgc tcc	528
Leu Ala Asp Asn Gly Tyr Arg Ser Arg Ile Arg Tyr Glu Ala Arg Ser	
165 170 175	
ggc cag cga cgc gcc aaa gaa tcc gtt agc cct acc atc acc tca tcc	576
Gly Gln Arg Arg Ala Lys Glu Ser Val Ser Pro Thr Ile Thr Ser Ser	
180 185 190	
agg cca gtg ctc cgt ctc cac ccg ggc aca cca aac tgg gag aag cag	624
Arg Pro Val Leu Arg Leu His Pro Gly Thr Pro Asn Trp Glu Lys Gln	
195 200 205	
ctc atc cac gct gaa acc ctc ggc gca cgg atc gaa gtg ttc	666
Leu Ile His Ala Glu Thr Leu Gly Ala Arg Ile Glu Val Phe	
210 215 220	
tagttttatc ggctgatgat tct	689

&lt;210&gt; 454

85					90					95					
Thr	Asp	Val	Val	Ser	Val	Lys	Thr	Ala	Val	Tyr	Asp	Ala	Val	Lys	Ala
		100						105					110		
Arg	Asn	Met	Gln	His	Arg	Tyr	Val	Gly	Ser	His	Pro	Met	Ala	Gly	Thr
		115					120					125			
Ala	Asn	Ser	Gly	Trp	Ser	Ala	Ser	Met	Asp	Gly	Leu	Phe	Lys	Arg	Ala
		130				135					140				
Val	Trp	Val	Val	Thr	Phe	Asp	Gln	Leu	Phe	Asp	Gly	Thr	Asp	Ile	Asn
	145					150					155				160
Ser	Thr	Trp	Ile	Ser	Ile	Trp	Lys	Asp	Val	Val	Gln	Met	Ala	Leu	Ala
			165						170					175	
Val	Gly	Ala	Glu	Val	Val	Pro	Ser	Arg	Val	Gly	Pro	His	Asp	Ala	Ala
			180					185					190		
Ala	Ala	Arg	Val	Ser	His	Leu	Thr	His	Ile	Leu	Ala	Glu	Thr	Leu	Ala
		195					200					205			
Ile	Val	Gly	Asp	Asn	Gly	Gly	Ala	Leu	Ser	Leu	Ser	Leu	Ala	Ala	Gly
	210					215					220				
Ser	Tyr	Arg	Asp	Ser	Thr	Arg	Val	Ala	Gly	Thr	Asp	Pro	Gly	Leu	Val
	225					230					235				240
Arg	Ala	Met	Cys	Glu	Ser	Asn	Ala	Gly	Pro	Leu	Val	Lys	Ala	Leu	Asp
			245						250					255	
Glu	Ala	Leu	Ala	Ile	Leu	His	Glu	Ala	Arg	Glu	Gly	Leu	Thr	Ala	Glu
		260					265					270			
Gln	Pro	Asn	Ile	Glu	Gln	Leu	Ala	Asp	Asn	Gly	Tyr	Arg	Ser	Arg	Ile
	275						280					285			
Arg	Tyr	Glu	Ala	Arg	Ser	Gly	Gln	Arg	Arg	Ala	Lys	Glu	Ser	Val	Ser
	290					295					300				
Pro	Thr	Ile	Thr	Ser	Ser	Arg	Pro	Val	Leu	Arg	Leu	His	Pro	Gly	Thr
	305					310					315				320
Pro	Asn	Trp	Glu	Lys	Gln	Leu	Ile	His	Ala	Glu	Thr	Leu	Gly	Ala	Arg
			325						330					335	
Ile	Glu	Val	Phe												
		340													

&lt;210&gt; 453

&lt;211&gt; 689

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(666)

&lt;223&gt; FRXA00448

ggt ggc gca ctg tct ctc tct tta gcc gct ggc agc tac cgc gac tcc 787  
 Gly Gly Ala Leu Ser Leu Ser Leu Ala Ala Gly Ser Tyr Arg Asp Ser  
 215 220 225  
 acc cgc gtt gca ggc acc gac cca gga ctc gtc cgc gcc atg tgt gaa 835  
 Thr Arg Val Ala Gly Thr Asp Pro Gly Leu Val Arg Ala Met Cys Glu  
 230 235 240 245  
 agc aac gcc ggc cca ctg gtc aaa gcc ctc gac gaa gca ctg gcg atc 883  
 Ser Asn Ala Gly Pro Leu Val Lys Ala Leu Asp Glu Ala Leu Ala Ile  
 250 255 260  
 ctc cac gaa gcc cgc gaa ggc ctc acc gca gaa cag cca aac atc gag 931  
 Leu His Glu Ala Arg Glu Gly Leu Thr Ala Glu Gln Pro Asn Ile Glu  
 265 270 275  
 caa ctt gcc gac aac ggc tac cga tcc cgc atc cgc tac gaa gcc cgc 979  
 Gln Leu Ala Asp Asn Gly Tyr Arg Ser Arg Ile Arg Tyr Glu Ala Arg  
 280 285 290  
 tcc ggc cag cga cgc gcc aaa gaa tcc gtt agc cct acc atc acc tca  
 1027  
 Ser Gly Gln Arg Arg Ala Lys Glu Ser Val Ser Pro Thr Ile Thr Ser  
 295 300 305  
 tcc agg cca gtg ctc cgt ctc cac ccg ggc aca cca aac tgg gag aag  
 1075  
 Ser Arg Pro Val Leu Arg Leu His Pro Gly Thr Pro Asn Trp Glu Lys  
 310 315 320 325  
 cag ctc atc cac gct gaa acc ctc ggc gca cgg atc gaa gtg ttc  
 1120  
 Gln Leu Ile His Ala Glu Thr Leu Gly Ala Arg Ile Glu Val Phe  
 330 335 340  
 tagttttatc ggctgatgat tct  
 1143

&lt;210&gt; 452

&lt;211&gt; 340

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 452

Val Thr Thr Lys Asp Ile Ser Arg Pro Val Cys Ile Leu Gly Leu Gly  
 1 5 10 15  
 Leu Ile Gly Gly Ser Leu Leu Arg Asp Leu His Ala Ala Asn His Ser  
 20 25 30  
 Val Phe Gly Tyr Asn Arg Ser Arg Ser Gly Ala Lys Ser Ala Val Asp  
 35 40 45  
 Glu Gly Phe Asp Val Ser Ala Asp Leu Glu Ala Thr Leu Gln Arg Ala  
 50 55 60  
 Ala Ala Glu Asp Ala Leu Ile Val Leu Ala Val Pro Met Thr Ala Ile  
 65 70 75 80  
 Asp Ser Leu Leu Asp Ala Val His Thr His Ala Pro Asn Asn Gly Phe

85								90				95			
Gly	Ala	Ala	Ala	Glu	Leu	Lys	Asn	Thr	Gly	Asp	Arg	Val	Tyr	Thr	Ser
100								105						110	
Leu	Thr	Pro	Met	Gln	Leu	Leu	Lys	Ala	Met	Asp	Ser	Leu	Gln	Gly	Ile
115								120						125	
Glu	Ala	Leu	Lys	Leu	Phe	Asp	Val	Ile	Leu	Val	Gly	Gly	Ala	Ala	Leu
130								135						140	
Ser	Lys	Gln	Ala	Arg	Ile	Ser	Ala	Glu	Gln	Leu	Asp	Ile	Asn	Ile	Val
145												155		160	
Thr	Thr	Tyr	Gly	Ser	Ser	Glu	Thr	Ser	Gly	Gly	Cys	Val	Tyr	Asp	Gly
				165								175			
Lys	Pro	Ile	Pro	Gly	Ala	Lys	Val	Arg	Ile	Ser	Asp	Glu	Arg	Ile	Glu
				180				185				190			
Leu	Gly	Gly	Pro	Met	Ile	Ala	Gln	Gly	Tyr	Arg	Asn	Ala	Pro	Glu	His
				195				200				205			
Pro	Asp	Phe	Ala	Asn	Glu	Gly	Trp	Phe	Thr	Thr	Ser	Asp	Ser	Gly	Glu
210								215						220	
Leu	His	Asp	Gly	Ile	Leu	Thr	Val	Thr	Gly	Arg	Val	Asp	Thr	Arg	His
225				230								235		240	

<210> 477  
<211> 1017  
<212> DNA  
<213> *Corynebacterium glutamicum*

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<220>  
<221> CDS  
<222> (101) .. (994)  
<223> RXS00393
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tctattcatt tcacaatagc gtttcacact ccccatagc ctgccgaacg tattttaacg 60

aattgcgcga tcgagtatgt gatggggaaa gatagagggt atg tct cac acg gaa 115
Met Ser His Thr Glu
1 5

ccc cag ccg aat tct gta act ttg tcc gat tgg att caa ggc gca cgc 163
Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp Ile Gln Gly Ala Arg
10 15 20

ccg cgt acc tgg gca aat gcg ttc gcg cct gtc att gcc ggt tca ggt 211
Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val Ile Ala Gly Ser Gly
25 30 35

gtc gcc gct ttt cat gat ggt ttt gtg tgg tgg aag gcc ttg ctg gcg 259
Val Ala Ala Phe His Asp Gly Phe Val Trp Trp Lys Ala Leu Leu Ala
40 45 50
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ctg aaa aat acc ggc gac cgc gtc tat aca tcc ttg act cca atg cag 451  
 Leu Lys Asn Thr Gly Asp Arg Val Tyr Thr Ser Leu Thr Pro Met Gln  
                   105                                  110                                  115  
  
 tta ctt aaa gca atg gac tcc ttg caa ggc att gaa gcc ctg aaa ctt 499  
 Leu Leu Lys Ala Met Asp Ser Leu Gln Gly Ile Glu Ala Leu Lys Leu  
                   120                                  125                                  130  
  
 ttt gat gtc att ctt gtt ggc ggt gct gca ttg tct aag cag gcc cga 547  
 Phe Asp Val Ile Leu Val Gly Gly Ala Ala Leu Ser Lys Gln Ala Arg  
                   135                                  140                                  145  
  
 att tct gcg gag cag cta gac atc aac att gtc acc acc tac ggc tcc 595  
 Ile Ser Ala Glu Gln Leu Asp Ile Asn Ile Val Thr Thr Tyr Gly Ser  
                   150                                  155                                  160                                  165  
  
 tca gag act tca ggt ggc tgc gtt tat gat ggc aag ccc att ccc ggc 643  
 Ser Glu Thr Ser Gly Gly Cys Val Tyr Asp Gly Lys Pro Ile Pro Gly  
                   170                                  175                                  180  
  
 gcg aaa gtc cgt att tcg gat gag cgc att gag ttg ggt ggc ccg atg 691  
 Ala Lys Val Arg Ile Ser Asp Glu Arg Ile Glu Leu Gly Gly Pro Met  
                   185                                  190                                  195  
  
 att gcg cag ggc tac aga aat gca cct gaa cat ccg gat ttc gcc aac 739  
 Ile Ala Gln Gly Tyr Arg Asn Ala Pro Glu His Pro Asp Phe Ala Asn  
                   200                                  205                                  210  
  
 gag ggt tgg ttt acc acc tct gat tca ggt gaa ctc cac gac ggg att 787  
 Glu Gly Trp Phe Thr Thr Ser Asp Ser Gly Glu Leu His Asp Gly Ile  
                   215                                  220                                  225  
  
 ctc acc gtg act ggt cgc gtg gat acc cgt cat tgattccggt ggattgaagt 840  
 Leu Thr Val Thr Gly Arg Val Asp Thr Arg His  
                   230                                  235                                  240  
  
 tgc 843

&lt;210&gt; 476

&lt;211&gt; 240

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 476

Leu Leu Arg Asp Ser Gln Arg Val Gly Leu Ala Ile Asp Pro Ser Ile  
   1                                  5                                  10                                  15  
  
 Ala Leu Val Met Ala Thr Ser Gly Ser Thr Gly Thr Pro Lys Gly Ala  
                   20                                  25                                  30  
  
 Gln Leu Thr Pro Leu Asn Leu Val Ser Ser Ala Asp Ala Thr His Gln  
                   35                                  40                                  45  
  
 Phe Leu Gly Gly Glu Gly Gln Trp Leu Leu Ala Met Pro Ala His His  
                   50                                  55                                  60  
  
 Ile Ala Gly Met Gln Val Leu Leu Arg Ser Leu Ile Ala Gly Val Glu  
                   65                                  70                                  75                                  80  
  
 Pro Leu Ala Ile Asp Leu Ser Thr Gly Phe His Ile Asp Ala Phe Ala

<400> 475																	
atcttgtaga tcccaccgca attctgggag atctcgagga cgcaatctct ggaagaaaac																	60
tttctctccc atccctgtac aagataaaac ccgtgcacag ttg ctg cgc gat tct																	115
Leu Leu Arg Asp Ser																	
1 5																	
caa cga gtt ggc ctc gcc atc gat cct tcg atc gct ttg gtg atg gcc																	163
Gln Arg Val Gly Leu Ala Ile Asp Pro Ser Ile Ala Leu Val Met Ala																	
10 15 20																	
act tct ggt tct aca ggt acc ccg aag ggc gct cag ctc act ccg ttg																	211
Thr Ser Gly Ser Thr Gly Thr Pro Lys Gly Ala Gln Leu Thr Pro Leu																	
25 30 35																	
aat ttg gtg agt tcc gcc gat gct acg cat cag ttt tta ggt ggc gaa																	259
Asn Leu Val Ser Ser Ala Asp Ala Thr His Gln Phe Leu Gly Gly Glu																	
40 45 50																	
ggc cag tgg ttg ctt gcc atg cca gca cac cac att gca ggc atg cag																	307
Gly Gln Trp Leu Leu Ala Met Pro Ala His His Ile Ala Gly Met Gln																	
55 60 65																	
gtg ctt ctt cga agc ctc att gct gga gtt gag cca cta gct att gat																	355
Val Leu Leu Arg Ser Leu Ile Ala Gly Val Glu Pro Leu Ala Ile Asp																	
70 75 80 85																	
ctc agc aca ggt ttt cac att gac gct ttc gca ggc gcc gcg gca gaa																	403
Leu Ser Thr Gly Phe His Ile Asp Ala Phe Ala Gly Ala Ala Glu																	
90 95 100																	

ggt cct cgt cgg atg tta gag atc gcg tcg gag cag att ctc ggg gga 211  
 Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu Gln Ile Leu Gly Gly  
                   25                                  30                                  35

aat aat cag tat tcg gcg ggg cgt ggg gat gct tcg ttg agg gca gct 259  
 Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala Ser Leu Arg Ala Ala  
                   40                                  45                                  50

gtg gct cgt gat cat ttg gag agg ttt gat ctg gag tac aac cct gat 307  
 Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu Glu Tyr Asn Pro Asp  
                   55                                  60                                  65

tcg gag gtg ttg atc acg gtg ggg gcc act gag gcg att acg gcg act 355  
 Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu Ala Ile Thr Ala Thr  
                   70                                  75                                  80                                  85

gtg ttg ggt ttg gtg gag cct ggg gat gaa gtg atc gtt ttg gaa ccg 403  
 Val Leu Gly Leu Val Glu Pro Gly Asp Glu Val Ile Val Leu Glu Pro  
                                   90                                  95                                  100

tat tac gat gcg tat gcg gcg gct att gcg ttg gcg ggg gcg acg cgg 451  
 Tyr Tyr Asp Ala Tyr Ala Ala Ala Ile Ala Leu Ala Gly Ala Thr Arg  
                   105                                  110                                  115

gtg gcg gtt cct ttg cag gag gtg gag aac tcg tgg gat gtg gat gtc 499  
 Val Ala Val Pro Leu Gln Glu Val Glu Asn Ser Trp Asp Val Asp Val  
                   120                                  125                                  130

gat aag ttg cat gcg gcg gtg act aag aag acg cgg atg att atc gtt 547  
 Asp Lys Leu His Ala Ala Val Thr Lys Lys Thr Arg Met Ile Ile Val  
                   135                                  140                                  145

aat tcg ccg cat aat ccg acg ggt tcg gtg ttt tct aag aag gcg ttg 595  
 Asn Ser Pro His Asn Pro Thr Gly Ser Val Phe Ser Lys Lys Ala Leu  
                   150                                  155                                  160                                  165

aag cag ttg gcg 607  
 Lys Gln Leu Ala

&lt;210&gt; 474

&lt;211&gt; 169

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 474

Met Thr Gln Arg Ala Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly  
   1                                  5                                  10                                  15

Phe Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu  
                   20                                  25                                  30

Gln Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala  
                   35                                  40                                  45

Ser Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu  
                   50                                  55                                  60

Glu Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu  
                   65                                  70                                  75                                  80



Arg Ala Tyr Asp Leu Leu Val Leu Ser Asp Glu Val Tyr Glu His Leu  
 195 200 205  
 Val Phe Asp Asp Gln Lys His Val Ser Val Ala Lys Leu Pro Gly Met  
 210 215 220  
 Trp Asp Arg Thr Val Thr Val Ser Ser Ala Ala Lys Thr Phe Asn Val  
 225 230 235 240  
 Thr Gly Trp Lys Thr Gly Trp Ala Leu Ala Pro Glu Pro Leu Leu Glu  
 245 250 255  
 Ala Val Leu Lys Ala Lys Gln Phe Met Ser Tyr Val Gly Ala Thr Pro  
 260 265 270  
 Phe Gln Pro Ala Val Ala His Ala Ile Glu His Glu Gln Lys Trp Val  
 275 280 285  
 Ser Lys Met Ser Lys Gly Leu Glu Leu Lys Arg Asp Ile Leu Arg Thr  
 290 295 300  
 Ala Leu Asp Lys Ala Gly Leu Lys Thr His Asp Ser Met Gly Thr Tyr  
 305 310 315 320  
 Phe Ile Val Ala Asp Ile Gly Asp Arg Asp Gly Ala Glu Phe Cys Phe  
 325 330 335  
 Glu Leu Ile Glu Lys Val Gly Val Ala Ala Ile Pro Val Gln Ala Phe  
 340 345 350  
 Val Asp His Pro Lys Lys Trp Ser Ser Lys Val Arg Phe Ala Phe Cys  
 355 360 365  
 Lys Lys Glu Glu Thr Leu Arg Glu Ala Ala Glu Arg Leu Lys Gly Ile  
 370 375 380  
 Lys Lys Leu  
 385

<210> 473  
 <211> 607  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(607)  
 <223> FRXA00116

<400> 473  
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 ttctaggctt agaccctttg gtgaaacgat ttttgcaacc atg acc cag cga gct 115  
 Met Thr Gln Arg Ala  
 1 5  
 gtt gag gcg ggt gca atc aat ctt ggt cag ggc ttt cct gat gag gat 163  
 Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly Phe Pro Asp Glu Asp  
 10 15 20

gtt ggg gtg gcg gcg att ccg gtg cag gcg ttt gtg gat cat ccg aag  
 1171  
 Val Gly Val Ala Ala Ile Pro Val Gln Ala Phe Val Asp His Pro Lys  
                   345                  350                  355

aag tgg tcg tcg aag gtt cgt ttt gcg ttt tgc aaa aaa gaa gag acg  
 1219  
 Lys Trp Ser Ser Lys Val Arg Phe Ala Phe Cys Lys Lys Glu Glu Thr  
                   360                  365                  370

ctc cgc gaa gct gcg gag cgt ctc aag ggg att aag aaa cta  
 1261  
 Leu Arg Glu Ala Ala Glu Arg Leu Lys Gly Ile Lys Lys Leu  
                   375                  380                  385

tagtttgaac aggttggttg ggg  
 1284

<210> 472

<211> 387

<212> PRT

<213> Corynebacterium glutamicum

<400> 472

Met Ser Asn Asp Phe Val Val Ser Arg Leu Arg Pro Phe Gly Glu Thr  
   1                  5                  10                  15

Ile Phe Ala Thr Met Thr Gln Arg Ala Val Glu Ala Gly Ala Ile Asn  
                   20                  25                  30

Leu Gly Gln Gly Phe Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu  
                   35                  40                  45

Ile Ala Ser Glu Gln Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly  
                   50                  55                  60

Arg Gly Asp Ala Ser Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu  
                   65                  70                  75                  80

Arg Phe Asp Leu Glu Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val  
                   85                  90                  95

Gly Ala Thr Glu Ala Ile Thr Ala Thr Val Leu Gly Leu Val Glu Pro  
                   100                  105                  110

Gly Asp Glu Val Ile Val Leu Glu Pro Tyr Tyr Asp Ala Tyr Ala Ala  
                   115                  120                  125

Ala Ile Ala Leu Ala Gly Ala Thr Arg Val Ala Val Pro Leu Gln Glu  
                   130                  135                  140

Val Glu Asn Ser Trp Asp Val Asp Val Asp Lys Leu His Ala Ala Val  
                   145                  150                  155                  160

Thr Lys Lys Thr Arg Met Ile Ile Val Asn Ser Pro His Asn Pro Thr  
                   165                  170                  175

Gly Ser Val Phe Ser Lys Lys Ala Leu Lys Gln Leu Ala Gly Val Ala  
                   180                  185                  190

105								110				115				
gtt	ttg	gaa	ccg	tat	tac	gat	gcg	tat	gcg	gcg	gct	att	gcg	ttg	gcg	499
Val	Leu	Glu	Pro	Tyr	Tyr	Asp	Ala	Tyr	Ala	Ala	Ala	Ile	Ala	Leu	Ala	
120				125				130								
ggg	gcg	acg	cgg	gtg	gcg	gtt	cct	ttg	cag	gag	gtg	gag	aac	tcg	tgg	547
Gly	Ala	Thr	Arg	Val	Ala	Val	Pro	Leu	Gln	Glu	Val	Glu	Asn	Ser	Trp	
135				140				145								
gat	gtg	gat	gtc	gat	aag	ttg	cat	gcg	gcg	gtg	act	aag	aag	acg	cgg	595
Asp	Val	Asp	Val	Asp	Lys	Leu	His	Ala	Ala	Val	Thr	Lys	Lys	Thr	Arg	
150				155				160								
atg	att	atc	gtt	aat	tcg	ccg	cat	aat	ccg	acg	ggt	tcg	gtg	ttt	tct	643
Met	Ile	Ile	Val	Asn	Ser	Pro	His	Asn	Pro	Thr	Gly	Ser	Val	Phe	Ser	
170				175				180								
aag	aag	gcg	ttg	aag	cag	ttg	gcg	ggt	gtt	gct	cgt	gcg	tat	gac	ttg	691
Lys	Lys	Ala	Leu	Lys	Gln	Leu	Ala	Gly	Val	Ala	Arg	Ala	Tyr	Asp	Leu	
185				190				195								
ttg	gtg	ttg	tca	gat	gag	gtg	tat	gag	cat	ctt	gtt	ttt	gat	gat	cag	739
Leu	Val	Leu	Ser	Asp	Glu	Val	Tyr	Glu	His	Leu	Val	Phe	Asp	Asp	Gln	
200				205				210								
aag	cat	gtg	agt	gtc	gcg	aag	ctg	ccc	ggt	atg	tgg	gat	cgc	acg	gtg	787
Lys	His	Val	Ser	Val	Ala	Lys	Leu	Pro	Gly	Met	Trp	Asp	Arg	Thr	Val	
215				220				225								
acg	gtg	tcg	tcg	gcg	gcg	aaa	acg	ttc	aat	gtg	act	ggt	tgg	aag	acg	835
Thr	Val	Ser	Ser	Ala	Ala	Lys	Thr	Phe	Asn	Val	Thr	Gly	Trp	Lys	Thr	
230				235				240								
ggg	tgg	gcg	ttg	gca	ccg	gag	ccg	ttg	ttg	gag	gcg	gtg	ttg	aag	gcg	883
Gly	Trp	Ala	Leu	Ala	Pro	Glu	Pro	Leu	Leu	Glu	Ala	Val	Leu	Lys	Ala	
250				255				260								
aag	cag	ttt	atg	tct	tat	gtg	ggg	gct	aca	cct	ttt	cag	ccg	gct	gtg	931
Lys	Gln	Phe	Met	Ser	Tyr	Val	Gly	Ala	Thr	Pro	Phe	Gln	Pro	Ala	Val	
265				270				275								
gcg	cat	gcg	att	gaa	cat	gag	cag	aag	tgg	gtg	tca	aag	atg	tct	aag	979
Ala	His	Ala	Ile	Glu	His	Glu	Gln	Lys	Trp	Val	Ser	Lys	Met	Ser	Lys	
280				285				290								
ggg	ctt	gag	ctc	aag	cgg	gat	att	ttg	cgt	act	gcg	tta	gat	aag	gcg	1027
Gly	Leu	Glu	Leu	Lys	Arg	Asp	Ile	Leu	Arg	Thr	Ala	Leu	Asp	Lys	Ala	
295				300				305								
ggg	ctg	aag	act	cat	gac	agt	atg	ggc	acg	tat	ttc	atc	gtt	gcg	gat	1075
Gly	Leu	Lys	Thr	His	Asp	Ser	Met	Gly	Thr	Tyr	Phe	Ile	Val	Ala	Asp	
310				315				320								
att	ggg	gat	cgt	gat	ggt	gcg	gag	ttc	tgt	ttt	gag	ttg	att	gag	aag	1123
Ile	Gly	Asp	Arg	Asp	Gly	Ala	Glu	Phe	Cys	Phe	Glu	Leu	Ile	Glu	Lys	
330				335				340								

165 170 175  
 Glu Ala Leu Ala Thr Trp Asp Phe Thr Asp Arg Leu Gly Glu Ile Thr  
 180 185 190  
 Val Pro Val Leu Thr Ile Ala Gly Ala Asp Asp Pro Ser Thr Pro Pro  
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 Met Ser Asn Asp Phe  
 1 5  
 gtc gtt tct agg ctt aga ccc ttt ggt gaa acg att ttt gca acc atg 163  
 Val Val Ser Arg Leu Arg Pro Phe Gly Glu Thr Ile Phe Ala Thr Met  
 10 15 20  
 acc cag cga gct gtt gag gcg ggt gca atc aat ctt ggt cag ggc ttt 211  
 Thr Gln Arg Ala Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly Phe  
 25 30 35  
 cct gat gag gat ggt cct cgt cgg atg tta gag atc gcg tcg gag cag 259  
 Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu Gln  
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 Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala Ser  
 55 60 65  
 ttg agg gca gct gtg gct cgt gat cat ttg gag agg ttt gat ctg gag 355  
 Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu Glu  
 70 75 80 85  
 tac aac cct gat tcg gag gtg ttg atc acg gtg ggg gcc act gag gcg 403  
 Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu Ala  
 90 95 100  
 att acg gcg act gtg ttg ggt ttg gtg gag cct ggg gat gaa gtg atc 451  
 Ile Thr Ala Thr Val Leu Gly Leu Val Glu Pro Gly Asp Glu Val Ile

Gly Thr Pro Ser Glu Gly Tyr Ala Leu Cys Cys Glu Ala Leu Ala Thr  
 170 175 180  
 tgg gat ttc acc gat cgc ctg gga gaa atc acc gtg cca gtg ctc acc 691  
 Trp Asp Phe Thr Asp Arg Leu Gly Glu Ile Thr Val Pro Val Leu Thr  
 185 190 195  
 atc gca ggt gcc gat gac ccc tcc act cct cca gca acc gtg cag atc 739  
 Ile Ala Gly Ala Asp Asp Pro Ser Thr Pro Pro Ala Thr Val Gln Ile  
 200 205 210  
 att gcc gat ggc gtt ggc ggc gag tcc cgc gca gag gtc cta agc cca 787  
 Ile Ala Asp Gly Val Gly Gly Glu Ser Arg Ala Glu Val Leu Ser Pro  
 215 220 225  
 gcc gcg cac gta cca acc gtg gaa cgt cca aac gag gta aat gaa ctg 835  
 Ala Ala His Val Pro Thr Val Glu Arg Pro Asn Glu Val Asn Glu Leu  
 230 235 240 245  
 cta gca cag cat ttc gct taatgttgta ggcattgttca caa 876  
 Leu Ala Gln His Phe Ala  
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&lt;210&gt; 470

&lt;211&gt; 251

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 470

Met Ala Ile Leu His Ser Val Ser Tyr Gly Thr Ser Asp Asn Thr Leu  
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 Val Phe Ile Gly Ser Leu Gly Ser Thr Thr Asp Met Trp Leu Pro Gln  
 20 25 30  
 Leu Asp Ala Leu His Lys Asp Phe Arg Val Ile Ala Val Asp His Arg  
 35 40 45  
 Gly His Gly Leu Ser Glu Leu Ile Glu Gly Thr Pro Thr Val Ala Asp  
 50 55 60  
 Leu Ala Gln Asp Val Leu Asp Thr Leu Asp Asp Leu Gly Val Gly Asn  
 65 70 75 80  
 Phe Gly Val Ile Gly Leu Ser Leu Gly Gly Ala Val Ala Gln Tyr Leu  
 85 90 95  
 Ala Ala Thr Ser Asp Arg Val Thr Lys Ala Ala Phe Met Cys Thr Ala  
 100 105 110  
 Ala Lys Phe Gly Glu Pro Gln Gly Trp Leu Asp Arg Ala Ala Ala Cys  
 115 120 125  
 Arg Glu Asn Gly Thr Gly Ser Leu Ser Glu Ala Val Ile Gln Arg Trp  
 130 135 140  
 Phe Ser Pro Thr Trp Leu Glu Asn Asn Pro Ala Ser Arg Glu His Phe  
 145 150 155 160  
 Glu Ala Met Val Ala Gly Thr Pro Ser Glu Gly Tyr Ala Leu Cys Cys

195

200

&lt;210&gt; 469

&lt;211&gt; 876

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(853)

&lt;223&gt; RXN01115

&lt;400&gt; 469

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                                         Met Ala Ile Leu His
                                         1           5

agc gtt tcc tac gga act tcc gac aac acc ttg gtg ttc att ggc tcg 163
Ser Val Ser Tyr Gly Thr Ser Asp Asn Thr Leu Val Phe Ile Gly Ser
                        10                        15                        20

ttg ggt tcc acc acc gac atg tgg ctg cca cag ctg gat gcc ttg cat 211
Leu Gly Ser Thr Thr Asp Met Trp Leu Pro Gln Leu Asp Ala Leu His
                        25                        30                        35

aag gat ttc cgc gtc atc gct gtt gat cac cgc gga cat ggt ctg tct 259
Lys Asp Phe Arg Val Ile Ala Val Asp His Arg Gly His Gly Leu Ser
                        40                        45                        50

gaa ctc atc gaa ggc acc ccc act gtg gcg gat ctg gcg cag gat gtg 307
Glu Leu Ile Glu Gly Thr Pro Thr Val Ala Asp Leu Ala Gln Asp Val
                        55                        60                        65

ctg gat acc ctc gat gac ctg ggt gtc gga aac ttc ggc gtc atc gga 355
Leu Asp Thr Leu Asp Asp Leu Gly Val Gly Asn Phe Gly Val Ile Gly
                        70                        75                        80                        85

cta tct ctc ggc gga gcg gtt gca caa tac ttg gcg gcc acc tct gat 403
Leu Ser Leu Gly Gly Ala Val Ala Gln Tyr Leu Ala Ala Thr Ser Asp
                        90                        95                        100

cgt gtc acc aag gca gca ttc atg tgt acc gct gca aaa ttc ggc gag 451
Arg Val Thr Lys Ala Ala Phe Met Cys Thr Ala Ala Lys Phe Gly Glu
                        105                        110                        115

ccc cag ggc tgg cta gat cgc gcc gca gcg tgc cgc gaa aac ggc act 499
Pro Gln Gly Trp Leu Asp Arg Ala Ala Ala Cys Arg Glu Asn Gly Thr
                        120                        125                        130

ggt tct ctg tcc gaa gct gtg atc cag cgc tgg ttc tcc ccc act tgg 547
Gly Ser Leu Ser Glu Ala Val Ile Gln Arg Trp Phe Ser Pro Thr Trp
                        135                        140                        145

ttg gag aac aac cca gcg tcc cgc gag cac ttc gaa gcc atg gtt gcc 595
Leu Glu Asn Asn Pro Ala Ser Arg Glu His Phe Glu Ala Met Val Ala
                        150                        155                        160                        165

ggc acc cca tct gag ggt tac gcg ctg tgc tgc gag gcg ttg gca acc 643

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gag tgt cgc ctc cca ctg act ggc gcg aag tgc gtg gac atg att gtc 595  
 Glu Cys Arg Leu Pro Leu Thr Gly Ala Lys Cys Val Asp Met Ile Val  
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acc acc cac gct gtg ttc tct gtg gac cct gaa gaa ggc ctc acg ctc 643  
 Thr Thr His Ala Val Phe Ser Val Asp Pro Glu Glu Gly Leu Thr Leu  
 170 175 180

atc gag tgc gcc gac ggt gtc acc gtt gag gaa ctc cgc gaa atc acc 691  
 Ile Glu Cys Ala Asp Gly Val Thr Val Glu Glu Leu Arg Glu Ile Thr  
 185 190 195

gaa gcc gat ttc aaa gtt gct taagcaaacg ctgcgcaatt aag 735  
 Glu Ala Asp Phe Lys Val Ala  
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<210> 468

<211> 204

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 468

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Leu Gly Ile Gly Met Pro Thr Leu Ile Pro Gly Tyr Leu Pro Glu Gly  
 20 25 30

Leu Glu Val Ile Leu His Ser Glu Asn Gly Val Leu Gly Val Gly Pro  
 35 40 45

Tyr Pro Thr Glu Glu Glu Leu Asp Pro Glu Leu Ile Asn Ala Gly Lys  
 50 55 60

Glu Thr Ile Thr Val Ala Pro Gly Ala Ser Tyr Phe Ser Ser Ser Asp  
 65 70 75 80

Ser Phe Ala Met Ile Arg Ser Lys Ser Val Asp Val Ala Val Leu Gly  
 85 90 95

Val Met Glu Val Ser Gln Tyr Gly Asp Leu Ala Asn Trp Met Ile Pro  
 100 105 110

Gly Lys Leu Val Lys Gly Met Gly Gly Ala Met Asp Leu Val His Gly  
 115 120 125

Ala Ser Lys Ile Ile Ala Met Thr Asp His Ile Thr Lys Lys Gly Ala  
 130 135 140

Pro Lys Ile Leu Lys Glu Cys Arg Leu Pro Leu Thr Gly Ala Lys Cys  
 145 150 155 160

Val Asp Met Ile Val Thr Thr His Ala Val Phe Ser Val Asp Pro Glu  
 165 170 175

Glu Gly Leu Thr Leu Ile Glu Cys Ala Asp Gly Val Thr Val Glu Glu  
 180 185 190

Leu Arg Glu Ile Thr Glu Ala Asp Phe Lys Val Ala

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115              120              125
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130              135              140

Gln Leu Asp
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<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(712)
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Met Ala Ala Arg Val
1 5

gcc cag gaa ctt gaa gac ggc cag tac gtc aac ctc ggc atc ggc atg 163
Ala Gln Glu Leu Glu Asp Gly Gln Tyr Val Asn Leu Gly Ile Gly Met
10 15 20

cct aca ctt atc ccc ggc tac ctg cct gag gga cta gag gtt atc ctt 211
Pro Thr Leu Ile Pro Gly Tyr Leu Pro Glu Gly Leu Glu Val Ile Leu
25 30 35

cac tcc gaa aac ggt gtg ctg ggc gtt gga cct tac cca act gaa gag 259
His Ser Glu Asn Gly Val Leu Gly Val Gly Pro Tyr Pro Thr Glu Glu
40 45 50

gaa ctt gat cct gag ctg atc aac gcc ggc aag gaa acc atc acg gtt 307
Glu Leu Asp Pro Glu Leu Ile Asn Ala Gly Lys Glu Thr Ile Thr Val
55 60 65

gca cct ggc gca tcc tac ttc tcc tct tct gat tct ttc gcc atg atc 355
Ala Pro Gly Ala Ser Tyr Phe Ser Ser Ser Asp Ser Phe Ala Met Ile
70 75 80 85

cgc tcc aag tct gtc gac gtt gca gtc ttg ggc gtt atg gaa gtc tcc 403
Arg Ser Lys Ser Val Asp Val Ala Val Leu Gly Val Met Glu Val Ser
90 95 100

cag tac ggc gac ctg gcc aac tgg atg att ccc ggc aag ctg gtc aag 451
Gln Tyr Gly Asp Leu Ala Asn Trp Met Ile Pro Gly Lys Leu Val Lys
105 110 115

ggt atg ggt ggc gca atg gat ctg gtg cac ggc gca tcc aag atc atc 499
Gly Met Gly Gly Ala Met Asp Leu Val His Gly Ala Ser Lys Ile Ile
120 125 130

gcc atg acc gat cac atc acc aag aag ggc gct ccg aag atc ctt aag 547
Ala Met Thr Asp His Ile Thr Lys Lys Gly Ala Pro Lys Ile Leu Lys
135 140 145

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25										30										35										
acc	ctg	ttc	ggg	gat	tta	ggt	tta	gac	gga	ctc	tct	gga	aac	tac	acc	259														
Thr	Leu	Phe	Gly	Asp	Leu	Gly	Leu	Asp	Gly	Leu	Ser	Gly	Asn	Tyr	Thr															
		40					45					50																		
gac	act	gag	att	gac	ggc	tac	ggc	gac	gca	ttc	ctg	ctg	gtt	gca	gcg	307														
Asp	Thr	Glu	Ile	Asp	Gly	Tyr	Gly	Asp	Ala	Phe	Leu	Leu	Val	Ala	Ala															
	55					60					65																			
cta	tcc	gtg	ttg	atg	gct	gaa	aac	aaa	gca	aca	ggt	ggc	gtg	aat	ctg	355														
Leu	Ser	Val	Leu	Met	Ala	Glu	Asn	Lys	Ala	Thr	Gly	Gly	Val	Asn	Leu															
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Gly	Glu	Leu	Gly	Gly	Ala	Asp	Lys	Ser	Ile	Arg	Leu	His	Val	Glu	Ser															
			90					95					100																	
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Lys	Glu	Asn	Thr	Gln	Ile	Asn	Thr	Ala	Leu	Lys	Tyr	Phe	Ala	Leu	Ser															
		105						110					115																	
cca	gaa	gac	cac	gca	gca	gca	gat	cgc	ttc	gat	gag	gat	gac	ctg	tct	499														
Pro	Glu	Asp	His	Ala	Ala	Ala	Asp	Arg	Phe	Asp	Glu	Asp	Asp	Leu	Ser															
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Glu	Leu	Ala	Asn	Leu	Ser	Glu	Glu	Leu	Arg	Gly	Gln	Leu	Asp																	
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&lt;210&gt; 466

&lt;211&gt; 147

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 466

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Glu	Glu	Ala	Thr	Ala	Leu	Val	Ser	Tyr	Leu	Ala	Gln	Ala	Ser	Gly	Asp
		20						25					30		

Pro	Ile	Glu	Val	His	Thr	Leu	Phe	Gly	Asp	Leu	Gly	Leu	Asp	Gly	Leu
	35					40					45				

Ser	Gly	Asn	Tyr	Thr	Asp	Thr	Glu	Ile	Asp	Gly	Tyr	Gly	Asp	Ala	Phe
	50				55					60					

Leu	Leu	Val	Ala	Ala	Leu	Ser	Val	Leu	Met	Ala	Glu	Asn	Lys	Ala	Thr
	65				70				75						80

Gly	Gly	Val	Asn	Leu	Gly	Glu	Leu	Gly	Gly	Ala	Asp	Lys	Ser	Ile	Arg
			85					90						95	

Leu	His	Val	Glu	Ser	Lys	Glu	Asn	Thr	Gln	Ile	Asn	Thr	Ala	Leu	Lys
		100					105					110			

Tyr	Phe	Ala	Leu	Ser	Pro	Glu	Asp	His	Ala	Ala	Ala	Asp	Arg	Phe	Asp
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Val Ser Ser Lys Ser Gly 469  
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<211> 123  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 464  
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Val Gly Glu Tyr Asp Asp Val His Ile Ala Ala Leu Leu Ala Thr Ile  
35 40 45  
Arg Thr Arg Gly Glu Gln Phe Ala Asp Ile Ala Gly Ala Ala Lys Ala  
50 55 60  
Phe Leu Ala Ala Ala Arg Pro Phe Pro Ile Thr Gly Ala Gly Leu Leu  
65 70 75 80  
Asp Ser Ala Gly Thr Gly Gly Asp Gly Ala Asn Thr Ile Asn Ile Thr  
85 90 95  
Thr Gly Ala Ser Leu Ile Ala Ala Ser Gly Gly Val Lys Leu Val Lys  
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His Gly Asn Arg Ser Val Ser Ser Lys Ser Gly  
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<213> Corynebacterium glutamicum

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<223> RXN02918

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Met Ser Glu Ile Leu  
1 5  
gaa acc tat tgg gca ccc cac ttt gga aaa acc gaa gaa gcc aca gca 163  
Glu Thr Tyr Trp Ala Pro His Phe Gly Lys Thr Glu Glu Ala Thr Ala  
10 15 20  
ctc gtt tca tac ctg gca caa gct tcc ggc gat ccc att gag gtt cac 211  
Leu Val Ser Tyr Leu Ala Gln Ala Ser Gly Asp Pro Ile Glu Val His

130	135	140
Ser Leu Gly Cys Val Val Ala Pro Asp Gly Ile Glu Ser Leu Gly Thr		
145	150	155 160
Cys Ser Ser Glu Ile Gly Asp Val Ile Met Ala Ala Arg Thr Thr Asp		
	165	170 175
Gly Lys Ala Ile Gly Leu Gln Phe His Pro Glu Ser Val Leu Ser Pro		
	180	185 190
Thr Gly Pro Val Ile Leu Ser Arg Cys Val Glu Gln Leu Leu Ala Asn		
	195	200 205

&lt;210&gt; 463

&lt;211&gt; 469

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(469)

&lt;223&gt; RXN03007

&lt;400&gt; 463

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gaacagcttc tcgcgaacta ataaaaaaag gatttgattc	atg act tct cca gca	115
	Met Thr Ser Pro Ala	
	1 5	

aca ctg aaa gtt ctc aac gcc tac ttg gat aac ccc act cca acc ctg	163
Thr Leu Lys Val Leu Asn Ala Tyr Leu Asp Asn Pro Thr Pro Thr Leu	
	10 15 20

gag gag gca att gag gtg ttc acc ccg ctg acc gtg ggt gaa tac gat	211
Glu Glu Ala Ile Glu Val Phe Thr Pro Leu Thr Val Gly Glu Tyr Asp	
	25 30 35

gac gtg cac atc gca gcg ctg ctt gcc acc atc cgt act cgc ggt gag	259
Asp Val His Ile Ala Ala Leu Leu Ala Thr Ile Arg Thr Arg Gly Glu	
	40 45 50

cag ttc gct gat att gcc ggc gct gcc aag gcg ttc ctc gcg gcg gct	307
Gln Phe Ala Asp Ile Ala Gly Ala Ala Lys Ala Phe Leu Ala Ala Ala	
	55 60 65

cgt ccg ttc ccg att act ggc gca ggt ttg cta gat tcc gct ggt act	355
Arg Pro Phe Pro Ile Thr Gly Ala Gly Leu Leu Asp Ser Ala Gly Thr	
	70 75 80 85

ggt ggc gac ggt gcc aac acc atc aac atc acc acc ggc gca tcc ctg	403
Gly Gly Asp Gly Ala Asn Thr Ile Asn Ile Thr Thr Gly Ala Ser Leu	
	90 95 100

atc gca gca tcc ggt gga gtg aag ctg gtt aag cac ggc aac cgt tcg	451
Ile Ala Ala Ser Gly Gly Val Lys Leu Val Lys His Gly Asn Arg Ser	

Gly Thr Thr Asp Asn Met Ile Leu Thr Asp Ala Gly Val Gln Ser Pro  
 105 110 115  
 gtt ttt gca ggt ctt gcc act gat gtt gag cct gat cat cca gaa atc 499  
 Val Phe Ala Gly Leu Ala Thr Asp Val Glu Pro Asp His Pro Glu Ile  
 120 125 130  
 cca ggc cgc aag gtt cca att ggc cgt tat cac tca ctg ggc tgc gtg 547  
 Pro Gly Arg Lys Val Pro Ile Gly Arg Tyr His Ser Leu Gly Cys Val  
 135 140 145  
 gtt gcc cca gac ggt att gaa tca cta ggt acc tgt tcc tcg gag att 595  
 Val Ala Pro Asp Gly Ile Glu Ser Leu Gly Thr Cys Ser Ser Glu Ile  
 150 155 160 165  
 ggt gat gtc atc atg gcg gca cgc acc acc gat gga aag gcc att ggc 643  
 Gly Asp Val Ile Met Ala Ala Arg Thr Thr Asp Gly Lys Ala Ile Gly  
 170 175 180  
 ctg cag ttt cac cct gag tca gtg cta agc cca acg ggt cct gtc att 691  
 Leu Gln Phe His Pro Glu Ser Val Leu Ser Pro Thr Gly Pro Val Ile  
 185 190 195  
 ttg tcc cgc tgt gtc gaa cag ctt ctc gcg aac taataaaaaa aggatttgat 744  
 Leu Ser Arg Cys Val Glu Gln Leu Leu Ala Asn  
 200 205  
 tca 747

&lt;210&gt; 462

&lt;211&gt; 208

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 462

Met Thr His Val Val Leu Ile Asp Asn His Asp Ser Phe Val Tyr Asn  
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 Leu Val Asp Ala Phe Ala Val Ala Gly Tyr Lys Cys Thr Val Phe Arg  
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 Asn Thr Val Pro Val Glu Thr Ile Leu Ala Ala Asn Pro Asp Leu Ile  
 35 40 45  
 Cys Leu Ser Pro Gly Pro Gly Tyr Pro Ala Asp Ala Gly Asn Met Met  
 50 55 60  
 Ala Leu Ile Glu Arg Thr Leu Gly Gln Ile Pro Leu Leu Gly Ile Cys  
 65 70 75 80  
 Leu Gly Tyr Gln Ala Leu Ile Glu Tyr His Gly Gly Lys Val Glu Pro  
 85 90 95  
 Cys Gly Pro Val His Gly Thr Thr Asp Asn Met Ile Leu Thr Asp Ala  
 100 105 110  
 Gly Val Gln Ser Pro Val Phe Ala Gly Leu Ala Thr Asp Val Glu Pro  
 115 120 125  
 Asp His Pro Glu Ile Pro Gly Arg Lys Val Pro Ile Gly Arg Tyr His

ggc cac aag tgg att cgt ttg agc ctg tgc gcg tca aag gaa gac acc 595  
 Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser Lys Glu Asp Thr  
 150 155 160 165

att gaa ggt gtg cgc aaa atc gga gaa ttc atc aaa aaa tagcagcgac 644  
 Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys Lys  
 170 175

taggttagtt tcg 657

<210> 488

<211> 178

<212> PRT

<213> Corynebacterium glutamicum

<400> 488

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Ala Ile Val Val Gly Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp  
 20 25 30

Arg Val Gly Trp Ile Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu  
 35 40 45

Asn Leu Gln Ala Ser Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala  
 50 55 60

Ala Gly Arg Ala Ala Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala  
 65 70 75 80

His Val Glu Ala Tyr Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu  
 85 90 95

Pro Glu Ile Gly Leu Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr  
 100 105 110

Leu Trp Val Asp Val Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala  
 115 120 125

Leu Arg Leu Leu Asp Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp  
 130 135 140

Phe Asp Pro Glu Glu Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala  
 145 150 155 160

Ser Lys Glu Asp Thr Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile  
 165 170 175

Lys Lys

<210> 489

<211> 385

<212> DNA

<213> Corynebacterium glutamicum

<220>

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Lys		
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	Met Ser Phe Gly Arg	
	1 5	
cgc ctg gca act gcg cat cag ttt tcc aag aac gcc atc gtg gtg ggt	163	
Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala Ile Val Val Gly		
10 15 20		
acc ttg tcc aag tac ttc tcc atg acg ggt tgg cgc gtg ggt tgg atc	211	
Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg Val Gly Trp Ile		
25 30 35		
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Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn Leu Gln Ala Ser		
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Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala Gly Arg Ala Ala		
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Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His Val Glu Ala Tyr		
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Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro Glu Ile Gly Leu		
90 95 100		
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Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu Trp Val Asp Val		
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Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu Arg Leu Leu Asp		
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Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe Asp Pro Glu Glu		
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Thr Leu Met Phe Cys Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala  
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 Thr Thr Gly Ser Ser Gly Gly Phe Val Ala Ser Phe Ile Ala Thr Leu  
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 Asp His Gly Asp Tyr Val Ala Met Pro Thr Pro Gly Tyr Pro Ala Tyr  
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 Pro His Lys Pro Lys Ala Val Ile Val Thr Ser Pro Gly Asn Pro Thr  
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 Asp Asp Asn Asp Ala Val Leu Ile Ser Asp Glu Asp Tyr His Gly Met  
 180 185 190  
 Ser Phe Gly Arg Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala  
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 Gly Arg Ala Ala Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His  
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 Val Glu Ala Tyr Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro  
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 Glu Ile Gly Leu Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu  
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 Trp Val Asp Val Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu  
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 Arg Leu Leu Asp Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe  
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 Asp Pro Glu Glu Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser

Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala Ile Val Val Gly Thr  
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 gtt cca gat gag ctg gtc aca ccg att gaa aac ctg cag gct tct ctt 835  
 Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn Leu Gln Ala Ser Leu  
 230 235 240 245  
 tcc ttg tgt gct cct gcc atc ggg cag gct gcg gga cgc gca gcc ttc 883  
 Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala Gly Arg Ala Ala Phe  
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 act ttg gag gct ggg gcc gaa ctt gat gcc cac gtt gaa gcg tat cgc 931  
 Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His Val Glu Ala Tyr Arg  
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 Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro Glu Ile Gly Leu Gly  
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 Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu Trp Val Asp Val Ser  
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 Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe Asp Pro Glu Glu Gly  
 330 335 340  
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 His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser Lys Glu Asp Thr Ile  
 345 350 355  
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 360 365  
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 1230

&lt;210&gt; 486

&lt;211&gt; 369

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 486

Met Gln Met Leu Asp Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp  
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&lt;221&gt; CDS

&lt;222&gt; (101)..(1207)

&lt;223&gt; RXS00618

&lt;400&gt; 485

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                                         Met Gln Met Leu Asp
                                         1 5

cga gtc cac cgt cgc agg cgc gaa ggc aaa gac acc tta atg ttc tgc 163
Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp Thr Leu Met Phe Cys
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Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala Val Ile Glu Glu Ala
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gag atc gct ctt cgc tcg ggt cct ttg gga tac acc gag gtg att ggt 259
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gat cgt gag ttc cgt gaa cgc atc gcc gat tgg cac tct gct act tat 307
Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp His Ser Ala Thr Tyr
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Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val Thr Thr Gly Ser Ser
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Val Ala Met Pro Thr Pro Gly Tyr Pro Ala Tyr Arg Asn Ile Leu Glu
                        105 110 115

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Ser Leu Gly Ala Lys Val Leu Asn Leu Arg Cys Thr Ala Glu Thr Arg
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Phe Gln Pro Thr Ala Gln Met Leu Glu Glu Leu Pro His Lys Pro Lys
                        135 140 145

gct gtt att gtc acc agc cca gga aac cca acg ggc acc atc att gat 595
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ccg gaa gag cta gag cgc atc gcc aag tgg tgc gat gac aat gat gct 643
Pro Glu Glu Leu Glu Arg Ile Ala Lys Trp Cys Asp Asp Asn Asp Ala
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gtt ctt atc tct gat gag gac tac cac ggc atg agc ttt ggt cgt ccg 691
Val Leu Ile Ser Asp Glu Asp Tyr His Gly Met Ser Phe Gly Arg Pro
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cgc gcg ttc ccc gag ggt gcg cgc att tcg gtg acc aac gcc gag gaa 480  
 Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu  
 145 150 155 160

act gac aag ctg ctg cgc gcg tgg gag gcc atc aat gct ggg 522  
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<211> 174

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 484

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His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr  
 35 40 45

Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile  
 50 55 60

Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala  
 65 70 75 80

Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met  
 85 90 95

Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala  
 100 105 110

Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu  
 115 120 125

Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile  
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Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly  
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<210> 485

<211> 1230

<212> DNA

<213> *Corynebacterium glutamicum*

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 225 230 235 240  
 Gly Glu Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile  
 245 250 255  
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 Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile  
 20 25 30  
 cac cgc cac gac aac gtg att ggt ttg cgc acg ttc tcc aag gcg tat 144  
 His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr  
 35 40 45  
 ggc ctg gcg ggc ttg cgt gtt ggt tac gcc ttc gga aac gca gag atc 192  
 Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile  
 50 55 60  
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 Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala  
 65 70 75 80  
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 Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met  
 85 90 95  
 gaa cgg gtg gag gaa acc gtc gaa aag cgt gat gct gtg gtg tca gcg 336  
 Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala  
 100 105 110  
 ctt ggt gct gcg ccg acg cag gcc aat ttc gtc tgg ctg ccg ggc gag 384  
 Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu  
 115 120 125

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 Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile Arg Ala Phe  
                     250                    255                    260

ccc gag ggt gcg cgc att tcg gtg acc aac gcc gag gaa act gac aag 931  
 Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu Thr Asp Lys  
                     265                    270                    275

ctg ctg cgc gcg tgg gag gcc atc aat gct ggg tagtctttgg cgttttgccg 984  
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tgc 987

<210> 482

<211> 288

<212> PRT

<213> Corynebacterium glutamicum

<400> 482

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Gln Leu Val Gln Ala Thr Cys Ala Gln Gly Asp Glu Val Ile Phe Pro  
                     35                    40                    45

Trp Arg Ser Phe Glu Ala Tyr Pro Ile Phe Ala Gln Val Ala Gly Ala  
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Thr Pro Val Ala Ile Pro Leu Thr Ala Asp Gln Asn His Asp Leu Asp  
                     65                    70                    75                    80

Ala Met Ala Ala Ala Ile Thr Asp Lys Thr Arg Leu Ile Phe Ile Cys  
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Asn Pro Asn Asn Pro Ser Gly Thr Thr Ile Thr Gln Ala Gln Phe Asp  
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Asn Phe Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu  
                     115                    120                    125

Ala Tyr Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu  
                     130                    135                    140

Glu Ile His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys  
                     145                    150                    155                    160

Ala Tyr Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala  
                     165                    170                    175

Glu Ile Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn  
                     180                    185                    190

Ser Ala Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu  
                     195                    200                    205

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ctc	cgt	gag	gct	ctt	gca	gag	cat	tta	gag	gtt	gag	ttt	gac	cag	gtc	163	
Leu	Arg	Glu	Ala	Leu	Ala	Glu	His	Leu	Glu	Val	Glu	Phe	Asp	Gln	Val		
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Thr	Val	Gly	Cys	Gly	Ser	Ser	Ala	Leu	Cys	Gln	Gln	Leu	Val	Gln	Ala		
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acg	tgc	gct	cag	ggc	gat	gag	gtc	att	ttt	cca	tgg	cgc	agc	ttt	gag	259	
Thr	Cys	Ala	Gln	Gly	Asp	Glu	Val	Ile	Phe	Pro	Trp	Arg	Ser	Phe	Glu		
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Ala	Tyr	Pro	Ile	Phe	Ala	Gln	Val	Ala	Gly	Ala	Thr	Pro	Val	Ala	Ile		
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Pro	Leu	Thr	Ala	Asp	Gln	Asn	His	Asp	Leu	Asp	Ala	Met	Ala	Ala	Ala		
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Ile	Thr	Asp	Lys	Thr	Arg	Leu	Ile	Phe	Ile	Cys	Asn	Pro	Asn	Asn	Pro		
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Ser	Gly	Thr		Ile	Thr	Gln	Ala	Gln	Phe	Asp	Asn	Phe	Met	Glu	Lys		
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Asn	Arg	Ala	Asp	Asp	Thr	Pro	Val	Ala	Thr	Glu	Glu	Ile	His	Arg	His		
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Asp	Asn	Val	Ile	Gly	Leu	Arg	Thr	Phe	Ser	Lys	Ala	Tyr	Gly	Leu	Ala		
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Gly	Leu	Arg	Val	Gly	Tyr	Ala	Phe	Gly	Asn	Ala	Glu	Ile	Ile	Ala	Ala		
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Met	Asn	Lys	Val	Ala	Ile	Pro	Phe	Ala	Val	Asn	Ser	Ala	Ala	Gln	Ala		
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Ala	Ala	Leu	Ala	Ser	Leu	Asn	Ser	Ala	Asp	Glu	Leu	Met	Glu	Arg	Val		
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gag	gaa	acc	gtc	gaa	aag	cgt	gat	gct	gtg	gtg	tca	gcg	ctt	ggg	gct	787	
Glu	Glu	Thr	Val	Glu	Lys	Arg	Asp	Ala	Val	Val	Ser	Ala	Leu	Gly	Ala		
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gcg	ccg	acg	cag	gcc	aat	ttc	gtc	tgg	ctg	ccg	ggc	gag	ggc	gcc	gct	835	
Ala	Pro	Thr	Gln	Ala	Asn	Phe	Val	Trp	Leu	Pro	Gly	Glu	Gly	Ala	Ala		
				230					235					240			
														245			

Asn Tyr Ala Asn Asp Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp  
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 Arg Thr Gly Pro Leu Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys  
 85 90 95  
 Lys Val Lys Ala Ala Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala  
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 Ile Leu Cys Val Leu Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro  
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 Tyr Gly Tyr Arg Gly Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly  
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 180 185 190  
 Val Asn Leu Ala Asn Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr  
 195 200 205  
 Gly Lys Ile Thr Leu Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys  
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 Ala Leu Lys Ala Ala Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp  
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 Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser Trp Ala Gly Leu Ala  
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 gcc gca gtt ggc gtg ggg tcg atg tct gct ggc gtg aac ttg gcc aac 691  
 Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly Val Asn Leu Ala Asn  
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 Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys Leu Phe Leu Ala Leu  
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 265 270 275  
  
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 Lys Ala Leu Leu Ala Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val  
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260 265 270

Leu Ile Pro Val Ile Gly Ser Thr Gly Arg Ala Met Ala Leu Trp Ala  
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 Val Ala Ala Phe His Asp Gly Phe Val Trp Trp Lys Ala Leu Leu Ala  
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 ctt gtc gtg gcg tgg gct ttg atc atc ggt gtg aat tac gcc aat gat 307  
 Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val Asn Tyr Ala Asn Asp  
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 Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp Arg Thr Gly Pro Leu  
 70 75 80 85  
 cga ctc act ggt tct ggg ttg gct gag ccg aag aaa gtg aaa gct gcg 403  
 Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys Lys Val Lys Ala Ala  
 90 95 100  
 gcg ttt att tct ttc ggt atc gca ggt gtc gcc ggc acc gcg ctg agc 451  
 Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala Gly Thr Ala Leu Ser  
 105 110 115  
 ctg ttg agc gcg tgg tgg ctg atc ctc atc ggc atc ctg tgt gtg ctg 499  
 Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly Ile Leu Cys Val Leu  
 120 125 130  
 ggc gcg tgg ttc tac acc ggc ggt aaa aat cct tat ggt tac cgc ggc 547  
 Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro Tyr Gly Tyr Arg Gly  
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 Lys Ala Leu Leu Ala Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val  
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 Asn Tyr Ala Asn Asp Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp  
 65 70 75 80  
 Arg Thr Gly Pro Leu Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys  
 85 90 95  
 Lys Val Lys Ala Ala Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala  
 100 105 110  
 Gly Thr Ala Leu Ser Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly  
 115 120 125  
 Ile Leu Cys Val Leu Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro  
 130 135 140  
 Tyr Gly Tyr Arg Gly Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly  
 145 150 155 160  
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 165 170 175  
 Trp Ala Gly Leu Ala Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly  
 180 185 190  
 Val Asn Leu Ala Asn Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr  
 195 200 205  
 Gly Lys Ile Thr Leu Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys  
 210 215 220  
 Leu Phe Leu Ala Leu Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu  
 225 230 235 240  
 Ala Phe Val Ala Trp Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu  
 245 250 255  
 Ala Leu Lys Ala Ala Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp

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tac tct gat ggc att cgt ggc acc gat gaa gac cgc acc ggt cct ctg Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp Arg Thr Gly Pro Leu 70 75 80 85	355
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gcc gca gtt ggc gtg ggg tgc atg tct gct ggc gtg aac ttg gcc aac Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly Val Asn Leu Ala Asn 185 190 195	691
aat att cgc gat att cca acc gat agc aag acc gga aaa att acc ctc Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr Gly Lys Ile Thr Leu 200 205 210	739
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<211> 437

<212> PRT

<213> Corynebacterium glutamicum

<400> 496

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35 40 45

Ile Arg Gly Pro Val Ala Ala Glu Ala Glu Arg Met Glu Leu Asp Gly  
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His Asn Ile Leu Lys Leu Asn Thr Gly Asn Pro Ala Val Phe Gly Phe  
65 70 75 80

Asp Ala Pro Asp Val Ile Met Arg Asp Met Ile Ala Asn Leu Pro Thr  
85 90 95

Ser Gln Gly Tyr Ser Thr Ser Lys Gly Ile Ile Pro Ala Arg Arg Ala  
100 105 110

Val Val Thr Arg Tyr Glu Val Val Pro Gly Phe Pro His Phe Asp Val  
115 120 125

Asp Asp Val Phe Leu Gly Asn Gly Val Ser Glu Leu Ile Thr Met Thr  
130 135 140

Thr Gln Ala Leu Leu Asn Asp Gly Asp Glu Val Leu Ile Pro Ala Pro  
145 150 155 160

Asp Tyr Pro Leu Trp Thr Ala Ala Thr Ser Leu Ala Gly Gly Lys Pro  
165 170 175

Val His Tyr Leu Cys Asp Glu Glu Asp Asp Trp Asn Pro Ser Ile Glu  
180 185 190

Asp Ile Lys Ser Lys Ile Ser Glu Lys Thr Lys Ala Ile Val Val Ile  
195 200 205

Asn Pro Asn Asn Pro Thr Gly Ala Val Tyr Pro Arg Arg Val Leu Glu  
210 215 220

Gln Ile Val Glu Ile Ala Arg Glu His Asp Leu Leu Ile Leu Ala Asp  
225 230 235 240

Glu Ile Tyr Asp Arg Ile Leu Tyr Asp Asp Ala Glu His Ile Ser Leu  
245 250 255

Ala Thr Leu Ala Pro Asp Leu Leu Cys Ile Thr Tyr Asn Gly Leu Ser  
260 265 270

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 230 235 240 245

att ctc tac gat gat gcc gag cac atc agc ctg gca acc ctt gca cca 883  
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gat ctc ctt tgc atc aca tac aac ggt cta tcc aag gca tac cgc gtc 931  
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gca gga tac cga gct ggc tgg atg gta ttg act gga cca aag caa tac 979  
 Ala Gly Tyr Arg Ala Gly Trp Met Val Leu Thr Gly Pro Lys Gln Tyr  
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 Ala Arg Gly Phe Ile Glu Gly Leu Glu Leu Leu Ala Gly Thr Arg Leu  
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tgc cca aat gtc cca gct cag cac gct att cag gta gct ctg ggt gga  
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 Cys Pro Asn Val Pro Ala Gln His Ala Ile Gln Val Ala Leu Gly Gly  
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 1123  
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 1219  
 Cys Val Lys Pro Met Gly Ala Leu Tyr Ala Phe Pro Lys Leu Asp Pro  
 360 365 370

aac gtg tac gaa atc cac gac gac acc caa ctc atg ctg gat ctt ctc  
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 1315  
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cat cac gat cac ttc cga gtg gtc acc ctg cca tgg gca tcc cag ttg  
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 His His Asp His Phe Arg Val Val Thr Leu Pro Trp Ala Ser Gln Leu  
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 Glu Asn Ala Ile Glu Arg Leu Gly Asn Phe Leu Ser Thr Tyr Lys Gln  
 425 430 435

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Arg Lys Thr Ser Lys Thr Thr Asp Thr Ala Asn Lys Ala Val Gly Ala		
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Gln Ser Glu Lys Met Lys Asp Val Leu Tyr Glu Ile Arg Gly Pro Val		
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Leu Asn Thr Gly Asn Pro Ala Val Phe Gly Phe Asp Ala Pro Asp Val		
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Ile Met Arg Asp Met Ile Ala Asn Leu Pro Thr Ser Gln Gly Tyr Ser		
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acc tcc aaa ggc att att ccg gcc cgg cga gca gtg gtc acc cgc tac	451	
Thr Ser Lys Gly Ile Ile Pro Ala Arg Arg Ala Val Val Thr Arg Tyr		
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Glu Val Val Pro Gly Phe Pro His Phe Asp Val Asp Asp Val Phe Leu		
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ggc aac ggt gtc tca gaa cta atc acc atg acc acc caa gca ctc ctc	547	
Gly Asn Gly Val Ser Glu Leu Ile Thr Met Thr Thr Gln Ala Leu Leu		
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Thr Ala Ala Thr Ser Leu Ala Gly Gly Lys Pro Val His Tyr Leu Cys		
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gat gag gaa gat gac tgg aac cca tcc atc gaa gac atc aag tcc aaa	691	
Asp Glu Glu Asp Asp Trp Asn Pro Ser Ile Glu Asp Ile Lys Ser Lys		
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atc tca gag aaa acc aaa gct att gtg gtg atc aac ccc aac aac ccc	739	
Ile Ser Glu Lys Thr Lys Ala Ile Val Val Ile Asn Pro Asn Asn Pro		
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Asp Ile Ile Thr Asp Pro Gly Arg His Ala Asp Gln Val Gly Ser Thr  
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 Val Lys Val Thr Gly Thr Gln Glu Lys Gln Trp Leu Lys Ile Cys Ser  
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 Gln Glu Phe Gly Phe Thr Gly Leu His Val Ala Ala Ala Val Ala Asp  
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 Arg Asp Leu Ser Leu Val Gly Met Pro Phe Asp Gly Val Asp Thr Phe  
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 Ser Pro Arg Gly Val Ala Gly Ile Asp Gly Ser Val Ala Gln Ala Ile  
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 Gly Thr Ser Leu Ala Val Gln Ser Arg His Pro Asp Glu Ile Arg Ala  
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 465 470 475 480  
 Pro His Asp Ala Ser Ile Ala Asp Leu Cys Ala Gly Tyr Gly Ile Glu  
 485 490 495  
 His Gln Val Val Asp Asn Leu Gln Asp Leu Ile Ile Ala Leu Val Asp  
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&lt;210&gt; 495

&lt;211&gt; 1434

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

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&lt;222&gt; (101)..(1411)

&lt;223&gt; RXS02550

&lt;400&gt; 495

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<400> 494

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Val Arg Ile Asp Glu Arg Ser Ala Ser Phe Leu Ala Leu Ser Leu Ala
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Arg Thr Gln Ala Arg Pro Val Ala Val Val Met Thr Ser Gly Thr Ala
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Pro Leu Ile Val Leu Ser Ala Asp Arg Pro Ala His Leu Val Gly Thr
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Gly Ala Ser Gln Thr Ile Asn Gln Thr Gly Ile Phe Gly Asp Leu Ala
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Pro Thr Val Gly Ile Thr Glu Leu Asp Gln Val Ala Gln Ile Ala Glu
          130          135          140

Ser Leu Ala Gln Gly Ala Ser Gln Ile Pro Arg His Phe Asn Leu Ala
          145          150          155          160

Leu Asp Val Pro Leu Val Ala Pro Glu Leu Pro Glu Leu His Gly Glu
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Ala Val Gly Ala Ser Trp Thr His Arg Trp Ile Asn His Gly Glu Val
          180          185          190

Thr Val Asp Leu Gly Glu His Thr Leu Val Ile Ala Gly Asp Glu Ala
          195          200          205

Trp Glu Val Glu Gly Leu Glu Asp Val Pro Thr Ile Ala Glu Pro Thr
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Ala Pro Lys Pro Tyr Asn Pro Val His Pro Leu Ala Ala Glu Ile Leu
          225          230          235          240

Leu Lys Glu Gln Val Ser Ala Glu Gly Tyr Val Val Asn Thr Arg Pro
          245          250          255

Asp His Val Ile Val Val Gly His Pro Thr Leu His Arg Gly Val Leu
          260          265          270

Lys Leu Met Ser Asp Pro Gly Ile Lys Leu Thr Val Leu Ser Arg Thr
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Asp Thr Leu Phe Ala Ala Ala Ser Asn Ser Ile Arg Asp Leu Ser Leu  
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 375 380 385  
 gca ggc att gat ggt tct gtt gct caa gca atc ggc act tca ctt gct  
 1315  
 Ala Gly Ile Asp Gly Ser Val Ala Gln Ala Ile Gly Thr Ser Leu Ala  
 390 395 400 405  
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 1363  
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 1603  
 Ile Ala Asp Leu Cys Ala Gly Tyr Gly Ile Glu His Gln Val Val Asp  
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 aac ctc caa gac ctc atc atc gcg cta gtt gat acc acc gaa gta tcc  
 1651  
 Asn Leu Gln Asp Leu Ile Ile Ala Leu Val Asp Thr Thr Glu Val Ser  
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 1699  
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 1749  
 Gln Gln Gln Ala Leu Met Asp Thr Val His  
 535 540  
 gcg  
 1752



Thr	Glu	Leu	Asp	Gln	Val	Ala	Gln	Ile	Ala	Glu	Ser	Leu	Ala	Gln	Gly		
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Val	Ala	Pro	Glu	Leu	Pro	Glu	Leu	His	Gly	Glu	Ala	Val	Gly	Ala	Ser	180	
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Trp	Thr	His	Arg	Trp	Ile	Asn	His	Gly	Glu	Val	Thr	Val	Asp	Leu	Gly	195	
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Glu	His	Thr	Leu	Val	Ile	Ala	Gly	Asp	Glu	Ala	Trp	Glu	Val	Glu	Gly	210	
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Leu	Glu	Asp	Val	Pro	Thr	Ile	Ala	Glu	Pro	Thr	Ala	Pro	Lys	Pro	Tyr	225	
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Ser	Ala	Glu	Gly	Tyr	Val	Val	Asn	Thr	Arg	Pro	Asp	His	Val	Ile	Val	260	
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Val	Gly	His	Pro	Thr	Leu	His	Arg	Gly	Val	Leu	Lys	Leu	Met	Ser	Asp	275	
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Pro	Gly	Ile	Lys	Leu	Thr	Val	Leu	Ser	Arg	Thr	Asp	Ile	Ile	Thr	Asp	290	
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Pro	Gly	Arg	His	Ala	Asp	Gln	Val	Gly	Ser	Thr	Val	Lys	Val	Thr	Gly	305	
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Thr	Gln	Glu	Lys	Gln	Trp	Leu	Lys	Ile	Cys	Ser	Ala	Ala	Ser	Glu	Leu	325	
310					315					320							
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acc	ggc	ctc	cat	ggt	gcc	gca	gcc	gtg	gcg	gat	acc	tta	ggc	acc	ggc	1171	
Thr	Gly	Leu	His	Val	Ala	Ala	Ala	Val	Ala	Asp	Thr	Leu	Gly	Thr	Gly	355	
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<213> *Corynebacterium glutamicum*

<223> RXS02315

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&lt;400&gt; 492

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 35 40 45  
 Leu Val Ala Thr Val Asp Lys Ile Ala Thr Glu Leu Asn Arg Tyr Pro  
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 Glu Arg Asp Ala Val Glu Leu Arg Asp Glu Leu Ala Ala Tyr Ile Thr  
 65 70 75 80  
 Lys Gln Thr Gly Val Ala Val Thr Arg Asp Asn Leu Trp Ala Ala Asn  
 85 90 95  
 Gly Ser Asn Glu Ile Leu Gln Gln Leu Leu Gln Ala Phe Gly Gly Pro  
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 Gly Arg Thr Ala Leu Gly Phe Gln Pro Ser Tyr Ser Met His Pro Ile  
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 Leu Ala Lys Gly Thr His Thr Glu Phe Ile Ala Val Ser Arg Gly Ala  
 130 135 140  
 Asp Phe Arg Ile Asp Met Asp Val Ala Leu Glu Glu Ile Arg Ala Lys  
 145 150 155 160  
 Gln Pro Asp Ile Val Phe Val Thr Thr Pro Asn Asn Pro Thr Gly Asp  
 165 170 175  
 Val Thr Ser Leu Asp Asp Val Glu Arg Ile Ile Asn Val Ala Pro Gly  
 180 185 190  
 Ile Val Ile Val Asp Glu Ala Tyr Ala Glu Phe Ser Pro Ser Pro Ser  
 195 200 205  
 Ala Thr Thr Leu Leu Glu Lys Tyr Pro Thr Lys Leu Val Val Ser Arg  
 210 215 220  
 Thr Met Ser Lys Ala Phe Asp Phe Ala Gly Gly Arg Leu Gly Tyr Phe  
 225 230 235 240  
 Val Ala Asn Pro Ala Phe Ile Asp Ala Val Met Leu Val Arg Leu Pro  
 245 250 255  
 Tyr His Leu Ser Ala Leu Ser Gln Ala Ala Ala Ile Val Ala Leu Arg  
 260 265 270  
 His Ser Ala Asp Thr Leu Gly Thr Val Glu Lys Leu Ser Val Glu Arg  
 275 280 285  
 Val Arg Val Ala Ala Arg Leu Glu Glu Leu Gly Tyr Ala Val Val Pro  
 290 295 300  
 Ser Glu Ser Asn Phe Val Phe Phe Gly Asp Phe Ser Asp Gln His Ala  
 305 310 315 320

gat gtt gag cgc atc atc aac gtt gcc cca ggc atc gtg atc gtg gat 691  
 Asp Val Glu Arg Ile Ile Asn Val Ala Pro Gly Ile Val Ile Val Asp  
 185 190 195

gaa gct tat gcg gaa ttc tcc cca tca cct tca gca acc act ctt ctg 739  
 Glu Ala Tyr Ala Glu Phe Ser Pro Ser Pro Ser Ala Thr Thr Leu Leu  
 200 205 210

gag aag tac cca acc aag ctg gtg gtg tcc cgc acc atg agt aag gct 787  
 Glu Lys Tyr Pro Thr Lys Leu Val Val Ser Arg Thr Met Ser Lys Ala  
 215 220 225

ttt gat ttc gca ggt gga cgc ctc ggc tac ttc gtg gcc aac cca gcg 835  
 Phe Asp Phe Ala Gly Gly Arg Leu Gly Tyr Phe Val Ala Asn Pro Ala  
 230 235 240 245

ttt atc gac gcc gtg atg cta gtc cgc ctt ccg tat cat ctt tca gcg 883  
 Phe Ile Asp Ala Val Met Leu Val Arg Leu Pro Tyr His Leu Ser Ala  
 250 255 260

ctg agc caa gca gcc gca atc gta gcg ctg cgt cac tcc gct gac acg 931  
 Leu Ser Gln Ala Ala Ala Ile Val Ala Leu Arg His Ser Ala Asp Thr  
 265 270 275

ctg gga acc gtc gaa aag ctc tct gta gag cgt gtt cgc gtg gca gca 979  
 Leu Gly Thr Val Glu Lys Leu Ser Val Glu Arg Val Arg Val Ala Ala  
 280 285 290

cgc ttg gag gaa ctg ggc tac gct gtg gtt cca agt gag tcc aac ttt  
 1027  
 Arg Leu Glu Glu Leu Gly Tyr Ala Val Val Pro Ser Glu Ser Asn Phe  
 295 300 305

gtg ttc ttt gga gat ttc tcc gat cag cac gcg gca tgg cag gca ttt  
 1075  
 Val Phe Phe Gly Asp Phe Ser Asp Gln His Ala Ala Trp Gln Ala Phe  
 310 315 320 325

ttg gat agg gga gtg ctc atc cgc gat gtg gga atc gct ggg cac ttg  
 1123  
 Leu Asp Arg Gly Val Leu Ile Arg Asp Val Gly Ile Ala Gly His Leu  
 330 335 340

cgc act acc att ggt gtg cct gag gaa aat gat gcg ttt ttg gac gca  
 1171  
 Arg Thr Thr Ile Gly Val Pro Glu Glu Asn Asp Ala Phe Leu Asp Ala  
 345 350 355

gct gca gag atc atc aag ctg aac ctg taagagagaa gaatttttca  
 1218  
 Ala Ala Glu Ile Ile Lys Leu Asn Leu  
 360 365

tga  
 1221

<210> 492  
 <211> 366  
 <212> PRT  
 <213> Corynebacterium glutamicum

<210> 491  
 <211> 1221  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1198)  
 <223> RXS01105

<400> 491  
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gctttgaaaa cctccccacc accgacgagg cctaagaaaa atg acc aaa att act 115  
 Met Thr Lys Ile Thr  
 1 5

ttg agc gat ttg cca ttg cgt gaa gaa ctg cgc ggt gag cac gct tac 163  
 Leu Ser Asp Leu Pro Leu Arg Glu Glu Leu Arg Gly Glu His Ala Tyr  
 10 15 20

ggc gca ccc cag ctc aac gtt gat att cgc ctc aac acc aac gaa aac 211  
 Gly Ala Pro Gln Leu Asn Val Asp Ile Arg Leu Asn Thr Asn Glu Asn  
 25 30 35

cct tac cca ccg tca gag gca ttg gtc gct gac ttg gtt gcc acc gtg 259  
 Pro Tyr Pro Pro Ser Glu Ala Leu Val Ala Asp Leu Val Ala Thr Val  
 40 45 50

gat aag atc gcc acc gag ctg aac cgc tac cca gag cgc gat gct gtg 307  
 Asp Lys Ile Ala Thr Glu Leu Asn Arg Tyr Pro Glu Arg Asp Ala Val  
 55 60 65

gaa ctg cgt gat gag ttg gct gcg tac atc acc aag caa acc ggc gtg 355  
 Glu Leu Arg Asp Glu Leu Ala Ala Tyr Ile Thr Lys Gln Thr Gly Val  
 70 75 80 85

gct gtc acc agg gat aac ctg tgg gct gcc aat ggt tcc aat gaa att 403  
 Ala Val Thr Arg Asp Asn Leu Trp Ala Ala Asn Gly Ser Asn Glu Ile  
 90 95 100

ctg cag cag ctg ctg cag gct ttt ggt gga cct gga cgc acc gcg ttg 451  
 Leu Gln Gln Leu Leu Gln Ala Phe Gly Gly Pro Gly Arg Thr Ala Leu  
 105 110 115

gga ttc caa ccc agc tat tcc atg cac cca att ttg gct aaa ggc acc 499  
 Gly Phe Gln Pro Ser Tyr Ser Met His Pro Ile Leu Ala Lys Gly Thr  
 120 125 130

cac act gaa ttc att gcg gtg tcc cga ggt gct gat ttc cgc atc gat 547  
 His Thr Glu Phe Ile Ala Val Ser Arg Gly Ala Asp Phe Arg Ile Asp  
 135 140 145

atg gat gtg gcg ctg gaa gaa att cgt gca aag cag cct gac att gtt 595  
 Met Asp Val Ala Leu Glu Glu Ile Arg Ala Lys Gln Pro Asp Ile Val  
 150 155 160 165

ttt gtc acc acc ccg aac aac ccg acc ggt gat gtg acc tcg ctg gac 643  
 Phe Val Thr Thr Pro Asn Asn Pro Thr Gly Asp Val Thr Ser Leu Asp  
 170 175 180

&lt;221&gt; CDS

&lt;222&gt; (101)..(385)

&lt;223&gt; FRXA00627

&lt;400&gt; 489

gctgcattag agggtcgtat ctcgatctaa aagcagtagc cagataggct tgtctcttat 60

gaagccaagc actagaagca atgttcagcc gtttcgcgtc atg cag atg ttg gac 115  
Met Gln Met Leu Asp  
1 5

cga gtc cac cgt cgc agg cgc gaa ggc aaa gac acc tta atg ttc tgc 163  
Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp Thr Leu Met Phe Cys  
10 15 20

gct ggc cag ccg tca act ggt gcg cca gaa gca gtc atc gaa gaa gca 211  
Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala Val Ile Glu Glu Ala  
25 30 35

gag atc gct ctt cgc tcg ggt cct ttg gga tac acc gag gtg att ggt 259  
Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr Thr Glu Val Ile Gly  
40 45 50

gat cgt gag ttc cgt gaa cgc atc gcc gat tgg cac tct gct act tat 307  
Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp His Ser Ala Thr Tyr  
55 60 65

gac gta gac acc aac cct gac aat gtt att gtc acc acc ggt tct tca 355  
Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val Thr Thr Gly Ser Ser  
70 75 80 85

ggt gga ttc gtg gca tcg ttt atc gcc acc 385  
Gly Gly Phe Val Ala Ser Phe Ile Ala Thr  
90 95

&lt;210&gt; 490

&lt;211&gt; 95

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 490

Met Gln Met Leu Asp Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp  
1 5 10 15

Thr Leu Met Phe Cys Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala  
20 25 30

Val Ile Glu Glu Ala Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr  
35 40 45

Thr Glu Val Ile Gly Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp  
50 55 60

His Ser Ala Thr Tyr Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val  
65 70 75 80

Thr Thr Gly Ser Ser Gly Gly Phe Val Ala Ser Phe Ile Ala Thr  
85 90 95

aag gca atg gtc act gaa gcc cag ggg cta gct aca gaa gac aat ccc  
2323  
Lys Ala Met Val Thr Glu Ala Gln Gly Leu Ala Thr Glu Asp Asn Pro  
730 735 740

gat tac gca tca ctt gcc atg gcg atg cgc acc tgc gga ctg ttc acc  
2371  
Asp Tyr Ala Ser Leu Ala Met Ala Met Arg Thr Cys Gly Leu Phe Thr  
745 750 755

gag gaa cca acc cac ctt gtg gtg aag aag gaa aag aca cca aag cct  
2419  
Glu Glu Pro Thr His Leu Val Val Lys Lys Glu Lys Thr Pro Lys Pro  
760 765 770

gcg aca cgt gat ggt ttc ggt gcc tcc gac tac acc gtc aag ggc atg  
2467  
Ala Thr Arg Asp Gly Phe Gly Ala Ser Asp Tyr Thr Val Lys Gly Met  
775 780 785

gca gcc atc gcc gct gtg gtg atc atc ttg gtt tcc ctg gtg gcc gcc  
2515  
Ala Ala Ile Ala Ala Val Val Ile Ile Leu Val Ser Leu Val Ala Ala  
790 795 800 805

ggt acc gcg ttc ctc acc agc ttc ttc ggc agc agc acc aac gaa caa  
2563  
Gly Thr Ala Phe Leu Thr Ser Phe Phe Gly Ser Ser Thr Asn Glu Gln  
810 815 820

tcc ccg ttg gcc tct gtt gaa gcc acc acc tct gca aca cca gaa cct  
2611  
Ser Pro Leu Ala Ser Val Glu Ala Thr Thr Ser Ala Thr Pro Glu Pro  
825 830 835

gtg ggg cca ccg gtc tac ctg gat ctg gat caa gcc cgc acg tgg gat  
2659  
Val Gly Pro Pro Val Tyr Leu Asp Leu Asp Gln Ala Arg Thr Trp Asp  
840 845 850

gac ggt gca gga aca gat gtc acc gac gtc acc gac ggc aac acc tcc  
2707  
Asp Gly Ala Gly Thr Asp Val Thr Asp Val Thr Asp Gly Asn Thr Ser  
855 860 865

acc gca tgg acc tcc acc ggc ggc gac ggc ctc cta gtt gac ctg tcc  
2755  
Thr Ala Trp Thr Ser Thr Gly Gly Asp Gly Leu Leu Val Asp Leu Ser  
870 875 880 885

acg cct gcc cgc ctc gac cgc gtc atc ttg acc acc ggc acc ggc tcc  
2803  
Thr Pro Ala Arg Leu Asp Arg Val Ile Leu Thr Thr Gly Thr Gly Ser  
890 895 900

gac agc aac gtg acc tcg acc gtg aag atc tac gca ttc aac gac gcc  
2851  
Asp Ser Asn Val Thr Ser Thr Val Lys Ile Tyr Ala Phe Asn Asp Ala  
905 910 915

gtt ccc ggc gcc cca gtc ggc gac ggt cgt ttc cgt ctg ctc gcc gat  
 1747  
 Val Pro Gly Ala Pro Val Gly Asp Gly Arg Phe Arg Leu Leu Ala Asp  
 535 540 545  
 cac ggc ggc gtc caa ggc gcg cgt ttc tgg cag gcc cgc gag atc gcc  
 1795  
 His Gly Gly Val Gln Gly Ala Arg Phe Trp Gln Ala Arg Glu Ile Ala  
 550 555 560 565  
 acc ggc aag gaa gtc gcg ctg atc ttt gtg gat act tcc ggc aac gcc  
 1843  
 Thr Gly Lys Glu Val Ala Leu Ile Phe Val Asp Thr Ser Gly Asn Ala  
 570 575 580  
 cca ttt gcg cca ctg tct tcg gca gcc gca gcg ggc atc gcc tac gag  
 1891  
 Pro Phe Ala Pro Leu Ser Ser Ala Ala Ala Ala Gly Ile Ala Tyr Glu  
 585 590 595  
 gtg cag cgc cgc acc aag aag ctg gcc agc ttg ggc agc ttg gcg gta  
 1939  
 Val Gln Arg Arg Thr Lys Lys Leu Ala Ser Leu Gly Ser Leu Ala Val  
 600 605 610  
 gcc ccc aac atc cac tcc gag gcg tac cgc aac ggt tgc ctc att gtg  
 1987  
 Ala Pro Asn Ile His Ser Glu Ala Tyr Arg Asn Gly Cys Leu Ile Val  
 615 620 625  
 gcc gat tgg gtg cct ggc tcc agc ttg agc gcc gtc gcg gaa tcc ggt  
 2035  
 Ala Asp Trp Val Pro Gly Ser Ser Leu Ser Ala Val Ala Glu Ser Gly  
 630 635 640 645  
 gcc gat ccc cgc gcc gcc gcg ttc gcg ctc gcg gaa cta act gaa acc  
 2083  
 Ala Asp Pro Arg Ala Ala Ala Phe Ala Leu Ala Glu Leu Thr Glu Thr  
 650 655 660  
 atc ggc gag gcc cac gag atg ggt atc ccg gcc ggc ttg gac aac aag  
 2131  
 Ile Gly Glu Ala His Glu Met Gly Ile Pro Ala Gly Leu Asp Asn Lys  
 665 670 675  
 tgc cga att cgt atc aac acc gac ggc cat gcc gtc ctc gcc ttg ccg  
 2179  
 Cys Arg Ile Arg Ile Asn Thr Asp Gly His Ala Val Leu Ala Leu Pro  
 680 685 690  
 gcg att ttg ccc gat gcc tca gag ctc cgc gac gcc aag tcc ctg gcc  
 2227  
 Ala Ile Leu Pro Asp Ala Ser Glu Leu Arg Asp Ala Lys Ser Leu Ala  
 695 700 705  
 tcg gcc gcc gag atg ctt atc gac gcg acc ctc gct ccc agc gac gtc  
 2275  
 Ser Ala Ala Glu Met Leu Ile Asp Ala Thr Leu Ala Pro Ser Asp Val  
 710 715 720 725



gcc ggc atc acc gcc acc aag gtc gtg ctt tcc ctg ttg gca ccg ctg  
 1171  
 Ala Gly Ile Thr Ala Thr Lys Val Val Leu Ser Leu Leu Ala Pro Leu  
 345 350 355

ctg tcg agc tcc ccg gag cgt gtg gtg gtg ctt ctt ggt gcg gcc aac  
 1219  
 Leu Ser Ser Ser Pro Glu Arg Val Val Val Leu Leu Gly Ala Ala Asn  
 360 365 370

ggt ttc agt ttc atc acc ggc gcg gtc atc ggc gcg tat ctg ttg cgc  
 1267  
 Gly Phe Ser Phe Ile Thr Gly Ala Val Ile Gly Ala Tyr Leu Leu Arg  
 375 380 385

aac aaa ctc ggc ctg ttg ggt atg cgc tct ttg gct aaa acc tcc ctg  
 1315  
 Asn Lys Leu Gly Leu Leu Gly Met Arg Ser Leu Ala Lys Thr Ser Leu  
 390 395 400 405

tgg gcg ttg ggc tct gcg gcg gtt ggt gca gca gca gca tgg gcg ttg  
 1363  
 Trp Ala Leu Gly Ser Ala Ala Val Gly Ala Ala Ala Ala Trp Ala Leu  
 410 415 420

ggg tgg ctg att caa gcc gtc gtg ggc gat ttc ttg ctg ggc act cta  
 1411  
 Gly Trp Leu Ile Gln Ala Val Val Gly Asp Phe Leu Leu Gly Thr Leu  
 425 430 435

agc tcc gta ggc tac ttg ttg aac ctg gct gtg ttg ggt gtc ttc ttc  
 1459  
 Ser Ser Val Gly Tyr Leu Leu Asn Leu Ala Val Leu Gly Val Phe Phe  
 440 445 450

atc ttc gtc acc ggc atc gtg ttg tca cgt tct ggt ttg ccg gag gtc  
 1507  
 Ile Phe Val Thr Gly Ile Val Leu Ser Arg Ser Gly Leu Pro Glu Val  
 455 460 465

caa aac ttg ggc cag gca ctg acc cgc atc cca ggt ttg agc cgg ttt  
 1555  
 Gln Asn Leu Gly Gln Ala Leu Thr Arg Ile Pro Gly Leu Ser Arg Phe  
 470 475 480 485

att cgc ccg aat acc aag atc tct ttg gat gtc ggc gaa gtc tcc gag  
 1603  
 Ile Arg Pro Asn Thr Lys Ile Ser Leu Asp Val Gly Glu Val Ser Glu  
 490 495 500

cag gat ttc tcc acc cag ctg gtc gcg cca agc gag ttc gca gca acc  
 1651  
 Gln Asp Phe Ser Thr Gln Leu Val Ala Pro Ser Glu Phe Ala Ala Thr  
 505 510 515

cct gtg ccg cca ccg atg tcc gcc ggt att gtc cgc gga cct cgc ctg  
 1699  
 Pro Val Pro Pro Pro Met Ser Ala Gly Ile Val Arg Gly Pro Arg Leu  
 520 525 530

ctg ggc gtg tac atg gtg ctg cct gcg cgt ttg cac ccg cat gag cag 499  
 Leu Gly Val Tyr Met Val Leu Pro Ala Arg Leu His Pro His Glu Gln  
 120 125 130

gtg ggc att ttt gat ccg cag atc att ttc ctc ggc gtg ggc acc acc 547  
 Val Gly Ile Phe Asp Pro Gln Ile Ile Phe Leu Gly Val Gly Thr Thr  
 135 140 145

ctt ggt gtg gtt gca cag tgt cta atc atg att ccg tac ctg cgt cgc 595  
 Leu Gly Val Val Ala Gln Cys Leu Ile Met Ile Pro Tyr Leu Arg Arg  
 150 155 160 165

gcg ggc att gat atg cgc cct ctg tgg ggt atc gat gcg cgt ttg aag 643  
 Ala Gly Ile Asp Met Arg Pro Leu Trp Gly Ile Asp Ala Arg Leu Lys  
 170 175 180

caa ttc ggt ggc atg gcg atg gcg atc atc gtg tac gtg gca atc tcc 691  
 Gln Phe Gly Gly Met Ala Met Ala Ile Ile Val Tyr Val Ala Ile Ser  
 185 190 195

cag ttc ggt tac atc atc acc act cgc att gcg tcg att gca gac gat 739  
 Gln Phe Gly Tyr Ile Ile Thr Thr Arg Ile Ala Ser Ile Ala Asp Asp  
 200 205 210

gct gcg ccg ttt att tat cag cag cac tgg atg ttg ctg caa gtt cct 787  
 Ala Ala Pro Phe Ile Tyr Gln Gln His Trp Met Leu Leu Gln Val Pro  
 215 220 225

tat ggc atc atc ggc gtc acc ttg ctc acc gcg att atg ccg cga ctg 835  
 Tyr Gly Ile Ile Gly Val Thr Leu Leu Thr Ala Ile Met Pro Arg Leu  
 230 235 240 245

tcc cgc aac gcg gca gac ggc gat gat agg gca gta gtc tct gac ctt 883  
 Ser Arg Asn Ala Ala Asp Gly Asp Asp Arg Ala Val Val Ser Asp Leu  
 250 255 260

cag ttg ggt tcc aag cta acc ttc atc gca ctg atc ccc atc gtg gtg 931  
 Gln Leu Gly Ser Lys Leu Thr Phe Ile Ala Leu Ile Pro Ile Val Val  
 265 270 275

ttc ttc acc gcc ttc ggt gtc cct att gcc aat ggc ctt ttt gcc tac 979  
 Phe Phe Thr Ala Phe Gly Val Pro Ile Ala Asn Gly Leu Phe Ala Tyr  
 280 285 290

ggc caa ttc gat gcc aac gcc gcc aac atc ctt ggt tgg act ctg agc 1027  
 Gly Gln Phe Asp Ala Asn Ala Ala Asn Ile Leu Gly Trp Thr Leu Ser  
 295 300 305

ttc tct gct ttc acg ctg att cct tac gct ttg gtg ctg cta cat ctg 1075  
 Phe Ser Ala Phe Thr Leu Ile Pro Tyr Ala Leu Val Leu Leu His Leu  
 310 315 320 325

cgt gtg ttt tat gcg cgt gaa gag gtc tgg acc cca acc ttc atc atc 1123  
 Arg Val Phe Tyr Ala Arg Glu Glu Val Trp Thr Pro Thr Phe Ile Ile  
 330 335 340

Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr  
 100 105 110

Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr  
 115 120 125

Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe  
 130 135 140

Ile Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr  
 145 150 155 160

Glu Ala Pro Ile Lys Gln  
 165

&lt;210&gt; 507

&lt;211&gt; 3075

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(3052)

&lt;223&gt; RXC01434

&lt;400&gt; 507

ggtttcctgc gcaccgtgat gattgggtgcg gcgctgtcgc cggccatcgc ttccggcggttc 60

aacactgccacacgctgcc caacctgatc actggaaatc gtg ttg ggt gcg gtg 115  
 Val Leu Gly Ala Val  
 1 5

ctg aca tcg ctg gtt att ccg gtc ctt acc cgc gcg gaa aaa gaa gac 163  
 Leu Thr Ser Leu Val Ile Pro Val Leu Thr Arg Ala Glu Lys Glu Asp  
 10 15 20

gcc gac ggc ggt tcc ggg ttc ttc agg cgg ctg ctc acc ctg tcg gtg 211  
 Ala Asp Gly Gly Ser Gly Phe Phe Arg Arg Leu Leu Thr Leu Ser Val  
 25 30 35

acg ctg ctg ggt ggt gtc acc atc ctg tcg att atc ggc gcg ccg ctg 259  
 Thr Leu Leu Gly Gly Val Thr Ile Leu Ser Ile Ile Gly Ala Pro Leu  
 40 45 50

ctg aca cgg atg atg ctg tcc tct gag gga caa gtc aac gtg gtc atg 307  
 Leu Thr Arg Met Met Leu Ser Ser Glu Gly Gln Val Asn Val Val Met  
 55 60 65

tcc acg gcc ttt gcg tat tgg ctg ctg cca cag att ttc ttc tac ggc 355  
 Ser Thr Ala Phe Ala Tyr Trp Leu Leu Pro Gln Ile Phe Phe Tyr Gly  
 70 75 80 85

ctg ttt gcc ctg ttc atg gct gtg ttg aac acc cgt gaa gtg ttc aaa 403  
 Leu Phe Ala Leu Phe Met Ala Val Leu Asn Thr Arg Glu Val Phe Lys  
 90 95 100

ccc ggc gcg tgg gca cct gtt gtc aac aat gtg atc acc ttg acc gtg 451  
 Pro Gly Ala Trp Ala Pro Val Val Asn Asn Val Ile Thr Leu Thr Val  
 105 110 115

ttc cac gga ata ata acc acc gtg aaa tgc ttc caa gac aac gcc ctc 259  
 Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu  
           40                          45                          50  
 ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc 307  
 Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile  
           55                          60                          65  
 gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca 355  
 Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala  
           70                          75                          80                          85  
 gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403  
 Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala  
                           90                          95                          100  
 att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc 451  
 Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala  
                           105                          110                          115  
 ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499  
 Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg  
                           120                          125                          130  
 gac gta gtg gta tcg att ggt ggc att gac ttc att cct ggt cat tac 547  
 Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr  
           135                          140                          145  
 gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595  
 Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys  
                           150                          155                          160                          165  
 cag taatttgttt tgacgacgca gta 621  
 Gln

&lt;210&gt; 506

&lt;211&gt; 166

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 506

Met Thr Gln Ser Ala Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp  
   1                          5                          10                          15  
 Ile Ile Gly Asp Asn Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu  
           20                          25                          30  
 Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe  
           35                          40                          45  
 Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly  
           50                          55                          60  
 Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val  
           65                          70                          75                          80  
 Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val  
                           85                          90                          95

His Gln Gly Glu Leu Ile Asp Ala Leu His Asn Ala Arg Gly Thr His  
 55 60 65  
 atc ggt tgc gtg att aac ccc ggc ggc ctg act aca ctt cgg tgg cgc 355  
 Ile Gly Cys Val Ile Asn Pro Gly Gly Leu Thr Thr Leu Arg Trp Arg  
 70 75 80 85  
 ttt tgg atg ctg tgaaggcgctc tgagcttcct acc 390  
 Phe Trp Met Leu

<210> 504  
 <211> 89  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 504  
 Met Pro Gly Lys Ile Leu Leu Leu Asn Gly Pro Asn Leu Asn Met Leu  
 1 5 10 15  
 Gly Lys Arg Glu Pro Asp Ile Tyr Gly His Asp Thr Leu Glu Asp Val  
 20 25 30  
 Val Ala Leu Ala Thr Ala Glu Ala Ala Lys His Gly Leu Glu Val Glu  
 35 40 45  
 Ala Leu Gln Ser Asn His Gln Gly Glu Leu Ile Asp Ala Leu His Asn  
 50 55 60  
 Ala Arg Gly Thr His Ile Gly Cys Val Ile Asn Pro Gly Gly Leu Thr  
 65 70 75 80  
 Thr Leu Arg Trp Arg Phe Trp Met Leu  
 85

<210> 505  
 <211> 621  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(598)  
 <223> RXS03074

<400> 505  
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 tagcaggaca agcatactgt tttagttcta tgctgtgggc atg act caa agt gct 115  
 Met Thr Gln Ser Ala  
 1 5  
 cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac 163  
 Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn  
 10 15 20  
 gcg caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa 211  
 Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu  
 25 30 35

724

Glu	Leu	Arg	Ala	Ala	Ile	Arg	Gly	Ala	Leu	Glu	Arg	Arg	Tyr	Asn	Met	
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Thr	Lys	Leu	Val	Asp	Ala	Ser	Leu	Leu	Pro	Val	Val	Gly	Thr	Lys	Glu	
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gca	att	gcc	ctt	ctt	cca	ttc	gcg	ttg	ggg	att	tcc	ggc	acc	gtt	gtc	451
Ala	Ile	Ala	Leu	Leu	Pro	Phe	Ala	Leu	Gly	Ile	Ser	Gly	Thr	Val	Val	
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atc	cca	gag	att	gcg	tac	cca	acc	tac	gaa	gtc	gct	gtc	gtg	gcc	gca	499
Ile	Pro	Glu	Ile	Ala	Tyr	Pro	Thr	Tyr	Glu	Val	Ala	Val	Val	Ala	Ala	
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gga	tgc	acc	gtg	ttg	cgt	tct	gat	tcg	ctg	ttt	aag	ctc	ggc	ccg	cag	547
Gly	Cys	Thr	Val	Leu	Arg	Ser	Asp	Ser	Leu	Phe	Lys	Leu	Gly	Pro	Gln	
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atc	ccg	tcg	atg	atg	ttt	atc	aac	tca	cca	tcc	aac	ccc	aca	ggc	aag	595
Ile	Pro	Ser	Met	Met	Phe	Ile	Asn	Ser	Pro	Ser	Asn	Pro	Thr	Gly	Lys	
	150				155					160					165	
gtt	ctg	ggc	atc	cca	cac	ttg	cgc	aag	gtt	gtg	aag	tgg	gcg	cag	gaa	643
Val	Leu	Gly	Ile	Pro	His	Leu	Arg	Lys	Val	Val	Lys	Trp	Ala	Gln	Glu	
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aac	aac	gtg	atc	ctc	gca	gct	gat	gaa	tgc	tac	ttg	ggg	ctt	ggc	tgg	691
Asn	Asn	Val	Ile	Leu	Ala	Ala	Asp	Glu	Cys	Tyr	Leu	Gly	Leu	Gly	Trp	
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gac	gat	gaa	aac	cca	ccg	atc	tca	att	ttg	gat	cca	cgt	gtc	tgc	gat	739
Asp	Asp	Glu	Asn	Pro	Pro	Ile	Ser	Ile	Leu	Asp	Pro	Arg	Val	Cys	Asp	
		200					205					210				
ggc	gac	cac	acc	aac	ttg	atc	gcc	att	cac	tcg	ctg					775
Gly	Asp	His	Thr	Asn	Leu	Ile	Ala	Ile	His	Ser	Leu					
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 35 40 45  
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 Thr Ile Gly Thr Pro Glu Leu Arg Ala Ala Ile Arg Gly Ala Leu Glu  
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 Gln Ala Ile Val Ala Ala Tyr Ser Gly Ser Ile Ser Pro Ser Glu Val  
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 Ile Glu Gly Leu Asp Asp Leu Pro Arg Trp Gln Leu Pro Lys Arg Leu  
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   Met Thr Ser Arg Thr  
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 ccg ctt gtt tct gtt ctt cct gat ttt ccg tgg gat tcg ctc gct tcc 163  
 Pro Leu Val Ser Val Leu Pro Asp Phe Pro Trp Asp Ser Leu Ala Ser  
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 gca aaa gcc aaa gct gcg tct cac ccg gat ggg atc gtg aat ctt tct 211  
 Ala Lys Ala Lys Ala Ala Ser His Pro Asp Gly Ile Val Asn Leu Ser  
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 gtt ggc act ccg gtt gat ccg gtc gcg ccc agc att cag atc gcg ttg 259  
 Val Gly Thr Pro Val Asp Pro Val Ala Pro Ser Ile Gln Ile Ala Leu  
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 gca gaa gca gcg ggg ttt tcg ggt tac cct caa acc atc ggc acc ccg 307  
 Ala Glu Ala Ala Gly Phe Ser Gly Tyr Pro Gln Thr Ile Gly Thr Pro  
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Asp Ala Glu Arg Met Gln Gln Met Gly Ala Val Asn Ile Val Ala Asp		
225	230	235
His Gly Asp Leu Glu Lys Glu Ala Ile Gln Ala Ala Arg Glu Ile Asn		
245	250	255
Thr Lys Ser Pro Thr Gly Gln Arg Met Leu Lys Phe Ala Phe Asn Leu		
260	265	270
Thr Asp Asp Gly Leu Met Gly Gln Gln Val Phe Ala Gly Glu Ala Thr		
275	280	285
Arg Leu Ala Tyr Met Thr Asp Glu Ala Val Glu Gly Lys Glu Ala Phe		
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Leu Glu Lys Arg Glu Pro Asn Trp Asn Glu Phe Pro Tyr Tyr Tyr		
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&lt;211&gt; 384

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(361)

&lt;223&gt; RXS02908

&lt;400&gt; 499

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				Leu Lys	Leu His	Pro	
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Glu Val	Leu Glu	Arg Ala	Ile Ala	Asp Ile	Lys Gly	Val Thr	Ala Ala	
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tgt gtt	gtg ggt	att ccc	gat ccc	cga tta	ggc caa	gca att	gtg gcc	211
Cys Val	Val Gly	Ile Pro	Asp Pro	Arg Leu	Gly Gln	Ala Ile	Val Ala	
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gcg tac	tcc gga	tcg atc	agt ccg	tct gaa	gtt att	gaa ggc	ctc gac	259
Ala Tyr	Ser Gly	Ser Ile	Ser Pro	Ser Glu	Val Ile	Glu Gly	Leu Asp	
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gat cta	cct cgt	tgg cag	ctt ccc	aaa cgg	ctg aag	cat ctg	gaa tct	307
Asp Leu	Pro Arg	Trp Gln	Leu Pro	Lys Arg	Leu Lys	His Leu	Glu Ser	
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Leu Pro	Ser Ile	Gly Pro	Gly Lys	Ala Asp	Arg Arg	Ala Ile	Ala Lys	
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Leu Phe				

acg gat gaa gcc gta gag ggt aag gaa gca ttc cta gaa aag cgc gaa  
1027

Thr Asp Glu Ala Val Glu Gly Lys Glu Ala Phe Leu Glu Lys Arg Glu  
295 300 305

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<213> *Corynebacterium glutamicum*

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Pro Glu Val Arg Asn Ala Phe Arg Pro His Thr Val Asp Glu Leu Tyr  
50 55 60

Gln Ala Leu Asp His Ala Arg Arg Thr Pro Asp Val Gly Thr Ile Leu  
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Leu Thr Gly Asn Gly Pro Ser Glu Lys Asp Gly Gly Trp Ala Phe Cys  
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Ser Gly Gly Asp Gln Arg Ile Arg Gly Arg Ser Gly Tyr Gln Tyr Ala  
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Thr Glu His Ala Arg Asp Asp Ala Thr Ala Asp Val Phe Thr Val Asp  
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Ile Ala Arg Thr Lys Val Glu Gly Gly Arg Leu His Ile Leu Glu Val  
130 135 140

Gln Arg Leu Ile Arg Thr Met Pro Lys Val Val Ile Ala Val Val Asn  
145 150 155 160

Gly Trp Ala Ala Gly Gly Gly His Ser Leu His Val Val Cys Asp Leu  
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Thr Ile Ala Ser Arg Gln Glu Ala Arg Phe Lys Gln Thr Asp Ala Asp  
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Val Gly Gln Lys Asn Ala Arg Glu Ile Phe Phe Leu Gly Arg Thr Tyr

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Pro	Ser	Glu	Lys	Asp	Gly	Gly	Trp	Ala	Phe	Cys	Ser	Gly	Gly	Asp	Gln	
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105					110					115						
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Asp	Asp	Ala	Thr	Ala	Asp	Val	Phe	Thr	Val	Asp	Ile	Ala	Arg	Thr	Lys	
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Val	Glu	Gly	Gly	Arg	Leu	His	Ile	Leu	Glu	Val	Gln	Arg	Leu	Ile	Arg	
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acc	atg	cct	aaa	gtt	gtc	atc	gca	gta	gtc	aac	ggc	tgg	gca	gcc	ggc	595
Thr	Met	Pro	Lys	Val	Val	Ile	Ala	Val	Val	Asn	Gly	Trp	Ala	Ala	Gly	
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Gly	Gly	His	Ser	Leu	His	Val	Val	Cys	Asp	Leu	Thr	Ile	Ala	Ser	Arg	
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Gln	Glu	Ala	Arg	Phe	Lys	Gln	Thr	Asp	Ala	Asp	Val	Gly	Ser	Phe	Asp	
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Ala	Arg	Glu	Ile	Phe	Phe	Leu	Gly	Arg	Thr	Tyr	Asp	Ala	Glu	Arg	Met	
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Gln	Gln	Met	Gly	Ala	Val	Asn	Ile	Val	Ala	Asp	His	Gly	Asp	Leu	Glu	
230					235					240					245	
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Lys	Glu	Ala	Ile	Gln	Ala	Ala	Arg	Glu	Ile	Asn	Thr	Lys	Ser	Pro	Thr	
250					255					260						
ggg	caa	cgc	atg	ctg	aaa	ttc	gcc	ttc	aat	ctc	acc	gac	gat	ggc	ctc	931
Gly	Gln	Arg	Met	Leu	Lys	Phe	Ala	Phe	Asn	Leu	Thr	Asp	Asp	Gly	Leu	
265					270					275						
atg	gga	caa	caa	gtc	ttc	gcc	ggc	gaa	gcc	acc	cgc	ctg	gcc	tac	atg	979
Met	Gly	Gln	Gln	Val	Phe	Ala	Gly	Glu	Ala	Thr	Arg	Leu	Ala	Tyr	Met	
280					285					290						

Lys Ala Tyr Arg Val Ala Gly Tyr Arg Ala Gly Trp Met Val Leu Thr  
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 Gly Pro Lys Gln Tyr Ala Arg Gly Phe Ile Glu Gly Leu Glu Leu Leu  
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 Ala Gly Thr Arg Leu Cys Pro Asn Val Pro Ala Gln His Ala Ile Gln  
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 Val Ala Leu Gly Gly Arg Gln Ser Ile Tyr Asp Leu Thr Gly Glu His  
                                   325                                  330                                  335  
 Gly Arg Leu Leu Glu Gln Arg Asn Met Ala Trp Thr Lys Leu Asn Glu  
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 Ile Pro Gly Val Ser Cys Val Lys Pro Met Gly Ala Leu Tyr Ala Phe  
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 Pro Lys Leu Asp Pro Asn Val Tyr Glu Ile His Asp Asp Thr Gln Leu  
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 Met Leu Asp Leu Leu Arg Ala Glu Lys Ile Leu Met Val Gln Gly Thr  
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 Gly Phe Asn Trp Pro His His Asp His Phe Arg Val Val Thr Leu Pro  
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 Trp Ala Ser Gln Leu Glu Asn Ala Ile Glu Arg Leu Gly Asn Phe Leu  
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 Glu Glu Phe Thr Asp Ile Thr Tyr His Arg His Val Gly Thr Thr Arg  
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Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala
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Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe
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His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala
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Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp
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Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn
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Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val
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Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly
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Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly
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Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly
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 50 55 60  
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 65 70 75 80  
 Val Ala Lys Ala Val Gly Ala Ala Ala Ala Arg Phe Thr His Thr Cys  
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 Phe Met Val Ser Pro Tyr Glu Thr Tyr Val Ala Met Ala Glu Arg Leu  
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 Ser Gly Ala Glu Ala Val Glu Asn Ala Val Lys Val Ala Arg Ala Tyr  
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 Pro Leu Arg Asp Gly Leu Ser Gly Pro Glu Ala Ala Glu Arg Ala Ile  
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 Ile Glu Pro Ile Gln Gly Glu Gly Gly Phe Ile Val Pro Ala Pro Gly  
 225 230 235 240  
 Phe Leu Ala Ala Ile Ser Thr Trp Cys Arg Glu Asn Asp Val Val Phe  
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 Ile Ala Asp Glu Ile Gln Ser Gly Phe Leu Arg Thr Gly Asp Trp Phe  
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 Asn Pro Val Ala Cys Ala Ala Ala Leu Ala Ala Ile Glu Val Met Glu  
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 Ala Met Thr Ala Lys Asn Arg Pro Tyr Lys Ser Gly Phe Gly Pro Leu  
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 Ala Ala Asp Val Tyr Arg Ala Pro Met Ser Tyr Pro Leu Arg Asp Gly  
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 Ser Thr Trp Cys Arg Glu Asn Asp Val Val Phe Ile Ala Asp Glu Ile  
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&lt;210&gt; 516

&lt;211&gt; 344

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 516

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Lys Ser Lys Ala Leu Asp Glu Arg Arg Gln Ala Ala Val Ala Arg Ala
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Leu Ala Pro Gly Leu Pro Gly Tyr Val Val Asp Ala Asp Gly Gly Ile
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Leu Ala Asp Ala Asp Gly Asn Arg Phe Ile Asp Leu Ala Ser Gly Ile
                        55                        60                        65
gcc gtg acc acg gtc ggc gga tcc aac gcg gcc gtc gcg aaa gcc gtc 355
Ala Val Thr Thr Val Gly Ser Asn Ala Ala Val Ala Lys Ala Val
                        70                        75                        80                        85
ggc gcc gca gct gcc cgc ttc acc cac acc tgc ttc atg gtc tca cct 403
Gly Ala Ala Ala Ala Arg Phe Thr His Thr Cys Phe Met Val Ser Pro
                        90                        95                        100
tat gaa act tac gtg gcc atg gcg gag aga ctc aac gcc ttg act cca 451
Tyr Glu Thr Tyr Val Ala Met Ala Glu Arg Leu Asn Ala Leu Thr Pro
                        105                        110                        115
ggc gat cac gac aag aag agc gcg ctg ttt aac tct ggc gcc gaa gcc 499
Gly Asp His Asp Lys Lys Ser Ala Leu Phe Asn Ser Gly Ala Glu Ala
                        120                        125                        130
gtg gaa aac gcc gtc aag gtg gca cgc gcc tac acc ggc aag ggc gcg 547
Val Glu Asn Ala Val Lys Val Ala Arg Ala Tyr Thr Gly Lys Gly Ala
                        135                        140                        145
gtc gtg gtg ttc gac aac gcg tac cac gga cgg acc aac ctc acc atg 595
Val Val Val Phe Asp Asn Ala Tyr His Gly Arg Thr Asn Leu Thr Met
                        150                        155                        160                        165

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gtc gtc atg agc gtc tac ctc acc tgg caa caa atc caa gga atg 880  
 Val Val Met Ser Val Tyr Leu Thr Trp Gln Gln Ile Gln Gly Met  
                     250                    255                    260

tagataagtc ggggcaaact cta 903

<210> 514

<211> 260

<212> PRT

<213> Corynebacterium glutamicum

<400> 514

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Ala Ala Val Ala Gly Trp Ile Asp Ala Val Ile Gly Gly Gly Gly Leu  
                     20                    25                    30

Val Leu Ile Pro Leu Ile Leu Ala Val Met Pro Gln Leu Ala Pro Val  
                     35                    40                    45

Thr Ala Leu Ala Ser Asn Lys Leu Ala Ala Val Thr Gly Thr Ala Ser  
                     50                    55                    60

Ala Ala Phe Thr Leu Val Arg Arg Val Lys Pro Asp Lys Lys Leu Leu  
                     65                    70                    75                    80

Ala Leu Tyr Val Leu Val Ala Ala Val Cys Ser Gly Ala Gly Ala Leu  
                     85                    90                    95

Ala Ala Ser Leu Ile Asp Lys Gln Ile Met Arg Pro Leu Ile Ile Val  
                     100                    105                    110

Leu Met Leu Val Val Gly Leu Ile Val Val Phe Lys Pro Asn Phe Gly  
                     115                    120                    125

Thr Gly Glu Ser Lys Ala Leu Pro Thr Gly Trp Lys Arg Trp Ala Ala  
                     130                    135                    140

Ile Val Ala Val Gly Leu Ile Ala Ala Tyr Asp Gly Ile Phe Gly Pro  
                     145                    150                    155                    160

Gly Thr Gly Met Phe Leu Ile Met Ala Phe Thr Ala Leu Leu Ser Gln  
                     165                    170                    175

Asn Phe Leu Ser Ser Ala Ala Met Ala Lys Val Val Asn Thr Ala Thr  
                     180                    185                    190

Asn Leu Gly Ala Leu Ile Val Phe Ile Ile Gly Gly His Met Trp Trp  
                     195                    200                    205

Thr Leu Gly Leu Val Leu Ala Val Ala Asn Val Ala Gly Ala Gln Leu  
                     210                    215                    220

Gly Ala Arg Thr Val Leu Gly Gly Gly Thr Arg Leu Ile Arg Tyr Ala  
                     225                    230                    235                    240

Leu Leu Thr Leu Val Val Val Met Ser Val Tyr Leu Thr Trp Gln Gln  
                     245                    250                    255

gca gct agc ggg tgg ggc atc ctc atc gca ggc gcc gcc gta gcc gga 163  
 Ala Ala Ser Gly Trp Gly Ile Leu Ile Ala Gly Ala Val Ala Gly  
 10 15 20

tgg atc gac gca gta atc ggc ggt ggc gga ctc gtc ctc atc ccg ctg 211  
 Trp Ile Asp Ala Val Ile Gly Gly Gly Gly Leu Val Leu Ile Pro Leu  
 25 30 35

atc ctc gcg gtc atg ccg caa ctc gca cct gtg aca gcg ctg gcc tcc 259  
 Ile Leu Ala Val Met Pro Gln Leu Ala Pro Val Thr Ala Leu Ala Ser  
 40 45 50

aac aaa ctg gca gcc gtc acc ggc acg gca tcg gcg gca ttc acc ctg 307  
 Asn Lys Leu Ala Ala Val Thr Gly Thr Ala Ser Ala Ala Phe Thr Leu  
 55 60 65

gtc agg cgc gtc aaa ccc gac aaa aaa ctg ctt gcg ctc tac gtt ctg 355  
 Val Arg Arg Val Lys Pro Asp Lys Lys Leu Leu Ala Leu Tyr Val Leu  
 70 75 80 85

gtg gca gct gtg tgc tcc ggt gca ggc gcc ctg gct gcg agt ctc att 403  
 Val Ala Ala Val Cys Ser Gly Ala Gly Ala Leu Ala Ala Ser Leu Ile  
 90 95 100

gac aaa caa atc atg cga ccg ctg atc atc gtg ttg atg ctg gtc gtt 451  
 Asp Lys Gln Ile Met Arg Pro Leu Ile Ile Val Leu Met Leu Val Val  
 105 110 115

ggc ctg atc gtg gtg ttc aaa cca aac ttc gga acc ggc gaa agc aaa 499  
 Gly Leu Ile Val Val Phe Lys Pro Asn Phe Gly Thr Gly Glu Ser Lys  
 120 125 130

gcc ctg ccc acc gga tgg aaa cgc tgg gcc gcc atc gtt gca gtc gga 547  
 Ala Leu Pro Thr Gly Trp Lys Arg Trp Ala Ala Ile Val Ala Val Gly  
 135 140 145

ctc atc gca gcc tac gac ggc atc ttc gga ccc gga acc ggc atg ttc 595  
 Leu Ile Ala Ala Tyr Asp Gly Ile Phe Gly Pro Gly Thr Gly Met Phe  
 150 155 160 165

ctc atc atg gcg ttc acc gca ctg ctc tcc caa aat ttc ctg tcc tcc 643  
 Leu Ile Met Ala Phe Thr Ala Leu Leu Ser Gln Asn Phe Leu Ser Ser  
 170 175 180

gca gcc atg gcg aag gtc gta aac acc gca aca aac ctg ggt gcg cta 691  
 Ala Ala Met Ala Lys Val Val Asn Thr Ala Thr Asn Leu Gly Ala Leu  
 185 190 195

att gta ttc atc atc ggc ggc cac atg tgg tgg acc cta gga ctc gtg 739  
 Ile Val Phe Ile Ile Gly Gly His Met Trp Trp Thr Leu Gly Leu Val  
 200 205 210

ctg gca gtc gcc aat gtc gca ggc gca caa ctc ggt gcc cga acg gtg 787  
 Leu Ala Val Ala Asn Val Ala Gly Ala Gln Leu Gly Ala Arg Thr Val  
 215 220 225

ctt ggt ggc ggt acc agg cta att aga tac gca cta cta acc ctg gtt 835  
 Leu Gly Gly Gly Thr Arg Leu Ile Arg Tyr Ala Leu Leu Thr Leu Val  
 230 235 240 245



&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101) .. (646)

&lt;223&gt; RXC02789

&lt;400&gt; 511

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ttcttaacac taaacaatgg aaaggtaagc gggtttttct atg aag gtt tcc gcc 115
                                         Met Lys Val Ser Ala
                                         1           5

gat aca ccc ggt cac gat gat cca ggc cca ggc cgg cgc ctt ggc tta 163
Asp Thr Pro Gly His Asp Asp Pro Gly Pro Gly Arg Arg Leu Gly Leu
                        10                15                20

gat gtc ggc acc gtg cgc atc gga gtg gca gcc tct gac cgc gat gcc 211
Asp Val Gly Thr Val Arg Ile Gly Val Ala Ala Ser Asp Arg Asp Ala
                        25                30                35

aag ctt gcc atg cct gtg gaa acc gtt ccg cgg gaa act gga ttc aaa 259
Lys Leu Ala Met Pro Val Glu Thr Val Pro Arg Glu Thr Gly Phe Lys
                        40                45                50

ggg cca gac ctg gcc gat att gat cgg ttg gtc gcc atc gtt gag gaa 307
Gly Pro Asp Leu Ala Asp Ile Asp Arg Leu Val Ala Ile Val Glu Glu
                        55                60                65

tac aac gcc gtg gaa gtc att gtt ggt cta ccc aca gat ctg cag gga 355
Tyr Asn Ala Val Glu Val Ile Val Gly Leu Pro Thr Asp Leu Gln Gly
                        70                75                80                85

aat ggc tcc gcc agt gtg aag cat gca aag gaa att gct ttc cgc gtc 403
Asn Gly Ser Ala Ser Val Lys His Ala Lys Glu Ile Ala Phe Arg Val
                        90                95                100

cgt cgg cgc ctc acc aat gct gga aag aac att ccg gta cgg ctt ggc 451
Arg Arg Arg Leu Thr Asn Ala Gly Lys Asn Ile Pro Val Arg Leu Gly
                        105                110                115

gac gaa cgc ctc acc acc gtc gtg gcc acc caa gcc ttg cgg gcc tca 499
Asp Glu Arg Leu Thr Thr Val Val Ala Thr Gln Ala Leu Arg Ala Ser
                        120                125                130

gga gtc agc gaa aaa gcg gga cgt aaa gtt att gat caa gct gcc gca 547
Gly Val Ser Glu Lys Ala Gly Arg Lys Val Ile Asp Gln Ala Ala Ala
                        135                140                145

gta gaa atc ctt caa acc tgg ttg gat gct cgc acc cga gcc ctt gaa 595
Val Glu Ile Leu Gln Thr Trp Leu Asp Ala Arg Thr Arg Ala Leu Glu
                        150                155                160                165

cca caa tcc aca gac acc caa gat ttc gac gag aag gga aat ttc cca 643
Pro Gln Ser Thr Asp Thr Gln Asp Phe Asp Glu Lys Gly Asn Phe Pro
                        170                175                180

gga tgaaccaa at ccgaaaccgc cgg 669
Gly

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<210> 510  
 <211> 269  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 510

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Met Ser Ile Glu Trp Leu Gln Ile Val Glu Leu Gly Ala Ile Phe Gly
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Ala Gly Phe Leu Ala Gly Ser Ile Asn Val Ile Val Gly Ala Gly Thr
          20           25           30

Leu Val Ser Phe Pro Ile Leu Val Phe Leu Gly Leu Pro Pro Leu Thr
          35           40           45

Ala Thr Ile Ala Asn Thr Ile Gly Ile Val Pro Gly Ser Ile Ser Gly
          50           55           60

Val Val Ala Tyr Arg Arg Glu Leu His Ala His Val Lys Thr Ile Arg
          65           70           75           80

Phe Leu Leu Pro Ala Ser Ile Leu Gly Gly Ile Thr Gly Ala Ser Leu
          85           90           95

Leu Leu His Phe Ser Ala Asp Val Phe Thr Ala Val Ile Pro Trp Leu
          100          105          110

Ile Gly Phe Gly Thr Leu Leu Val Ile Ala Gly Pro Ser Ile Lys Lys
          115          120          125

His Val Gly Ala His Thr Ser Gly Gly Ile Ser Ala Gly Phe Arg Gln
          130          135          140

Leu Pro Phe Pro Ser Arg Thr Thr Phe Ile Val Ser Val Cys Gly Ala
          145          150          155          160

Leu Leu Leu Gly Met Tyr Gly Gly Tyr Phe Ser Ala Ala Gln Gly Ile
          165          170          175

Leu Leu Ile Ala Leu Leu Gly Ile Thr Ser Thr Leu Gln Met Gln Glu
          180          185          190

Leu Asn Ala Ile Lys Asn Leu Thr Val Ala Ala Val Asn Leu Ile Ala
          195          200          205

Ala Ser Val Phe Ile Ile Ile Ser Pro Glu Leu Ile Ser Trp Pro Thr
          210          215          220

Val Ala Leu Ile Ala Leu Gly Ser Ala Leu Gly Gly Tyr Ile Gly Gly
          225          230          235          240

Arg Tyr Ala Arg Arg Leu Arg Pro Ser Val Phe Arg Ala Phe Val Val
          245          250          255

Ile Val Gly Ile Thr Thr Val Ile Val Met Thr Ile Gly
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<210> 511  
 <211> 669  
 <212> DNA

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acc atc ggc atc gtt cct gga agt att tcg ggt gtg gtt gct tat aga Thr Ile Gly Ile Val Pro Gly Ser Ile Ser Gly Val Val Ala Tyr Arg 55 60 65	307
cgt gaa cta cac gcc cat gta aaa acc atc aga ttt ctg ctg cca gca Arg Glu Leu His Ala His Val Lys Thr Ile Arg Phe Leu Leu Pro Ala 70 75 80 85	355
tca atc ctc gga ggg atc acc ggc gcc tcg ctc ttg ctg cat ttc tcc Ser Ile Leu Gly Gly Ile Thr Gly Ala Ser Leu Leu Leu His Phe Ser 90 95 100	403
gca gat gtt ttt aca gca gta att ccc tgg ctg att gga ttc ggc acg Ala Asp Val Phe Thr Ala Val Ile Pro Trp Leu Ile Gly Phe Gly Thr 105 110 115	451
ctg ttg gtt atc gca ggt cca tca att aag aag cat gtt ggc gct cat Leu Leu Val Ile Ala Gly Pro Ser Ile Lys Lys His Val Gly Ala His 120 125 130	499
act tca ggt ggc atc tct gct ggg ttt agg caa ttg cct ttc ccg agc Thr Ser Gly Gly Ile Ser Ala Gly Phe Arg Gln Leu Pro Phe Pro Ser 135 140 145	547
cga acc acc ttc atc gtc tca gta tgt ggt gcc ctg ttg ctg ggc atg Arg Thr Thr Phe Ile Val Ser Val Cys Gly Ala Leu Leu Leu Gly Met 150 155 160 165	595
tat gga ggg tac ttc agc gca gct caa ggc att ctt ctc atc gca ttg Tyr Gly Gly Tyr Phe Ser Ala Ala Gln Gly Ile Leu Leu Ile Ala Leu 170 175 180	643
ctt ggc atc aca tca acg ctg cag atg cag gaa ctc aac gcc atc aaa Leu Gly Ile Thr Ser Thr Leu Gln Met Gln Glu Leu Asn Ala Ile Lys 185 190 195	691
aac ctc aca gtg gcg gca gtt aat ctc atc gca gcc agt gtt ttt ata Asn Leu Thr Val Ala Ala Val Asn Leu Ile Ala Ala Ser Val Phe Ile 200 205 210	739
atc atc tcc cct gag ttg atc tcc tgg ccg acc gtt gcc tta atc gcg Ile Ile Ser Pro Glu Leu Ile Ser Trp Pro Thr Val Ala Leu Ile Ala 215 220 225	787
ctt ggc tca gct tta ggt gga tac atc ggc gga cgg tac gcc cgc cga Leu Gly Ser Ala Leu Gly Gly Tyr Ile Gly Gly Arg Tyr Ala Arg Arg 230 235 240 245	835
ctt cgc ccc agt gtt ttt aga gca ttt gtg gtc atc gtc gga atc acc Leu Arg Pro Ser Val Phe Arg Ala Phe Val Val Ile Val Gly Ile Thr 250 255 260	883
acg gtc atc gtt atg acg atc ggt taatgcagca gactagtaac ccc Thr Val Ile Val Met Thr Ile Gly 265	930

805										810					815				
Ser	Thr	Asn	Glu	Gln	Ser	Pro	Leu	Ala	Ser	Val	Glu	Ala	Thr	Thr	Ser				
			820						825					830					
Ala	Thr	Pro	Glu	Pro	Val	Gly	Pro	Pro	Val	Tyr	Leu	Asp	Leu	Asp	Gln				
			835					840					845						
Ala	Arg	Thr	Trp	Asp	Asp	Gly	Ala	Gly	Thr	Asp	Val	Thr	Asp	Val	Thr				
			850				855					860							
Asp	Gly	Asn	Thr	Ser	Thr	Ala	Trp	Thr	Ser	Thr	Gly	Gly	Asp	Gly	Leu				
	865					870				875					880				
Leu	Val	Asp	Leu	Ser	Thr	Pro	Ala	Arg	Leu	Asp	Arg	Val	Ile	Leu	Thr				
				885					890					895					
Thr	Gly	Thr	Gly	Ser	Asp	Ser	Asn	Val	Thr	Ser	Thr	Val	Lys	Ile	Tyr				
			900					905						910					
Ala	Phe	Asn	Asp	Ala	Ser	Pro	His	Ser	Leu	Ser	Glu	Gly	Ile	Glu	Ile				
			915					920					925						
Gly	Thr	Val	Asp	Tyr	Ser	Gly	Arg	Ser	Leu	Ser	His	Ser	Ile	Arg	Asp				
	930						935					940							
Ser	Ser	Lys	Leu	Pro	Gly	Gln	Val	Glu	Ser	Val	Val	Ile	Leu	Val	Asp				
	945					950				955					960				
Glu	Val	Arg	Ser	Ser	Gln	Thr	Ser	Asp	Thr	Asn	Pro	Gln	Met	Gln	Ile				
				965					970					975					
Ala	Glu	Val	Gln	Leu	Val	Gly	Trp												
				980															

&lt;210&gt; 509

&lt;211&gt; 930

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(907)

&lt;223&gt; RXC02080

&lt;400&gt; 509

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tttgtcctgt	tgcttattgt	gcaggaattc	ggaggcggac	atg	tca	atc	gag	tgg	115
				Met	Ser	Ile	Glu	Trp	
				1				5	

tta	caa	att	gtt	gaa	tta	gga	gcg	atc	ttt	ggt	gca	ggt	ttc	ctc	gca	163
Leu	Gln	Ile	Val	Glu	Leu	Gly	Ala	Ile	Phe	Gly	Ala	Gly	Phe	Leu	Ala	
			10					15						20		

gga	agc	atc	aat	gta	att	gtc	gga	gca	gga	aca	tta	gtg	tcg	ttt	cct	211
Gly	Ser	Ile	Asn	Val	Ile	Val	Gly	Ala	Gly	Thr	Leu	Val	Ser	Phe	Pro	
			25					30					35			

Gly Leu Ser Arg Phe Ile Arg Pro Asn Thr Lys Ile Ser Leu Asp Val  
 485 490 495  
 Gly Glu Val Ser Glu Gln Asp Phe Ser Thr Gln Leu Val Ala Pro Ser  
 500 505 510  
 Glu Phe Ala Ala Thr Pro Val Pro Pro Pro Met Ser Ala Gly Ile Val  
 515 520 525  
 Arg Gly Pro Arg Leu Val Pro Gly Ala Pro Val Gly Asp Gly Arg Phe  
 530 535 540  
 Arg Leu Leu Ala Asp His Gly Gly Val Gln Gly Ala Arg Phe Trp Gln  
 545 550 555 560  
 Ala Arg Glu Ile Ala Thr Gly Lys Glu Val Ala Leu Ile Phe Val Asp  
 565 570 575  
 Thr Ser Gly Asn Ala Pro Phe Ala Pro Leu Ser Ser Ala Ala Ala  
 580 585 590  
 Gly Ile Ala Tyr Glu Val Gln Arg Arg Thr Lys Lys Leu Ala Ser Leu  
 595 600 605  
 Gly Ser Leu Ala Val Ala Pro Asn Ile His Ser Glu Ala Tyr Arg Asn  
 610 615 620  
 Gly Cys Leu Ile Val Ala Asp Trp Val Pro Gly Ser Ser Leu Ser Ala  
 625 630 635 640  
 Val Ala Glu Ser Gly Ala Asp Pro Arg Ala Ala Ala Phe Ala Leu Ala  
 645 650 655  
 Glu Leu Thr Glu Thr Ile Gly Glu Ala His Glu Met Gly Ile Pro Ala  
 660 665 670  
 Gly Leu Asp Asn Lys Cys Arg Ile Arg Ile Asn Thr Asp Gly His Ala  
 675 680 685  
 Val Leu Ala Leu Pro Ala Ile Leu Pro Asp Ala Ser Glu Leu Arg Asp  
 690 695 700  
 Ala Lys Ser Leu Ala Ser Ala Ala Glu Met Leu Ile Asp Ala Thr Leu  
 705 710 715 720  
 Ala Pro Ser Asp Val Lys Ala Met Val Thr Glu Ala Gln Gly Leu Ala  
 725 730 735  
 Thr Glu Asp Asn Pro Asp Tyr Ala Ser Leu Ala Met Ala Met Arg Thr  
 740 745 750  
 Cys Gly Leu Phe Thr Glu Glu Pro Thr His Leu Val Val Lys Lys Glu  
 755 760 765  
 Lys Thr Pro Lys Pro Ala Thr Arg Asp Gly Phe Gly Ala Ser Asp Tyr  
 770 775 780  
 Thr Val Lys Gly Met Ala Ala Ile Ala Ala Val Val Ile Ile Leu Val  
 785 790 795 800  
 Ser Leu Val Ala Ala Gly Thr Ala Phe Leu Thr Ser Phe Phe Gly Ser



Pro Tyr Leu Arg Arg Ala Gly Ile Asp Met Arg Pro Leu Trp Gly Ile  
 165 170 175  
 Asp Ala Arg Leu Lys Gln Phe Gly Gly Met Ala Met Ala Ile Ile Val  
 180 185 190  
 Tyr Val Ala Ile Ser Gln Phe Gly Tyr Ile Ile Thr Thr Arg Ile Ala  
 195 200 205  
 Ser Ile Ala Asp Asp Ala Ala Pro Phe Ile Tyr Gln Gln His Trp Met  
 210 215 220  
 Leu Leu Gln Val Pro Tyr Gly Ile Ile Gly Val Thr Leu Leu Thr Ala  
 225 230 235 240  
 Ile Met Pro Arg Leu Ser Arg Asn Ala Ala Asp Gly Asp Asp Arg Ala  
 245 250 255  
 Val Val Ser Asp Leu Gln Leu Gly Ser Lys Leu Thr Phe Ile Ala Leu  
 260 265 270  
 Ile Pro Ile Val Val Phe Phe Thr Ala Phe Gly Val Pro Ile Ala Asn  
 275 280 285  
 Gly Leu Phe Ala Tyr Gly Gln Phe Asp Ala Asn Ala Ala Asn Ile Leu  
 290 295 300  
 Gly Trp Thr Leu Ser Phe Ser Ala Phe Thr Leu Ile Pro Tyr Ala Leu  
 305 310 315 320  
 Val Leu Leu His Leu Arg Val Phe Tyr Ala Arg Glu Glu Val Trp Thr  
 325 330 335  
 Pro Thr Phe Ile Ile Ala Gly Ile Thr Ala Thr Lys Val Val Leu Ser  
 340 345 350  
 Leu Leu Ala Pro Leu Leu Ser Ser Ser Pro Glu Arg Val Val Val Leu  
 355 360 365  
 Leu Gly Ala Ala Asn Gly Phe Ser Phe Ile Thr Gly Ala Val Ile Gly  
 370 375 380  
 Ala Tyr Leu Leu Arg Asn Lys Leu Gly Leu Leu Gly Met Arg Ser Leu  
 385 390 395 400  
 Ala Lys Thr Ser Leu Trp Ala Leu Gly Ser Ala Ala Val Gly Ala Ala  
 405 410 415  
 Ala Ala Trp Ala Leu Gly Trp Leu Ile Gln Ala Val Val Gly Asp Phe  
 420 425 430  
 Leu Leu Gly Thr Leu Ser Ser Val Gly Tyr Leu Leu Asn Leu Ala Val  
 435 440 445  
 Leu Gly Val Phe Phe Ile Phe Val Thr Gly Ile Val Leu Ser Arg Ser  
 450 455 460  
 Gly Leu Pro Glu Val Gln Asn Leu Gly Gln Ala Leu Thr Arg Ile Pro  
 465 470 475 480

tca cca cac tcc ctg tcg gaa ggc atc gag atc ggc acc gtg gat tat  
2899  
Ser Pro His Ser Leu Ser Glu Gly Ile Glu Ile Gly Thr Val Asp Tyr  
920 925 930

tcc ggc cgc agt ctc agc cac agc atc cgc gat tcc tcc aag ctt ccg  
2947  
Ser Gly Arg Ser Leu Ser His Ser Ile Arg Asp Ser Ser Lys Leu Pro  
935 940 945

ggc cag gtg gaa tcc gtg gtg att ctg gtc gat gag gtt cgt tcc tca  
2995  
Gly Gln Val Glu Ser Val Val Ile Leu Val Asp Glu Val Arg Ser Ser  
950 955 960 965

caa acc tca gac acc aat cca cag atg cag atc gct gaa gta caa ctt  
3043  
Gln Thr Ser Asp Thr Asn Pro Gln Met Gln Ile Ala Glu Val Gln Leu  
970 975 980

gtt ggt tgg taaattacgc gtttgtgatt gac  
3075  
Val Gly Trp

<210> 508  
<211> 984  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 508  
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20 25 30  
Leu Thr Leu Ser Val Thr Leu Leu Gly Gly Val Thr Ile Leu Ser Ile  
35 40 45  
Ile Gly Ala Pro Leu Leu Thr Arg Met Met Leu Ser Ser Glu Gly Gln  
50 55 60  
Val Asn Val Val Met Ser Thr Ala Phe Ala Tyr Trp Leu Leu Pro Gln  
65 70 75 80  
Ile Phe Phe Tyr Gly Leu Phe Ala Leu Phe Met Ala Val Leu Asn Thr  
85 90 95  
Arg Glu Val Phe Lys Pro Gly Ala Trp Ala Pro Val Val Asn Asn Val  
100 105 110  
Ile Thr Leu Thr Val Leu Gly Val Tyr Met Val Leu Pro Ala Arg Leu  
115 120 125  
His Pro His Glu Gln Val Gly Ile Phe Asp Pro Gln Ile Ile Phe Leu  
130 135 140  
Gly Val Gly Thr Thr Leu Gly Val Val Ala Gln Cys Leu Ile Met Ile  
145 150 155 160

Pro	Ile	Arg	Lys	Asp	Gly	Leu	Glu	Val	Pro	Glu	Thr	Glu	Ile	Arg	Leu	
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gat	gac	tcg	cca	agc	ggc	ccc	aac	gaa	ccc	ttc	cgc	atc	tac	cgc	acc	355
Asp	Asp	Ser	Pro	Ser	Gly	Pro	Asn	Glu	Pro	Phe	Arg	Ile	Tyr	Arg	Thr	
	70				75				80						85	
cgt	ggc	cca	gaa	acc	aac	ccc	aag	cag	gga	ctt	ccg	cgg	ctg	cgc	gag	403
Arg	Gly	Pro	Glu	Thr	Asn	Pro	Lys	Gln	Gly	Leu	Pro	Arg	Leu	Arg	Glu	
				90					95						100	
tca	tgg	atc	acc	gcc	cgc	ggc	gac	gtt	gcc	acc	tat	cag	ggg	cgc	gag	451
Ser	Trp	Ile	Thr	Ala	Arg	Gly	Asp	Val	Ala	Thr	Tyr	Gln	Gly	Arg	Glu	
			105					110					115			
cgt	ttg	ctt	atc	gac	gac	ggc	cgc	tcg	gca	atg	cgt	cga	ggt	caa	gct	499
Arg	Leu	Leu	Ile	Asp	Asp	Gly	Arg	Ser	Ala	Met	Arg	Arg	Gly	Gln	Ala	
			120				125					130				
tcg	gct	gag	tgg	aaa	ggc	caa	aaa	cca	gct	cct	ttg	aag	gcg	cta	cct	547
Ser	Ala	Glu	Trp	Lys	Gly	Gln	Lys	Pro	Ala	Pro	Leu	Lys	Ala	Leu	Pro	
	135					140					145					
ggc	aaa	aga	gtc	acc	caa	atg	gcc	tat	gca	cgt	gct	ggc	gtg	att	act	595
Gly	Lys	Arg	Val	Thr	Gln	Met	Ala	Tyr	Ala	Arg	Ala	Gly	Val	Ile	Thr	
	150				155				160						165	
cgt	gaa	atg	gag	ttt	gta	gcg	ctg	cgc	gaa	cac	gtt	gat	gcg	gag	ttt	643
Arg	Glu	Met	Glu	Phe	Val	Ala	Leu	Arg	Glu	His	Val	Asp	Ala	Glu	Phe	
				170					175					180		
gtg	cgc	tct	gag	gtg	gcg	cgc	ggc	cgg	gcc	att	att	ccc	aac	aac	gtc	691
Val	Arg	Ser	Glu	Val	Ala	Arg	Gly	Arg	Ala	Ile	Ile	Pro	Asn	Asn	Val	
			185					190					195			
aac	cac	ccc	gaa	tct	gaa	ccg	atg	att	att	ggc	cgc	aaa	ttt	ttg	acc	739
Asn	His	Pro	Glu	Ser	Glu	Pro	Met	Ile	Ile	Gly	Arg	Lys	Phe	Leu	Thr	
		200					205					210				
aaa	atc	aac	gcc	aat	att	ggc	aat	tct	gcg	gtc	acc	tct	tca	atc	gag	787
Lys	Ile	Asn	Ala	Asn	Ile	Gly	Asn	Ser	Ala	Val	Thr	Ser	Ser	Ile	Glu	
	215					220					225					
gaa	gag	gtg	tcc	aag	ctg	cag	tgg	gcc	acg	cgc	tgg	ggc	gcc	gat	acc	835
Glu	Glu	Val	Ser	Lys	Leu	Gln	Trp	Ala	Thr	Arg	Trp	Gly	Ala	Asp	Thr	
	230				235					240					245	
gtg	atg	gat	cta	tcc	acc	ggc	gat	gat	att	cac	acc	acc	cgc	gaa	tgg	883
Val	Met	Asp	Leu	Ser	Thr	Gly	Asp	Asp	Ile	His	Thr	Thr	Arg	Glu	Trp	
				250					255					260		
att	atc	cgc	aac	tcc	ccc	gtt	cct	atc	ggc	acc	gtc	ccg	atc	tac	caa	931
Ile	Ile	Arg	Asn	Ser	Pro	Val	Pro	Ile	Gly	Thr	Val	Pro	Ile	Tyr	Gln	
			265					270					275			
gcg	ctg	gaa	aaa	gta	aat	ggc	gtg	gcc	gca	gac	ctt	aac	tgg	gaa	gta	979
Ala	Leu	Glu	Lys	Val	Asn	Gly	Val	Ala	Ala	Asp	Leu	Asn	Trp	Glu	Val	
		280					285					290				
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					Leu	Lys	Ala	Val	Pro							
					1				5							
acg	ggc	gcc	cga	gca	cgg	gct	gag	atc	gcg	ctg	att	gct	gcg	cga	gca	163
Thr	Gly	Ala	Arg	Ala	Arg	Ala	Glu	Ile	Ala	Leu	Ile	Ala	Ala	Arg	Ala	
				10					15					20		
ccg	ttt	gaa	cct	gtc	cgg	tta	gca	ccg	gcg	aag	gaa	gag	agg	aat	ggg	211
Pro	Phe	Glu	Pro	Val	Arg	Leu	Ala	Pro	Ala	Lys	Glu	Glu	Arg	Asn	Gly	
			25					30					35			
gca	atg	acg	cct	acc	caa	aat	gag	atc	cac	ccg	aaa	cat	agc	tac	tcc	259
Ala	Met	Thr	Pro	Thr	Gln	Asn	Glu	Ile	His	Pro	Lys	His	Ser	Tyr	Ser	
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ccc	atc	cgc	aag	gac	ggg	ctc	gag	gtc	ccg	gag	acc	gaa	atc	cgc	ctc	307

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 Phe Lys Glu Arg Gly  
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 Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro  
 35 40 45  
 Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly  
 50 55 60  
 Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly  
 65 70 75 80  
 His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg  
 85 90 95  
 Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val  
 100 105 110  
 Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe  
 115 120 125  
 Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala  
 130 135 140  
 Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr  
 145 150 155 160  
 His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg  
 165 170 175  
 Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro  
 180 185 190  
 Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys  
 195 200 205  
 Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala  
 210 215 220  
 Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly  
 225 230 235 240  
 Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys  
 245 250 255

Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser  
 185 190 195  
 tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag 739  
 Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys  
 200 205 210  
 cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg 787  
 His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala  
 215 220 225  
 atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca 835  
 Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro  
 230 235 240 245  
 gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc 883  
 Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile  
 250 255 260  
 ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa 931  
 Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys  
 265 270 275  
 ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc 979  
 Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile  
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 acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc  
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 Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile  
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 gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc  
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 Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser  
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 1123  
 Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys  
 330 335 340  
 gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct  
 1171  
 Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala  
 345 350 355  
 cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa  
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 Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu  
 360 365 370  
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 1267  
 Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala  
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 Leu Ala Leu Lys Gly  
 1 5

tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163  
 Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala  
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aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211  
 Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe  
 25 30 35

cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259  
 His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala  
 40 45 50

gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307  
 Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp  
 55 60 65

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 Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg  
 70 75 80 85

tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac 403  
 Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn  
 90 95 100

ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg 451  
 Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val  
 105 110 115

tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc 499  
 Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly  
 120 125 130

gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga 547  
 Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly  
 135 140 145

cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga 595  
 Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly  
 150 155 160 165

tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc 643  
 Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr  
 170 175 180

acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc 691





gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa  
1315

Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu  
390 395 400 405

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1363

Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser Gly Asn Arg Phe His  
410 415 420

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1411

Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu Leu Val Ala Leu Leu  
425 430 435

gac gcg gtg gaa gct gca gcc caa gct gtc gag ctg acc ttc gct ggg  
1459

Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu Leu Thr Phe Ala Gly  
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1491

Ala Leu Phe  
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<213> Corynebacterium glutamicum

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35 40 45

Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly  
50 55 60

Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly  
65 70 75 80

His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg  
85 90 95

Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val  
100 105 110

Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe  
115 120 125

Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala  
130 135 140

Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr

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 Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr  
 170 175 180

acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc 691  
 Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser  
 185 190 195

tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag 739  
 Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys  
 200 205 210

cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg 787  
 His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala  
 215 220 225

atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca 835  
 Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro  
 230 235 240 245

gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc 883  
 Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile  
 250 255 260

ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa 931  
 Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys  
 265 270 275

ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc 979  
 Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile  
 280 285 290

acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc  
 1027  
 Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile  
 295 300 305

gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc  
 1075  
 Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser  
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ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag  
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 Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys  
 330 335 340

gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct  
 1171  
 Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala  
 345 350 355

cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa  
 1219  
 Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu  
 360 365 370

gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca  
 1267  
 Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala  
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Asn Ala Leu  
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Met Leu His Ile Ala
1 5

gat aaa act ttc gat tcc cac ctc atc atg ggc acc ggc gga gcc acc 163
Asp Lys Thr Phe Asp Ser His Leu Ile Met Gly Thr Gly Gly Ala Thr
10 15 20

tct cag gcg ttg ctg gag gaa tcc ctt gtc gcc agt gga act caa ttg 211
Ser Gln Ala Leu Leu Glu Glu Ser Leu Val Ala Ser Gly Thr Gln Leu
25 30 35

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Thr Thr Val Ala Met Arg Arg His Gln Ala Thr Thr Ser Ser Gly Glu
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Thr Ser Ser Gly Glu
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&lt;210&gt; 528

&lt;211&gt; 307

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 528

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          20           25           30
Arg Pro Lys Val Glu Val Ala Ala Glu Arg Leu Lys Glu Leu Gln Pro
          35           40           45
Asp Ile Thr Val Asn Ala Leu His Glu Arg Ile Thr Pro Glu Asn Ala
          50           55           60
Cys Glu Leu Leu Asn Ser Val Asp Leu Val Leu Asp Gly Ser Asp Ser
          65           70           75           80
Phe Ser Thr Lys Tyr Leu Val Ser Asp Ala Ala Glu Ile Thr Gly Thr
          85           90           95
Pro Leu Ile Trp Ala Thr Val Leu Arg Phe His Gly Glu Leu Ala Leu
          100          105          110
Phe Asn Ser Gly Pro Asp His Arg Gly Val Gly Leu Arg Asp Val Phe
          115          120          125
Pro Glu Gln Pro Ser Ala Asp Phe Val Pro Asp Cys Ala Thr Ala Gly
          130          135          140
Val Leu Gly Ala Thr Thr Ala Thr Ile Gly Ala Leu Met Ala Thr His
          145          150          155          160
Ala Ile Gly Phe Leu Thr Glu Ile Gly Asp Val Gln Pro Gly Thr Ile
          165          170          175
Leu Ser Tyr Asp Ala Phe Pro Ala Ala Thr Arg Ser Phe Arg Val Ser
          180          185          190
Ala Asp Pro Ala Arg Pro Leu Val Thr Arg Leu Arg Ala Ser Tyr Glu
          195          200          205
Ala Ala Arg Thr Asp Thr Thr Ser Leu Ile Asp Ala Thr Leu Asn Gly
          210          215          220
Ser Leu Thr Ala Leu Asp Ile Arg Glu Pro His Glu Val Leu Leu Lys
          225          230          235          240
Asp Leu Pro Glu Gly Ala Thr Ser Leu Lys Leu Pro Leu Ser Gln Ile
          245          250          255
Thr Ser Asp Ser Asp Ile Leu Glu Ala Leu Ser Gly Ile Asp Gly Asp
          260          265          270
Ile Leu Val Tyr Cys Ala Ser Gly Ile Arg Ser Ser Asp Phe Ile Asp
          275          280          285

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Phe Ser Thr Lys Tyr Leu Val Ser Asp Ala Ala Glu Ile Thr Gly Thr	85	90	95	
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Pro Leu Ile Trp Ala Thr Val Leu Arg Phe His Gly Glu Leu Ala Leu	100	105	110	
ttc aac tct ggc ccc gac cac cgc gga gtc ggc ctg cgc gac gtc ttc				384
Phe Asn Ser Gly Pro Asp His Arg Gly Val Gly Leu Arg Asp Val Phe	115	120	125	
ccc gaa caa ccc tcc gcc gat ttc gtc cct gac tgc gcc acc gct ggt				432
Pro Glu Gln Pro Ser Ala Asp Phe Val Pro Asp Cys Ala Thr Ala Gly	130	135	140	
gtt ctt ggc gcc acc aca gcc acc atc ggc gca ctc atg gcc act cac				480
Val Leu Gly Ala Thr Thr Ala Thr Ile Gly Ala Leu Met Ala Thr His	145	150	155	160
gcc atc gga ttt ctc aca gaa atc ggc gac gtc caa cca ggc aca atc				528
Ala Ile Gly Phe Leu Thr Glu Ile Gly Asp Val Gln Pro Gly Thr Ile	165	170	175	
ctc tcc tac gac gca ttc ccc gcc gcc acg cgc agc ttc cgc gtc tcc				576
Leu Ser Tyr Asp Ala Phe Pro Ala Ala Thr Arg Ser Phe Arg Val Ser	180	185	190	
gcc gac ccg gcg cgc cca ctg gtc acc cgc ctc cgc gcc tcc tac gag				624
Ala Asp Pro Ala Arg Pro Leu Val Thr Arg Leu Arg Ala Ser Tyr Glu	195	200	205	
gca gcg cgc acc gat aca act tcg ctt atc gac gcc acc ctc aac ggc				672
Ala Ala Arg Thr Asp Thr Thr Ser Leu Ile Asp Ala Thr Leu Asn Gly	210	215	220	
tcc ctc acc gcc ctc gat atc cga gag cca cat gaa gtt ctg ctc aaa				720
Ser Leu Thr Ala Leu Asp Ile Arg Glu Pro His Glu Val Leu Leu Lys	225	230	235	240
gac ctc ccc gag ggc gca acg tca ctg aag ctc ccc tta agc cag atc				768
Asp Leu Pro Glu Gly Ala Thr Ser Leu Lys Leu Pro Leu Ser Gln Ile	245	250	255	
acc tcg gac agc gac att tta gag gca ctg tct gga atc gac ggc gac				816
Thr Ser Asp Ser Asp Ile Leu Glu Ala Leu Ser Gly Ile Asp Gly Asp	260	265	270	
att ttg gtc tac tgc gct tcg gga atc cgc agt tcc gac ttc atc gac				864
Ile Leu Val Tyr Cys Ala Ser Gly Ile Arg Ser Ser Asp Phe Ile Asp	275	280	285	
aac tac tcc cac ctc ggc cac aaa ttt gtg aat ctt ccc ggt ggg gtc				912
Asn Tyr Ser His Leu Gly His Lys Phe Val Asn Leu Pro Gly Gly Val	290	295	300	
aac gcg ctg tagctgtcaa tttaagaggc cag				944
Asn Ala Leu				305

Met Arg Glu Leu Ala Ser Lys Val Ala Leu Glu Val Ala Arg Cys Ser  
 50 55 60

Pro Thr Thr Arg Val Leu Ile Asp Asp His Leu His Val Ala Ser Ser  
 65 70 75 80

Leu Met Arg Glu Gly Leu Pro Ile His Gly Val His Leu Gly Gln Asp  
 85 90 95

Asp Met Ser Val Leu Glu Ala Arg Glu Leu Leu Gly Pro Glu Ala Ile  
 100 105 110

Ile Gly Leu Thr Thr Gly Thr Leu Glu Leu Val Ala Ala Ala Asn Glu  
 115 120 125

Leu Ser Asp Val Leu Asp Tyr Ile Gly Ala Gly Pro Phe Arg Lys Thr  
 130 135 140

Pro Thr Lys Asp Ser Gly Arg Pro Pro Ile Gly Leu Ala Gly Tyr Pro  
 145 150 155 160

Pro Leu Val Glu Leu Ser Lys Val Pro Ile Val Ala Ile Gly Asp Val  
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 <223> RXA01381

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Ile Ser Asn Ile His Arg Gln Ile Leu Phe Gly Ala Ser Asp Val Gly	
20 25 30	
cga ccc aag gtc gag gtt gcc gcc gag cgc ctc aaa gaa ctc caa cca	144
Arg Pro Lys Val Glu Val Ala Ala Glu Arg Leu Lys Glu Leu Gln Pro	
35 40 45	
gac atc acc gtc aac gcg ttg cac gaa cgg atc act cca gaa aac gcc	192
Asp Ile Thr Val Asn Ala Leu His Glu Arg Ile Thr Pro Glu Asn Ala	
50 55 60	
tgc gag ctg ctc aat tcc gtg gac ctc gtc tta gac ggc tcc gat tct	240
Cys Glu Leu Leu Asn Ser Val Asp Leu Val Leu Asp Gly Ser Asp Ser	

25										30										35										
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Gln	Val	Arg	Ser	Lys	Pro	Ile	Ser	Pro	Glu	Ala	Met	Arg	Glu	Leu	Ala															
40					45					50																				
tca	aag	gtt	gcg	ctt	gag	gtt	gcg	cgg	tgc	agc	cca	aca	acg	agg	gtg	307														
Ser	Lys	Val	Ala	Leu	Glu	Val	Ala	Arg	Cys	Ser	Pro	Thr	Thr	Arg	Val															
55					60					65																				
ctt	atc	gac	gac	cac	ctc	cac	gtt	gct	tct	tcc	tta	atg	cgc	gaa	gga	355														
Leu	Ile	Asp	Asp	His	Leu	His	Val	Ala	Ser	Ser	Leu	Met	Arg	Glu	Gly															
70					75					80					85															
ctc	ccg	att	cac	ggg	gtg	cat	ctt	ggg	cag	gat	gat	atg	tcg	gtg	ctt	403														
Leu	Pro	Ile	His	Gly	Val	His	Leu	Gly	Gln	Asp	Asp	Met	Ser	Val	Leu															
90					95					100																				
gag	gct	cgt	gag	ttg	ttg	ggg	cct	gag	gcg	atc	att	ggg	ttg	act	act	451														
Glu	Ala	Arg	Glu	Leu	Leu	Gly	Pro	Glu	Ala	Ile	Ile	Gly	Leu	Thr	Thr															
105					110					115																				
gga	acc	cta	gaa	ctt	gtg	gcg	gcg	gcg	aat	gag	ctg	tcc	gat	gtg	ttg	499														
Gly	Thr	Leu	Glu	Leu	Val	Ala	Ala	Ala	Asn	Glu	Leu	Ser	Asp	Val	Leu															
120					125					130																				
gat	tac	atc	ggg	gct	ggg	ccg	ttt	cgg	aag	act	ccc	acc	aag	gat	tca	547														
Asp	Tyr	Ile	Gly	Ala	Gly	Pro	Phe	Arg	Lys	Thr	Pro	Thr	Lys	Asp	Ser															
135					140					145																				
ggg	cgg	cca	ccg	att	ggc	ctt	gcg	ggg	tat	ccc	cct	ttg	gtg	gaa	ttg	595														
Gly	Arg	Pro	Pro	Ile	Gly	Leu	Ala	Gly	Tyr	Pro	Pro	Leu	Val	Glu	Leu															
150					155					160					165															
tcc	aag	gtg	ccg	atc	gtt	gcg	att	ggg	gat	gtc	acc	cct	gcc	gat	gtg	643														
Ser	Lys	Val	Pro	Ile	Val	Ala	Ile	Gly	Asp	Val	Thr	Pro	Ala	Asp	Val															
170					175					180																				
cgc	gct	ctc	agc	gca	acc	ggg	gtg	gct	ggc	gtt	gcc	atg	gtg	cgg	gct	691														
Arg	Ala	Leu	Ser	Ala	Thr	Gly	Val	Ala	Gly	Val	Ala	Met	Val	Arg	Ala															
185					190					195																				
ttt	tct	gaa	tct	gat											706															
Phe	Ser	Glu	Ser	Asp																										
200																														

&lt;210&gt; 526

&lt;211&gt; 202

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 526

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Gly	Ser	Val	Asp	Glu	Val	Val	His	Thr	Ala	Ser	Ala	Ala	Ala	Arg	Gly
20					25					30					

Gly	Ala	Gly	Val	Val	Gln	Val	Arg	Ser	Lys	Pro	Ile	Ser	Pro	Glu	Ala
35					40					45					

Val Ile Ala Val Thr Ala Ile Gly Gln Leu Gly Gly Ser Leu Pro Glu  
 145 150 155 160  
 Leu Thr Leu Gly Arg Ala Arg Pro Gly Gln Thr Leu Val Ala His Gly  
 165 170 175  
 Lys Ile Gly Tyr Ser Ala Ala Gly Leu Ala Leu Leu Gln His Phe Gly  
 180 185 190  
 Pro Asp Asn Val Pro Glu His Leu Arg Pro Leu Val Asp Ala His Cys  
 195 200 205  
 Ala Pro Val Leu Thr Pro Gly Arg Gly Met Val Ala Arg Ala Ala Gly  
 210 215 220  
 Ala Thr Ala Met Thr Asp Asn Ser Asp Gly Leu Ile Val Asp Leu Asn  
 225 230 235 240  
 Gln Met Ala Met Lys Ser Gly Val Arg Ile Asp Val Asp Ser Cys Ser  
 245 250 255  
 Ile Ser Pro Asp Glu Leu Leu Ser Glu Ala Ala Ser Val Leu Gly Thr  
 260 265 270  
 Asp Ala Trp Arg Trp Ile Leu Ser Gly Gly Glu Asp His Thr Leu Leu  
 275 280 285  
 Ser Thr Thr Phe Gly Asp Ala Pro Ser Gly Phe Arg Thr Ile Gly Gln  
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 Pro Ala Phe Ser Asp Gly Trp Arg Ser Phe  
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 Val Phe Glu Asn Arg  
 1 5  
 ttt gac ctg cgt tgt tat gtt gtg act ggt gcg ggc tcg gtg gat gag 163  
 Phe Asp Leu Arg Cys Tyr Val Val Thr Gly Ala Gly Ser Val Asp Glu  
 10 15 20  
 gtt gtg cac act gcg tct gct gcg gct cgt ggt ggc gcg ggt gtg gtg 211  
 Val Val His Thr Ala Ser Ala Ala Ala Arg Gly Gly Ala Gly Val Val



caa atg gcc atg aag tct ggt gtg cgc atc gat gtg gat tcc tgt agc 768  
 Gln Met Ala Met Lys Ser Gly Val Arg Ile Asp Val Asp Ser Cys Ser  
 245 250 255

atc agc ccc gat gaa ctc ctt agc gaa gcc gct tcc gta ctc gga aca 816  
 Ile Ser Pro Asp Glu Leu Leu Ser Glu Ala Ala Ser Val Leu Gly Thr  
 260 265 270

gac gcc tgg cga tgg atc tta agc ggc ggg gaa gac cac acc ctg ctc 864  
 Asp Ala Trp Arg Trp Ile Leu Ser Gly Gly Glu Asp His Thr Leu Leu  
 275 280 285

tct acg acg ttt ggc gat gcc ccc tct gga ttc cgc acc atc ggc caa 912  
 Ser Thr Thr Phe Gly Asp Ala Pro Ser Gly Phe Arg Thr Ile Gly Gln  
 290 295 300

gtc acc aaa aca cgc cac gaa gac ctc gtc acc gta gat aag aaa acc 960  
 Val Thr Lys Thr Arg His Glu Asp Leu Val Thr Val Asp Lys Lys Thr  
 305 310 315 320

ccc gca ttt tcc gat gga tgg aga agc ttc taatgaccaa caccctatgg  
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 Pro Ala Phe Ser Asp Gly Trp Arg Ser Phe  
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aat  
 1013

<210> 524

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<212> PRT

<213> Corynebacterium glutamicum

<400> 524

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Gln Ala Gly Ser Ser Leu Asn Gly Asp Asp Ala Ala Val Leu Arg His  
 35 40 45

Ala Ser Pro Asn Ser Arg Ala Val Val Thr Thr Asp Met Leu Val Ala  
 50 55 60

Gly Arg His Phe Gln Leu Asp Trp Ser Thr Pro Glu Gln Ile Gly Gln  
 65 70 75 80

Lys Ala Ile Val Gln Asn Phe Ala Asp Ile Glu Ala Met Gly Ala Arg  
 85 90 95

Pro Val Ala Ala Leu Leu Ala Ile Ser Ala Pro Thr His Thr Pro Val  
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Glu Phe Val Arg Gly Leu Ala Arg Gly Met Asn Gln Arg Leu Glu Glu  
 115 120 125

Tyr Ser Ala Glu Leu Val Gly Gly Asp Ile Thr Ser Gly Asp Ser Leu  
 130 135 140

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 Thr Leu Ala His Ser Leu Ser Phe Pro Asp Ser Leu Arg Asp Gly Pro  
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 Thr Val Gly Asp Leu Gly Glu Phe Glu Val Ile Arg Val Ile Thr Glu  
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 Gln Ala Gly Ser Ser Leu Asn Gly Asp Asp Ala Ala Val Leu Arg His  
 35 40 45  
 gca tca ccc aat tcc agg gct gtt gtc acc acc gac atg ttg gtt gcg 192  
 Ala Ser Pro Asn Ser Arg Ala Val Val Thr Thr Asp Met Leu Val Ala  
 50 55 60  
 ggt agg cat ttc caa ttg gat tgg tcc acc ccg gaa caa ata ggg cag 240  
 Gly Arg His Phe Gln Leu Asp Trp Ser Thr Pro Glu Gln Ile Gly Gln  
 65 70 75 80  
 aag gcg att gtg cag aac ttt gct gat att gag gcg atg ggt gca cgt 288  
 Lys Ala Ile Val Gln Asn Phe Ala Asp Ile Glu Ala Met Gly Ala Arg  
 85 90 95  
 cca gta gcc gca ttg ttg gcg att tcc gcc ccc aca cac acc ccc gtg 336  
 Pro Val Ala Ala Leu Leu Ala Ile Ser Ala Pro Thr His Thr Pro Val  
 100 105 110  
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 Glu Phe Val Arg Gly Leu Ala Arg Gly Met Asn Gln Arg Leu Glu Glu  
 115 120 125  
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 Tyr Ser Ala Glu Leu Val Gly Gly Asp Ile Thr Ser Gly Asp Ser Leu  
 130 135 140  
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 Val Ile Ala Val Thr Ala Ile Gly Gln Leu Gly Gly Ser Leu Pro Glu  
 145 150 155 160  
 ctg acg ttg gga cgt gcc cga cca gga cag acc ctg gtg gcc cac gga 528  
 Leu Thr Leu Gly Arg Ala Arg Pro Gly Gln Thr Leu Val Ala His Gly  
 165 170 175  
 aag atc ggt tac tcc gca gca ggc ctt gct cta ctg cag cac ttt ggt 576  
 Lys Ile Gly Tyr Ser Ala Ala Gly Leu Ala Leu Leu Gln His Phe Gly  
 180 185 190  
 cca gac aac gtt cca gag cac ctt cgc ccc ttg gtg gat gca cac tgc 624  
 Pro Asp Asn Val Pro Glu His Leu Arg Pro Leu Val Asp Ala His Cys  
 195 200 205  
 gca cca gtt ctc acc cca ggc cga ggc atg gtg gca cgc gct gct gga 672  
 Ala Pro Val Leu Thr Pro Gly Arg Gly Met Val Ala Arg Ala Ala Gly  
 210 215 220  
 gcg acc gcc atg act gat aac tcg gac gga ctg att gtg gat ctt aac 720  
 Ala Thr Ala Met Thr Asp Asn Ser Asp Gly Leu Ile Val Asp Leu Asn  
 225 230 235 240

370	375	380
Asp Ala Ala Gln Phe Ala Glu Leu Lys Thr Ile Gly Glu Leu Thr Gln 385 390 395 400		
Arg Ala Trp Glu Tyr Asp Val Gln Val Met Val Glu Gly Pro Gly His 405 410 415		
Val Pro Leu Asn Met Ile Gln Glu Asn Asn Glu Leu Glu Gln Lys Trp 420 425 430		
Ala Ala Asp Ala Pro Phe Tyr Thr Leu Gly Pro Leu Val Thr Asp Ile 435 440 445		
Ala Pro Gly Tyr Asp His Ile Thr Ser Ala Ile Gly Ala Ala His Ile 450 455 460		
Ala Met Gly Gly Thr Ala Met Leu Cys Tyr Val Thr Pro Lys Glu His 465 470 475 480		
Leu Gly Leu Pro Asn Arg Asp Asp Val Lys Thr Gly Val Ile Thr Tyr 485 490 495		
Lys Leu Ala Ala His Ala Ala Asp Val Ala Lys Gly His Pro Gly Ala 500 505 510		
Arg Ala Trp Asp Asp Ala Met Ser Lys Ala Arg Phe Glu Phe Arg Trp 515 520 525		
Asn Asp Gln Phe Ala Leu Ser Leu Asp Pro Asp Thr Ala Ile Ala Tyr 530 535 540		
His Asp Glu Thr Leu Pro Ala Glu Pro Ala Lys Thr Ala His Phe Cys 545 550 555 560		
Ser Met Cys Gly Pro Lys Phe Cys Ser Met Arg Ile Ser Gln Asp Ile 565 570 575		
Arg Asp Met Phe Gly Asp Gln Ile Ala Glu Leu Gly Met Pro Gly Val 580 585 590		
Gly Asp Ser Ser Ser Ala Val Ala Ser Ser Gly Ala Arg Glu Gly Met 595 600 605		
Ala Glu Lys Ser Arg Glu Phe Ile Ala Gly Gly Ala Glu Val Tyr Arg 610 615 620		
Arg 625		

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 Arg Ile Tyr Arg Thr Arg Gly Pro Glu Thr Asn Pro Lys Gln Gly Leu  
 85 90 95  
 Pro Arg Leu Arg Glu Ser Trp Ile Thr Ala Arg Gly Asp Val Ala Thr  
 100 105 110  
 Tyr Gln Gly Arg Glu Arg Leu Leu Ile Asp Asp Gly Arg Ser Ala Met  
 115 120 125  
 Arg Arg Gly Gln Ala Ser Ala Glu Trp Lys Gly Gln Lys Pro Ala Pro  
 130 135 140  
 Leu Lys Ala Leu Pro Gly Lys Arg Val Thr Gln Met Ala Tyr Ala Arg  
 145 150 155 160  
 Ala Gly Val Ile Thr Arg Glu Met Glu Phe Val Ala Leu Arg Glu His  
 165 170 175  
 Val Asp Ala Glu Phe Val Arg Ser Glu Val Ala Arg Gly Arg Ala Ile  
 180 185 190  
 Ile Pro Asn Asn Val Asn His Pro Glu Ser Glu Pro Met Ile Ile Gly  
 195 200 205  
 Arg Lys Phe Leu Thr Lys Ile Asn Ala Asn Ile Gly Asn Ser Ala Val  
 210 215 220  
 Thr Ser Ser Ile Glu Glu Glu Val Ser Lys Leu Gln Trp Ala Thr Arg  
 225 230 235 240  
 Trp Gly Ala Asp Thr Val Met Asp Leu Ser Thr Gly Asp Asp Ile His  
 245 250 255  
 Thr Thr Arg Glu Trp Ile Ile Arg Asn Ser Pro Val Pro Ile Gly Thr  
 260 265 270  
 Val Pro Ile Tyr Gln Ala Leu Glu Lys Val Asn Gly Val Ala Ala Asp  
 275 280 285  
 Leu Asn Trp Glu Val Phe Arg Asp Thr Ile Ile Glu Gln Cys Glu Gln  
 290 295 300  
 Gly Val Asp Tyr Met Thr Ile His Ala Gly Val Leu Leu Ala Tyr Ile  
 305 310 315 320  
 Pro Leu Thr Thr Arg Arg Val Thr Gly Ile Val Ser Arg Gly Gly Ser  
 325 330 335  
 Ile Met Ala Gly Trp Cys Leu Ala His His Arg Glu Ser Phe Leu Tyr  
 340 345 350  
 Glu His Phe Asp Glu Leu Cys Glu Ile Phe Ala Gln Tyr Asp Val Ala  
 355 360 365  
 Phe Ser Leu Gly Asp Gly Leu Arg Pro Gly Ser Leu Ala Asp Ala Asn



Phe Arg Asp Thr Ile Ile Glu Gln Cys Glu Gln Gly Val Asp Tyr Met  
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 1075  
 Thr Ile His Ala Gly Val Leu Leu Ala Tyr Ile Pro Leu Thr Thr Arg  
 310 315 320 325  
 cgt gtc acc ggc att gtc tcc cgc ggc gga tcc att atg gcc ggt tgg  
 1123  
 Arg Val Thr Gly Ile Val Ser Arg Gly Gly Ser Ile Met Ala Gly Trp  
 330 335 340  
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 1171  
 Cys Leu Ala His His Arg Glu Ser Phe Leu Tyr Glu His Phe Asp Glu  
 345 350 355  
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 1219  
 Leu Cys Glu Ile Phe Ala Gln Tyr Asp Val Ala Phe Ser Leu Gly Asp  
 360 365 370  
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 1267  
 Gly Leu Arg Pro Gly Ser Leu Ala Asp Ala Asn Asp Ala Ala Gln Phe  
 375 380 385  
 gcc gag ctg aaa acc att ggt gag ctc acc caa cgc gcc tgg gaa tac  
 1315  
 Ala Glu Leu Lys Thr Ile Gly Glu Leu Thr Gln Arg Ala Trp Glu Tyr  
 390 395 400 405  
 gat gta caa gta atg gtc gaa gga cct gga cac gtg cca cta aac atg  
 1363  
 Asp Val Gln Val Met Val Glu Gly Pro Gly His Val Pro Leu Asn Met  
 410 415 420  
 atc cag gaa aac aac gag ctg gaa caa aag tgg gca gcg gac gca cct  
 1411  
 Ile Gln Glu Asn Asn Glu Leu Glu Gln Lys Trp Ala Ala Asp Ala Pro  
 425 430 435  
 ttt tac act ctt gga cca cta gtt acc gac atc gct cca ggt tat gac  
 1459  
 Phe Tyr Thr Leu Gly Pro Leu Val Thr Asp Ile Ala Pro Gly Tyr Asp  
 440 445 450  
 cac atc act tct gcc att ggt gca gct cac atc gcc atg ggt ggc acc  
 1507  
 His Ile Thr Ser Ala Ile Gly Ala Ala His Ile Ala Met Gly Gly Thr  
 455 460 465  
 gcc atg ctg tgt tat gtc acc ccg aaa gaa cac ctt ggc ctg ccc aac  
 1555  
 Ala Met Leu Cys Tyr Val Thr Pro Lys Glu His Leu Gly Leu Pro Asn  
 470 475 480 485  
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<212> PRT

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<400> 542

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Val Asp Ser Ala Ile Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp  
35 40 45

Lys Asn Ser Gly Val Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys  
50 55 60

Glu Leu Cys Asp Ala Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu  
65 70 75 80

Asp Ile Ala Val Glu Leu Gly Leu His Leu His Ile Gly Gln Gly Asp  
85 90 95

Thr Pro Tyr Thr Gln Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu  
100 105 110

Gly Leu Ser Ile Glu Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln  
115 120 125

Cys Ala Glu Thr Gly Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro  
130 135 140

Val Ala Ser Thr Ala Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val  
145 150 155 160

Glu Gly Ile Ala Glu Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala  
165 170 175

Ser Val Ala Ile Gly Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala  
180 185 190

Ala Thr Pro Ile Asp Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala  
195 200 205

Ala Asn Pro Ala Ala Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro  
210 215 220

Thr Phe Ser Pro Glu Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln  
225 230 235 240

Gly Ala Phe Val Asn Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala  
245 250 255

Gly Thr Asp Pro Thr Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser  
260 265 270

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 Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val Ala Gln Asn Thr His  
 280 285 290

ggc gtc aac acg atc cac acc cca ccc ttg acc ttt ttg gaa gaa cag  
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 Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr Phe Leu Glu Glu Gln  
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ctg gaa gcg gtc ttt tcc gat gtc acc gtc gat gcc atc aag ctc ggc  
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 Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp Ala Ile Lys Leu Gly  
 310 315 320 325

atg ttg ggc tct gcc gac acc gtc gat ctg gtg gct tca tgg ctt ggt  
 1123  
 Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val Ala Ser Trp Leu Gly  
 330 335 340

tcc cac gag cac ggt ccc gtg gtg ctt gat ccc gtc atg atc gcc acc  
 1171  
 Ser His Glu His Gly Pro Val Val Leu Asp Pro Val Met Ile Ala Thr  
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 1219  
 Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu Glu Ser Leu Arg Arg  
 360 365 370

ctg gcc gtg cac gtc gat gtg gtc acc ccg aat atc ccc gaa ctt gcc  
 1267  
 Leu Ala Val His Val Asp Val Val Thr Pro Asn Ile Pro Glu Leu Ala  
 375 380 385

gtg ttg tgc gac agt gct cct gcc atc acc atg gat gag gcc att gct  
 1315  
 Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met Asp Glu Ala Ile Ala  
 390 395 400 405

cag gct cag gga ttt gcg cgg act cat gac acc atc gtc att gtc aag  
 1363  
 Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr Ile Val Ile Val Lys  
 410 415 420

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 1411  
 Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn Ala Val Val Arg Pro  
 425 430 435

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 440 445 450

tcc cat ggc aca ggc tgt tcg ctc tct gcg tca ctt gcc acc aag atc  
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 Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser Leu Ala Thr Lys Ile  
 455 460 465

gcc gcc ggc gaa agc gtg gaa  
 1528



tcc ggc gga gtt tct gtg gtg cag ctg cgc gat aag aac tca ggc gtg	259
Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp Lys Asn Ser Gly Val	
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gaa gat gtt cgt gcg gca gca aag gag ctg aaa gaa ctc tgc gat gct	307
Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala	
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cgc ggg gtg gcg ctt gtt gtc aac gat tac tta gat atc gcc gtt gag	355
Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu Asp Ile Ala Val Glu	
70 75 80 85	
ctg ggt ctt cac ctg cac att ggt caa ggc gat aca cct tat acg caa	403
Leu Gly Leu His Leu His Ile Gly Gln Gly Asp Thr Pro Tyr Thr Gln	
90 95 100	
gca cgg gag ctg ctt cca gct cat ctt gaa ttg ggt ttg agc att gaa	451
Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu Gly Leu Ser Ile Glu	
105 110 115	
aac ctg gat caa ttg cat gct gtg atc gcg cag tgc gcc gag act ggt	499
Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln Cys Ala Glu Thr Gly	
120 125 130	
gtg gca ttg ccc gat gtg att ggc att ggt ccg gtg gcc tct act gcg	547
Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro Val Ala Ser Thr Ala	
135 140 145	
acc aaa cca gat gcg gca ccc gca ttg ggt gtg gag ggc atc gct gag	595
Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val Glu Gly Ile Ala Glu	
150 155 160 165	
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Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala Ser Val Ala Ile Gly	
170 175 180	
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Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala Ala Thr Pro Ile Asp	
185 190 195	
ggt ctg tgc gtg gtc tct gaa atc atg acc gcc gcc aat cca gca gct	739
Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala Ala Asn Pro Ala Ala	
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gcg gca act cgc ctg cgg act gct ttt caa cct act ttc tcg cct gaa	787
Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro Thr Phe Ser Pro Glu	
215 220 225	
act caa act gaa ctc tct caa aca gaa ctc caa gga gcc ttc gtg aat	835
Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln Gly Ala Phe Val Asn	
230 235 240 245	
tcg cct tct gcc cca cgt gtg ttg tct att gca ggc act gat ccc aca	883
Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala Gly Thr Asp Pro Thr	
250 255 260	
ggt ggt gca ggt att cag gct gat ctg aag tcc att gca gca ggt ggc	931
Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser Ile Ala Ala Gly Gly	
265 270 275	

Ala Gln Asn Thr His Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr  
 290 295 300  
 Phe Leu Glu Glu Gln Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp  
 305 310 315 320  
 Ala Ile Lys Leu Gly Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val  
 325 330 335  
 Ala Ser Trp Leu Gly Ser His Glu His Gly Pro Val Val Leu Asp Pro  
 340 345 350  
 Val Met Ile Ala Thr Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu  
 355 360 365  
 Glu Ser Leu Arg Arg Leu Ala Val His Val Asp Val Val Thr Pro Asn  
 370 375 380  
 Ile Pro Glu Leu Ala Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met  
 385 390 395 400  
 Asp Glu Ala Ile Ala Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr  
 405 410 415  
 Ile Val Ile Val Lys Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn  
 420 425 430  
 Ala Val Val Arg Pro Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg  
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 Met Cys Glu Arg Pro  
 1 5  
 gaa aag tac gtg act gat ttt tct ttg tat ctg gtc acc gat ccc gtt 163  
 Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu Val Thr Asp Pro Val  
 10 15 20  
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 Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile Val Asp Ser Ala Ile  
 25 30 35

&lt;210&gt; 540

&lt;211&gt; 476

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 540

Met Cys Glu Arg Pro Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu  
 1 5 10 15

Val Thr Asp Pro Val Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile  
 20 25 30

Val Asp Ser Ala Ile Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp  
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Lys Asn Ser Gly Val Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys  
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Glu Leu Cys Asp Ala Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu  
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Asp Ile Ala Val Glu Leu Gly Leu His Leu His Ile Gly Gln Gly Asp  
 85 90 95

Thr Pro Tyr Thr Gln Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu  
 100 105 110

Gly Leu Ser Ile Glu Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln  
 115 120 125

Cys Ala Glu Thr Gly Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro  
 130 135 140

Val Ala Ser Thr Ala Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val  
 145 150 155 160

Glu Gly Ile Ala Glu Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala  
 165 170 175

Ser Val Ala Ile Gly Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala  
 180 185 190

Ala Thr Pro Ile Asp Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala  
 195 200 205

Ala Asn Pro Ala Ala Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro  
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Thr Phe Ser Pro Glu Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln  
 225 230 235 240

Gly Ala Phe Val Asn Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala  
 245 250 255

Gly Thr Asp Pro Thr Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser  
 260 265 270

Ile Ala Ala Gly Gly Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val  
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ggc gtc aac acg atc cac acc cca ccc ttg acc ttt ttg gaa gaa cag  
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 Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr Phe Leu Glu Glu Gln  
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 1075  
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 1123  
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 Ser His Glu His Gly Pro Val Val Leu Asp Pro Val Met Ile Ala Thr  
 345 350 355  
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 1219  
 Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu Glu Ser Leu Arg Arg  
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 1267  
 Leu Ala Val His Val Asp Val Val Thr Pro Asn Ile Pro Glu Leu Ala  
 375 380 385  
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 1315  
 Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met Asp Glu Ala Ile Ala  
 390 395 400 405  
 cag gct cag gga ttt gcg cgg act cat gac acc atc gtc att gtc aag  
 1363  
 Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr Ile Val Ile Val Lys  
 410 415 420  
 ggt gga cat ctg act ggc gcg ctt gct gat aac gct gtc gtg cgc ccc  
 1411  
 Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn Ala Val Val Arg Pro  
 425 430 435  
 gac ggc tcg gtg ttc cag gtg gaa aac ctg cgt gtc aac acc acc aac  
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 Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg Val Asn Thr Thr Asn  
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 tcc cat ggc aca ggc tgt tcg ctc tct gcg tca ctt gcc acc aag atc  
 1507  
 Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser Leu Ala Thr Lys Ile  
 455 460 465  
 gcc gcc ggc gaa agc gtg gaa  
 1528  
 Ala Ala Gly Glu Ser Val Glu  
 470 475

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cgc ggg gtg gcg ctt gtt gtc aac gat tac tta gat atc gcc gtt gag Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu Asp Ile Ala Val Glu 70 75 80 85			355
ctg ggt ctt cac ctg cac att ggt caa ggc gat aca cct tat acg caa Leu Gly Leu His Leu His Ile Gly Gln Gly Asp Thr Pro Tyr Thr Gln 90 95 100			403
gca cgg gag ctg ctt cca gct cat ctt gaa ttg ggt ttg agc att gaa Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu Gly Leu Ser Ile Glu 105 110 115			451
aac ctg gat caa ttg cat gct gtg atc gcg cag tgc gcc gag act ggt Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln Cys Ala Glu Thr Gly 120 125 130			499
gtg gca ttg ccc gat gtg att ggc att ggt ccg gtg gcc tct act gcg Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro Val Ala Ser Thr Ala 135 140 145			547
acc aaa cca gat gcg gca ccc gca ttg ggt gtg gag ggc atc gct gag Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val Glu Gly Ile Ala Glu 150 155 160 165			595
atc gcc gct gta gct caa gac cac ggc atc gca tca gta gct att gga Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala Ser Val Ala Ile Gly 170 175 180			643
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ggt ctg tgc gtg gtc tct gaa atc atg acc gcc gcc aat cca gca gct Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala Ala Asn Pro Ala Ala 200 205 210			739
gcg gca act cgc ctg cgg act gct ttt caa cct act ttc tcg cct gaa Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro Thr Phe Ser Pro Glu 215 220 225			787
act caa act gaa ctc tct caa aca gaa ctc caa gga gcc ttc gtg aat Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln Gly Ala Phe Val Asn 230 235 240 245			835
tcg cct tct gcc cca cgt gtg ttg tct att gca ggc act gat ccc aca Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala Gly Thr Asp Pro Thr 250 255 260			883
ggt ggt gca ggt att cag gct gat ctg aag tcc att gca gca ggt ggc Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser Ile Ala Ala Gly Gly 265 270 275			931
ggc tac ggc atg tgc gtt gtg acc tcg ctg gtc gcg caa aac acc cac Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val Ala Gln Asn Thr His 280 285 290			979

Ser Ala Ala Leu Val Ala Cys Ser Pro Pro His Gln Gln Asp Ser Pro  
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 Val Gln Arg Thr Asn Glu Ile Leu Thr Thr Ser Gln Asn Pro Thr Ser  
                   35                                  40                                  45  
 Ala Ser Ser Thr Ser Thr Ser Ser Ala Thr Thr Thr Ser Ser Ala Pro  
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 Val Glu Glu Asp Val Glu Ile Val Val Ser Pro Ala Ala Leu Val Asp  
                   65                                  70                                  75                                  80  
 Gly Glu Gln Val Thr Phe Glu Ile Ser Gly Leu Asp Pro Glu Gly Gly  
                                   85                                  90                                  95  
 Tyr Tyr Ala Ala Ile Cys Asp Ser Val Ala Asn Pro Gly Asn Pro Val  
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 Pro Ser Cys Thr Gly Glu Met Ala Asp Phe Thr Ser Gln Ala Trp Leu  
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 Ala Thr Val Glu Leu Glu Ala Thr Ala Thr Gly Thr Gly Leu Asp Cys  
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 Thr Thr Gln Ala Cys Val Ala Lys Val Phe Gly Asp His Thr Glu Gly  
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 Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu Val Thr Asp Pro Val  
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 ttg ggt ggc ggg cca aaa aaa gta gct gga att gtt gac agc gca att 211  
 Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile Val Asp Ser Ala Ile  
                                   25                                  30                                  35  
 tcc ggc gga gtt tct gtg gtg cag ctg cgc gat aag aac tca ggc gtg 259  
 Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp Lys Asn Ser Gly Val